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ORGANISM Homo sapiens Enkaryota, Metazoa; Chordata; Craniata; Euteleostomi,  REPERENCE 1 (bases 1 to 29)  AUTHORS Salai.C., Toth, S. and Falus, A.  TITLE Exon-intron organization of the human gpl30 gene JOURNAL Gene 243 (1-2), 161-166 (2000)  MEDLINE 20156380  1055638  1056380  AUTHORS Salai.C.  TITLE Exon-intron organization of the human gpl30 gene JOURNAL Coloses 1 to 29)  AUTHORS Salai.C.  TITLE Direct Submissor POBOX 66, H-1958 Hungary  COMMENT Related 627-APR-1999) Szalai C., Heim Pal Pediatric Hospital  Budapest, Budapest POBOX 66, H-1958 Hungary  COMMENT Related sequence M57230.  FATURE Submitted (27-APR-1999) Szalai C., Heim Pal Pediatric Hospital  JOURNAL LOCATION/Qualifiers  SOURCE / Cramosome = "Fayon"  AD 1. 29  JOURNAL AD 29130"  JOHNAL AD 29130	2 3 al	ORGANISM Unknown.  Unclassified.  REFERENCE 1 (bases 1 to 24)  AUTHORS Chetverin,A.B. and Kramer,F.R.  TITLE Oligonuclectide arrays and their use for sorting, isolating, sequencing, and manipulating nucleic acids  JOURNAL Patent: US 6322971.A 6 27-NOV-2001;  FRATURES Location/Qualifiers  1. 24   /organism="unknown"    /mol_type="genomic DNA"  Query Match  Query Match  1.3%; Score 22.4; DB 1; Length 24; Best Local Similarity 95.8%; Pred. NO. 71; Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Oy 1731 TTTACAARAAAAAAAAAAAA 1754
ACCESSION: AX688602 ACCESSION: AX688694 ACCESSION: AX688140 ACCESSION: AX688140 ACCESSION: AX688141 ACCESSION: AX690555 ACCESSION: AX690555 ACCESSION: AX691282 ACCESSION: AX691282 ACCESSION: AX691283 ACCESSION: AX692610 ACCESSION: AX723728 ACCESSION: AX723729 ACCESSION: AX724111 ACCESSION: AX724111 ACCESSION: AX724111 ACCESSION: AX725448 ACCESSION: AX725967 ACCESSION: AX726840 ACCESSION: AX726840 ACCESSION: AX730114 ACCESSION: AX730114 ACCESSION: AX731099	ACCESSION: AXX 158 79 ACCESSION: AXX 158 79 ACCESSION: AXX 172 93 ACCESSION: AXX 174 45 ACCESSION: AXX 174 45 ACCESSION: AXX 174 20 ACCESSION: AXX 174 201 ACCESSION: AXX 174 201 ACCESSION: AXX 174 504 ACCESSION: AXX 178 1891 ACCESSION: AXX 1899 ACCESSION: AXX 1899 ACCESSION: AXX 1899 ACCESSION: AXX 184 080	· · · · · · · · · · · · · · · · · · ·	DNA linear PRI 24-FEB-2000 intron 14 splice acceptor site.
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BD248974.1 GI:33058744
JP 2002537839-A/35.
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BD248974/c
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AR174581/c
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ORGANISM
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JP 2001509271-A/1.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Eparatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosida II; Brassicales, Brassicaceae, Arabidopsis.
1 (bases 1 to 25)
                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

I (Dases I to 24)
Cohen, D., Blumefeld, M., Chumakov, I. and Bougueleret, L.
Prostatic cancer gene
Patent: JP 2002516657-A 8 11-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sets of labeled energy transfer fluorescent primers and their use in multi component analysis Patent: 19 2001509271-A 1 10-JUL-2001; INCYTE PHARMACEUTICALS INC PN JP 2001509271-A/1
PD 10-JUL-2001
                                                                                                                                                                                                                                                                 PR 22-DEC-1997 US 08/996306,09-SEP-1998 US 60/099658 PI DANIEL COHEN,MARTA BLUMENFELD,ILYA CHUMAKOV,LYDIE BOUGUELERET PC C12N15/09,C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N1/15, PC C12N1/19,
                                                                                                                                                                                                                                                                                                                        PC (12/1/21,C12N5/10,C12N5/10,C12P21/08,C12Q1/68,G01N33/50 PC (12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N15/00 CC primer oligonucleotide PGRT32 C primer oligonucleotide FF Key Location/Qualifiers FF T misc binding 1 24
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GOIN21/78,C12N15/09,C12Q1/68,C12N15/00
Strandedness: Single;
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15-JAN-1997 US 08/784162
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22-DEC-1997 US 08/99630
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                               BD196419.1 GI:33006189
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   Prostatic cancer gene.
BD196419
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Best Local Similarity 95.7%;
Matches 22; Conservative
                                               JP 2002516657-A/8.
Homo sapiens (human)
Homo sapiens
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CO7K14/54,CO7K14/55,CO7K16/24,CO7K19/00,C12N1/15,C12N1/19, PC
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Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
Hammond,A.K.
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synthetic construct
artificial sequences.
1 (bases 1 to 26)
Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
Hammond,A.K.
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                                                                                                             Gaps
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PR 09-MAR-1999 US 09/264908,11-MAR-1999 US
01-JUL-1999 US 60/142013
PI JULIA R MANAN A.
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Patent: JP 200237839-A 35 12-NOV-2002;
ZYMOGENETICS INC
OS Artificial Sequence
                                                                                                                                                                                                                                                                                                                    DNA
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Patent: US 6307024-A 38 23-OCT-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                    26 bp | Sequence 38 from patent US 6307024.
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Novel cytokine ZALPHAll ligand.
BD248974
/mol_type="genomic DNA"
/db_xref="taxon:3702"
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12-NOV-2002
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AR374073.1 GI:40076645
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AX106717/c
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C12N5/10, C12P21/02, C12P21/02, G01N33/53, C12N15/00, C12N5/00, PC
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                                                               /organism='Artificial Sequence'
Location/Qualifiers
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Molecular indexing for expressed gene analysis
Patent: US 5707807-A 1 13-JAN-1998;
Location/Qualifiers
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95.7%; Pred. No. 1.1e+02;
tive 0; Mismatches 1;
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                          Oligonucleotide primer ZC7764a
Key Location/Qualifiers

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|mol type="genomic DNA"
|db_xref="taxon:32630"

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Unknown.
Unclassified.
3 1 (bases 1 to 26)
S Adler, D.A. and Sheppard, P.O.
Secreted salivary ZSIG63 Polypeptide
AL Patent: US 6331413-A 7 18-DEC-2001;
Location/Qualifiers
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Sequence 1 from patent US 5707807.
I79494.1 GI:3207784
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Sequence 7 from patent US 6331413.
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AR263648.1 GI:28075581
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Best Local Similarity 95.74
Matches 22, Conservative
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AR263648/c
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Vovak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
Hammond,A.K.
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                                                                                                                                                                                                                                 Methods of using zalphall ligand
Patent: US 6605272-A 38 12-AUG-2003;
Location/Qualifiers
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Patent: WO 0125444-A 9 12-APR-2001;
ZymoGenetics, Inc. (US)
Location/Qualifiers
Sequence 38 from patent US 6605272. AR374073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9 from Patent W00125444. AXI06717
                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
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100.0%; Pred. No. 94;
tive 0; Mismatches 0; Indels
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                  linear
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Method for sorting single-stranded nucleic acids
Patent: WO 03072818-A 56 04-SEP-2003;
Degussa Bloactives GmbH (DE)
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Method for sorting single-stranded nucleic acids
Patent: WO 03072818-A & 2 04-SEP-2003;
Degussa Bloactives GmbH (DE)
                                                                                                                                                                                                                                                                  1. .21
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/db_xref="taxon:32650"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
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/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xxef="kaxon:32630"

/note="Beschreibung der kuenstlichen

Sequenz:Capture-Oligonukleotid"
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/mod_base=OTHER
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/mod_base=OTHER
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                AX825158 21 bp 1
Sequence 56 from Patent WO03072818.
AX825158
AX825158.1 GI:39750887
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Sequence 62 from Patent WO03072818.
AX825164
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                                1 (bases 1 to 27)
Garner, H.R., Wren, J.D., Minna, J.D. and Fondon, J.W. III.
Polymorphic repeats in human genes
Patent: US 6472154-A 153 29-OCT-2002;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="synthetic construct"
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Sequenz:Capture-Oligonukleotid"
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/mod_base=OTHER
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Sequence 29 from Patent WO03072818.
AX825131
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/organism="unknown"
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PAT 06-FEB-1997

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Aicolaides, N.C., Sass, P.M., Grasso, L., Vogelstein, B. and Kinzler, K.W.

Kinzler, K.W.

Method for generating hypermutable organisms

Patent: WO 0188192-A 4 22-NOV-2001;

The Johns Hopkins UNiversity School of Medicine (US); Morphotek Inc. (US); Nicolaides, Micholas, C. (US); Sass, Philip, M. (US) Grasso, Luigi (US); Vogelstein, Bert (US)

Location/Qualifiers
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100.0%; Pred. No. 1.1e+02;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 0; Indels
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    .25
    /organism="synthetic construct"
/mol_type="unassigned DNA"

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    .24
    /organism="synthetic construct
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/note="Viral vector sequence"

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Pickup, D.J., Patel, D. and Antczak, J.B.
Site-specific RNA cleavage
Patent: US 5578468-A 42 26-NOV-1996;
Location/Qualifiers
                           Vector constructs
Patent: WO 02068627-A 8 06-SEP-2002;
Location/Qualifiers
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Sequence 42 from patent US 5578468.
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Sequence 4 from Patent W00188192.
AX338548
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artificial sequences.
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AX338548
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I29929
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    .24 /note="Fig. 1C. SV40 early Poly(A) site"
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(mod_base=OTHER
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mod_base=OTHER
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/noTe="Viral vector sequence"
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Location/Qualifiers
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AX817782
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Sequence 8 from Patent W002068627.
AX838369
AX838369.1 GI:39922050
                 bound moiety="Biotin"
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AX817782
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AX838369
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PAT 09-JAN-2002

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Z6 bp DNA linear PAT 17-JUL-2003
Reagents and methods useful for detecting diseases of the breast.
BD192375.1 GI:33002114
JP 202516576-A/14.
                                                  PAT 10-JUN-1998
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A method for generating hypermutable organisms
Patent: WO 0188192-A 3 22-NOV-2001;
The Johns Hopkins University School of Medicine (US); Morphotek
Inc. (US); Nicolaides, Nicholas, C. (US); Sass, Philip, M. (US)
Grasso, Luigi (US); Vogelstein, Bert (US)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                  linear
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Patent: US 5707807-A 3 13-JAN-1998;
Location/Qualifiers
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Sequence 3 from patent US 5707807.
179496
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Sequence 3 from Patent WO0188192.
AX338547
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1 (bases 1 to 26)
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Patent: WO 0218538-A 52 07-MAR-2002,
Gemini Genomics PLC (GB)
Location/Qualifiers
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Patent: WO 0218618-A 59 07-MAR-2002;
Gemini Genomics PLC (GB)
Location/Qualifiers
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                                              Query Match 1.2%; Score 21; DB 1; Length 25; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 21; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="taxon:32630"
/noTe="Synthetic oligonucleotide"
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/mol_type="unassigned DNA"
/db xref="taxon:32630"
/noTe="Synthetic oligonucleotide"
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Sequence 59 from Patent W00218638.
AX394514
AX394514.1 GI:21065652
                                                                                                                                                                                                                             25 bp
Sequence 52 from Patent WO0218638.
AX394507
                 /note="Recombinant DNA"
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Best Local Similarity 100.
Matches 21; Conservative
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AX394514/c
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AX394507
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PAT 17-JUL-2003

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28-SEP-1999 JP 2000572365
28-SEP-1999 US 09/161939
RICHARD A SHIMKETS
C12N15/09, A01K67/027, A61K31/7088, A61K38/00, A61K39/395, A61K39/
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                                       BD237566 26 26 bp DNA linear PAT 17-JU Genes and proteins predicting and treating fit, hypertension,
                                                                                                                                                                                                                                                                                                                                                                                                                           Genes and proteins predicting and treating fit, hypertension,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PC C07KK4/47, C07KL6/18, C12N9/10, C12N9/88, C12Q1/25, C12Q1/52, C
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Patent: JP 2002525115-A | 13-AUG-2002;
CURAGEN CORP
OS Artificial Sequence
PN JP 2002525115-A/1
PP 340G-2002
PP 28-SEP-1999 JP 2000572365
PR 28-SEP-1999 JP 2000572365
PC 212N15/09, A01K67/027, AG193/99, AG1843/00, AG1943/00, AG1943/00, PC 207K14/47, C07K16/19, C12N9/10, C12N9/10

    .26
    forganism="synthetic construct"
|mol type="genomic DNA"
|db_xref="taxon:32630"

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Patent: US 6486299-A 43 26-NOV-2002;
Location/Qualifiers
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Sequence 43 from patent US 6486299.
AR257336
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/mol_type="genomic DNA"
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1 (bases 1 to 26)
                                                                                                        diabetes and obesity.
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Shimkets, R.A.
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AR257336/c
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                            1 (bases 1 to 26)
Medel, P.A.B., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J.,
Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D.,
Russell, J.C., Scheffel, C.P., Stroupe, S.D. and Yu, H.
Reagents and methods useful for detecting diseases of the breast
Patent: JP 2002516576-A 14 04-JUN-2002;
PN JP 2002516576-A/14
PD 04-JUN-2002
PP 19-JUN-1998 JP 1999504891
PF 20-JUN-1999 JB SP 1999504891
PR 20-JUN-1999 JB SP 1999504891
PR 20-JUN-1999 JB SP 1999504891
PR 20-JUN-1998 JP BEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA
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   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R
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Pred. No. 1.3e+02;
1; Mismatches 1; Indels
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1.2e+02;
hes 0;
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1.2%; Score 21; DB
Best Local Similarity 100.0%; Pred. No. 1.2
Matches 21; Conservative 0; Mismatches
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Patent: WO 0216618-A 21 28-FEB-2002;
DSM N.V. (NL)
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Sequence 21 from Patent WO0216618.
AX391871 GI:19700451

    '26
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    /db_xref="taxon:10095"

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21; Conservative ::
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Modulation of t-cell receptor interactions
Patent: WO 0190747-A 37 29-NOV-2001;
Sunol Molecular Corporation (US)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="taxon:32630"
/noTe="Primer"
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Sequence 42 from Patent WO02062135.
AX513052
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Sequence 37 from Patent WO0190747.
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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A human 2-19 protein homologue, Z219A.
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BD062456.1 GI:22608059
JP 2001507946-A/4.
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Sequence 36 from Patent W003064691.
AX814950
                                                                                                                                Sequence 6 from patent US 6331413.
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/organism="unknown"
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AR263647.1 GI:28075580
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                                        Egelrud, T. and Hansson, L. Scce modified transgenic mammals and their use as models of human
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Torrence P.F., Silverman, R.H., Maitra, R.K. and Lesiak, K. Chimeric molecules targeted to viral RNAs
Patent: US 6271369-A 19 07-AUG-2001;
Location/Qualifiers
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/note="5 -RACE cDNA synthesis primer."
                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                               disease
Patent: WO 02062135-A 42 15-AUG-2002;
Egelrud, Torbjorn (SE) ; Hansson, Lennart (SE)
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="primer"
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Enterovirus nucleic acids
Patent: WO 02103060-A 35 27-DEC-2002;
Innoventus Project AB (SE)
Location/Qualifiers
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Sequence 35 from Patent W002103060.
AX711956
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AR164336
AR164336.1 GI:16235464
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/organism="unknown"
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artificial sequences.
synthetic construct artificial sequences.
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23 bp DNA linear PAT 17-JUL-2003 Oligonucleotide primer capable of making the non-specific double BD244857
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1 (bases 1 to 22)
Torrence, P., Silverman, R., Maitra, R. and Lesiak, K.
Method of cleaving specific strands of RNA and medical treatments
                                              Gaps
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Torrence, P., Silverman, R., Maitra, R. and Lesiak, K. Method of cleaving specific strands of RNA Patent: US 5583032-A 19 10-DEC-1996;
Location/Qualifiers
                                           1; Indels
Query Match
1.2%; Score 20.4; DB 1; Length
Best Local Similarity 95.5%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels
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Sequence 19 from patent US 5583032.
I31828
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Sequence 19 from patent US 5677289.
1169425 1 GI:2831547
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PAT 29-SEP-1999
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Dellinger, D.J., Dahm, S.C., Ilsley, D.D., Ach, R.A. and Troll, M.A. Hybridization assay signal enhancement
Patent: US 6103474-A 7 15-AUG-2000;
Location/Qualifiers
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1 Unknown.
Unclassified.
1 (bases 1 to 24)
5 Johnson, E.M. and Bergemann, A.D.
Nonoclonal antibodies to the pur protein
AL Patent: US 5869622-A 50 09-FEB-1999;
Location/Qualifiers
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Best Local Similarity 95.5%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 1;
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95.5%; Pred. No. 1.3e+02;
tive 0; Mismatches 1;
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Unclassified.
1 (bases 1 to 24)
Dellinger, D.J., Dahm, S.C. and Troll, M.A.
Signal enhancement method and kit
Patent: US 585393-A 1 29-DEC-1998;
Location/Qualifiers
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    .24
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Sequence 7 from patent US 6103474.
AR105984 GI:12820049
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Sequence 1 from patent US 5853993.
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06-OCT-1999 JP 2000574722
06-OCT-1999 JP 2000574722
07-OCT-1999 JP 2000574722
07-OCT-1999 JP 2000574722
07-OCT-1999 JP 2000574722
07-007-1999 JP 2000574722
07-007-1999 JP 20005746623
07-007-1999 JP 2000574722
07-007-1999 JP 200057422
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    .23
    /organism="synthetic construct"

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1 (Bases 1 to 24)
Johnson, E.M. and Bergemann, A.D.
Cloning and expression of PUR protein
Patent: US 5756684-A 50 26-WAY-1998;
Location/Qualifiers
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Sequence 50 from patent US 5869622.
AR034772
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JP 2002532063-A/2
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AR034772
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1 (Dases 1 to 24)

1 (Dases 1 to 24)

Quantitative determination of nucleic acid amplification products
Patent: US 6365346-A 4 02-APR-2002;
Location/Qualifiers
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1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 1; Indels
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                                                                                                    DNA
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Patent: US 6346384-A 11 12-FEB-2002;
Location/Qualifiers
                            24 bp E
Sequence 25 from patent US 5545551.
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/organism="unknown"
/wol_type="unassigned DNA"
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AR184443
AR184443.1 GI:20230408
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/organism="unknown"
/wol_type="unassigned DNA"
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Sequence 4 from patent US 6365346.
AR202876.1 GI:21499117
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/organism="unknown"
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                                                       124762
124762.1 GI:1604632
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Pollner, R.B.
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Unclassified.
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RESULT 43
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AR202876
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                                                                      PAT 14-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Improved method for inserting nucleic acid into cyclic vector Patent: JP 2002532085-A 3 02-OCT-2002;
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    .24
    /organism='Artificial Sequence'

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Unclassified.
1 (bases I to 24)
3 Dellinger, D.J., Dahm, S.C. and Troll, M.A. Signal enhancement method and kit
AL Patent: US 6110682-A I 29-AUG-2000;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                      1.2%; Score 20.4; DB 1;
95.5%; Pred. No. 1.3e+02;
tive 0; Mismatches 1;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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                                                                      DNA
                                                                                                                                                                                                                                                 1. .24
/organism="unknown"
/wol_type="unassigned DNA"
                                                                      AR107972 24 bp
Sequence 1 from patent US 6110682.
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17-DEC-1998 US 09/2138
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DP 2002532085-A/3.
synthetic construct
synthetic construct
artificial sequences.
1 (Dases 1 to 24)
Romantchikov, Y.
  AAAAAAAAAAAAAAAAAAA
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JP 2002532085-A/3
02-OCT-2002
                                                                                                           AR107972.1 GI:12823459
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Best Local Similarity 95.5
Matches 21; Conservative
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AR107972
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Quantitative determination of nucleic acid amplification products
Patent: US 6573054-A 4 03-UUN-2003;
Location/Qualifiers
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1 (Dases 1 to 24)
Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
Polymorphic repeats in human genes
Patent: 16 (A72154-A 134 29-OCT-2002;
Location/Qualifiers
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llarity 95.5%; Pred. No. 1.3e+02;
Conservative 0; Mismatches 1; Indels
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Amplification of nucleic acids
Patent: US 6582938-A 1 24-UW-2003;
Location/Qualifiers
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Sequence 4 from patent US 6573054.
AR340571
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Sequence 1 from patent US 6582938.
                                                                                                                                                                        /organism="unknown"
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/mol_type="genomic DNA"
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/organism="unknown"
/mol_type="genomic DNA"
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AR345020.1 GI:33741140
 GI:27287658
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1 (bases 1 to 24)
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 AR241846.1
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Seguence 134 from patent US 6472154.
AR241846
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Front tube furrow opener attachment
Patent: US 6457426-A 1 01-OCT-2002;
Location/Qualifiers
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                          Patent: US 6406667-A 4 18-JUN-2002;
Location/Qualifiers
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Sequence 1 from patent US 6457426.
AR232949.1 GI:27275296
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PAT 30-APR-2001
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                            Krieg,A.M., Schetter,C. and Vollmer,J.C.
muniostimulatory nucleic acids
Patent: WO 0122972-A 433 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Krieg, A.M., Schetter, C. and Vollmer, J.C.
munuostimulatory nucleic acids
Patent: WO 0122972-A 96i 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical
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Immunostimulatory nucleic acids
Patent: WO 0122972-A 92 05-D48F2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
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    .24
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Vaisberg, E.A., Adams, C.L., Sabry, J.H. and Crompton, A.M.
Database system including computer code for predictive cellular
bioinformatics
Patent: US 6651008-A 4 18-NOV-2003;
Location/Qualifiers
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Vaisberg, E.A., Adams, C.L., Sabry, J.H. and Crompton, A.M.
Database system including computer code for predictive cellular
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Sequence 433 from Patent WO0122972.
AX104241
AX104241.1 GI:13920438
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Patent: US 6651008-A 1 18-NOV-2003;
Location/Qualifiers
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Sequence 4 from patent US 6651008.
AR431310
AR431310.1 GI:40193278
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/mol_type="genomic DNA"
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/organism="unknown"
/mol_type="genomic DNA"
              1734 ACAAAAAAAAAAAAAAAA 1755
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AR431307/C
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PAT 20-JUN-2002
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                                                                                                                                                                                                                                     Lin,S.L., Chuong,C.M. and Widelitz,R.B.
Gene silencing using mrna-cdna hybrids
Patent: WO 0210374-A 12 07-FEB-2002;
UNIVERSITY OF SOUTHERN CALIFORNIA (US)
Location/Qualifiers
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Sequence 433 from Patent WO02053141.
AX547294.1 GI:25812438
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                                                                        AX427163 24 bp
Sequence 12 from Patent WO0210374.
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Sequence 1 from Patent WO0184157.
AX428574 GI:21538485
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                             RESULT 58
AX427163/c
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AXS47294/c
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backbone"
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                               Query Match
1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 1; Indels
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UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
Location/Qualifiers
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Patent: WO 0173129-A 11 04-0CT-2001;
DADE BEHRING INC. (US)
Location/Qualifiers
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AX355813
AX355813.1 GI:18620481
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Sequence 11 from Patent WO0173129.
AX354553
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Query Match

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DEFINITION ACCESSION VERSION KEYWORDS SOURCE

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AX35453 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE

RESULT 56

ORGANISM

REFERENCE AUTHORS JOURNAL

TITLE

FEATURES

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Gaps

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Indels

Length 24;

PAT 29-MAR-2003

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Mack, D. and Gish, K.C.
Methods of diagnosing breast cancer and screening for modulators
Patent: WO 0221134-A 11 14-MR-2002;
EOS Biotechnology, Inc. (US)
Location/Qualifiers
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Methods of diagnosing colorectal cancer and/or breast cancer.
compositions, and methods of screening for colorectal cancer
breast cancer modulators
Patent: WO 02055609-A 13 01-AUG-2002;
EOS Biotechnology, Inc. (US)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="teaxon:32630"
/note="T7-(dT)-24 primer"
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   /note="Synthetic Sequence"
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AX750585
AX750585.1 GI:32133003
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AX684290/c
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AX750585/c
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                            Bratzler, R.L.
Inhibition of angiogenesis by nucleic acids
Patent: WO 02053141-A 433 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bratzler, R.L.
Inhibition of angiogenesis by nucleic acids
Patent: WO 02053141-A 961 11-JUL-2002,
Coley Pharmaceutical Group, Inc. (US)
Location/Qualifiers
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1.2%; Score 20.4; DB 1;
Best Local Similarity 95.5%; Pred, No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 1;
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1.2%; Score 20.4; DB 1;
Best Local Similarity 95.5%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 1;
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/mol_type="unassigned DNA"
/db_xref="teaxon:32630"
/noTe="Synthetic Sequence"
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/noTe="Synthetic Sequence"
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Sequence 961 from Patent W002053141.
AX547822.1 GI:25812966
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Sequence 962 from Patent WO02053141.
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1 AAAAAAAAAAAAAAAAAA 22
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AR105982/c
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BD234336/c
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                                          PAT 12-DEC-2003
                                                                                                                                                                        Mack, D.H., Gish, K.C. and Afar, D.
Methods of diagnosis of breast cancer, compositions and methods of
screening for medulators of breast cancer
Patent: WO 02059377-A 140 01-AUG-2002;
EOS Biotechnology, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                               1.24
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/note="t at positions 8-24 may be present or absent"
/mod_base=OTHER
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Switchetic construct
artificial sequences.

1 (base 1 to 24)
S Patel,R. and Kurn,N.
Quantitative assay of nucleic acid amplification product
Quantitative assay of nucleic acid amplification product
DADE BEHRING INC
OS Artificial Sequence
PN UP 2002504350-A/4
PD 12-FEB-1999 JP 2000532556
PR 17-FEB-1999 JP 2000532556
PR 18-FEB-1999 UP 2000532556
PR AJESH PATEL,NURITH KURN
PC C12Q1/68,C12N15/09,C12N15/O0
CC Synthetic DNA Probe
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Quantitative assay of nucleic acid amplification product.
BD136714
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1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 1; Indels
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                                 AX829247 24 bp DI
Sequence 140 from Patent WO02059377.
AX829247
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AX829247/c
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BD136714
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BD234336 17-JUL-2003 1mear PAT 17-JUL-2003 Improved method for inserting nucleic acid into cyclic vector. BD234336.1 GI:33044106
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C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/00, C12N5/
        PAT 14-FEB-2001
                                                                                                                                                                          1 (bases 1 to 25)
Dellinger,D.J., Dahm,S.C., Ilshey,D.D., Ach,R.A. and Troll,M.A. Hybridization assay signal enhancement
Patent: US 6103474-A 5 15-AUG-2000;
Location/Qualifiers
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synthetic construct
artificial sequences.

1 (bases 1 to 25)
Romantchikov, Y.
Improved method for inserting nucleic acid into cyclic vector
Patent: JP 2002532085-A 9 02-OCT-2002;
YURI ROMANTCHIKOV
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11; Conservative 0; Mismatches 1; Indels
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1.2%; Score 20.4; DB 1; Length 25;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels
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/organism='Artificial Sequence'
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           DNA
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25 bp
Sequence 5 from patent US 6103474.
AR105982
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17-DEC-1998 US 09/213834
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/organism="unknown"
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Probe carrier, Method and Apparatus for producing Probe carrier.
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artificial sequences.

1 (bases 1 to 25)
Okamura, N., Okamoto, T. and Kameyama, M.
Probe carrier, Method and Apparatus for producing Probe carrier
Patent: JP 2003014773-A 3 15-JAN-2003;
CANON INC
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                                                                                                                                                                                                                                                                                                                              Picoult-Newburg, L. and Pohl, M. Gencyping reagents, Kits and methods of use thereof Patent: WO 0129262-A 1311 26-APR-2001; Orchid BioSciences, Inc. (US) Location/Qualifiers
                                         Query Match 1.2%; Score 20.4; DB 1; Length 25; Best Local Similarity 95.5%; Pred. No. 1.4e+02; Matches 21; Conservative 0; Mismatches 1; Indels
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1 Similarity 95.5%; Pred. No. 1.4e+02;
21; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="synthetic construct"
/mol_type="unassigned DNA"
/mol_type="taxon:32630"
/nofe="primer"
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                               Sequence 1311 from Patent WO0129262.
AX116188
/organism="unknown"
/wol_type="genomic DNA"
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BD187513.1 GI:32997252
JP 2003014773-A/3.
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synthetic construct
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Production and use of magnetic porous inorganic materials
Patent: US 5734020-A 2 31-MAR-1998;
Location/Qualifiers
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                                                                                                                                           Unclassified.

1 (bases 1 to 25)
Nikiforov, T. and Knapp, M.R.
Method for immobilizing nucleic acid molecules
Patent: US 5610287-A 2 11.MAR-1997,
Location/Qualifiers
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95.5%; Pred. No. 1.4e+02;
tive 0; Mismatches 1;
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95.5%; Pred. No. 1.4e+02;
tive 0; Mismatches 1;
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Kuimelis,R.G. and Wagner,R.
Addressable protein arrays
Patent: US 6537749-A 23 25-MAR-2003;
Location/Qualifiers
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/organism="unknown"
/wol_type="unassigned DNA"
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Sequence 23 from patent US 6537749.
AR288252. GI:31675536
                                      25 bp
Sequence 2 from patent US 5610287.
I58009
I58009.1 GI:2483073
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Sequence 2 from patent US 5734020.
196072
196072.1 GI:3940542
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/organism="unknown"
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158009/c
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196072/c
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Novak, J.E., Presnell, S.R., Sprecher, C.A., Foster, D.C., Holly, R.D., Gross, J.A., Johnston, J.V., Nelson, A.J., Dillon, S.R. and Hammond, A.K.
Cytokine, A.K.
Cytokine zalphall Ligand
Patent: US 6307024-A 39 23-OCT-2001;
Location/Qualifiers
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Lin, S.-L., Chuong, C.-M. and Ying, S.-Y.
Method for generating full-length cDNA library from single cells
Patent: US 6197554-A 5 06-MAR-2001;
Location/Qualifiers
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                             ce 1. .25 /organism='Artificial Sequence'
Location/Qualifiers
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1.2%; Score 20.4; DB 1;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1;
   Location/Qualifiers

    .25
    ^crganism="synthetic construct"
    ^mol_type="genomic DNA"
    ^db_xref="taxon:32630"

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ARI74582
ARI74582.1 GI:17914902
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/organism="unknown"
/mol_type="unassigned DNA"
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/wol_type="unassigned DNA"
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Sequence 5 from patent US 6197554.
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Probe carrier, Method and Apparatus for producing Probe carrier.
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03-APR-1998 US 60/080686
ROBERT G KUIMELIS, RICHARD WAGNER
CIZNIS/09, CO7H21/02, CO7H21/04, C12M1/00, C12Q1/68, G01N33/566, PC
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Query Match 1.2%; Score 20.4; DB 1; Length 25; Best Local Similarity 95.5%; Pred. No. 1.4e+02; Matches 21; Conservative 0; Mismatches 1; Indels
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artificial sequences.

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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Capture probe sequence
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PAT 10-APR-2003

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Unclassified.

1 (bases 1 to 26)

Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D., Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and Hammond,A.K.
Methods of using zalphall ligand
Patent: US 6605272-A 39 12-AUG-2003;

Location/Qualifiers
                                                                                                                                                                                                                                                                                               Unknow...
Unclassified.
1 (basss 1 to 26)
0'Neill,R.A., Chen,J.-K., Chiesa,C. and Fry,G.
Multiplex polynucleotide capture methods and compositions
Patent: US 6514699-A 2 04-FEB-2003;
Location/Qualifiers
                y Match 1.2%; Score 20.4; DB 1; Length 26; Local Similarity 95.5%; Pred. No. 1.5e+02; hes 21; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.2%; Score 20.4; DB 1; Length 26; Best Local Similarity 95.5%; Pred. No. 1.5e+02; Matches 21; Conservative 0; Mismatches 1; Indels
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95.5%; Pred. No. 1.5e+02;
tive 0; Mismatches 1;
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Sequence 39 from patent US 6605272.
AR374074
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Sequence 2 from patent US 6514699.
AR279358
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AR404597
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/organism="unknown"
/mol_type="genomic DNA"
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/wol_type="genomic DNA"
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AR279358/c
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AR404597/c
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BD248975.1 GI:33058745
Synthetic construct
synthetic construct
artificial sequences.
I (base 1 to 20.1)
Novak, J.E., Pressell, S.R., Sprecher, C.A., Foster, D.C., Holly, R.D.,
Hammond, A.K.
Novel cytokine ZALPHA11 ligand
Patent: JP 2005337839-A 36 12-NOV-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RICHARD D HOLLY, JANE A GROSS, JANET V JOHNSTON, ANDREW J NELSON, STACEY R DILLON, ANGELA K HAMMOND CI2N15/09, AGIK38/00, AGIK4/52, CO7K14/53,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C07K14/54, C07K14/55, C07K16/24, C07K19/00, C12N1/15, C12N1/19, PC
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1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                     ZYMOGENETICS INC
OS Artificial Sequence
PN JP 2002537839-A/36
PD 12-NOV-2002
PF 09-MRR-2000 JP 2000603382
PR 09-MRR-1999 US 09/264908,11-MAR-1999 US
01-JUL-1999 US 60/142013
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Patent: US 5707807-A 2 13-JAN-1998;
Location/Qualifiers
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Key
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/organism="synthetic construct"
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/db_xref="taxon:32630"
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Sequence 2 from patent US 5707807.
                                                                           Novel cytokine ZALPHA11 ligand.
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25 AAAAAAAAAAAAAAAAAAA
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1 (bases 1 to 26)
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PC C12N
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BD248975/c
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PAT 18-DEC-2003

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PAT 18-DEC-2003

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Gaps

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Indels

Length 26;

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26 bp DNA linear PAT 31-JAN-2002
Method and composition for capturing multiple polynucleotide.
BD007174
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                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 26)
OGnell, R.A., Chen, J.C., Chiesa, C. and Fry, G.
Method and composition for capturing multiple polynucleotide
Patent: JP 2001503973-A 2 27-MAR-2001;
THE PERKIN ELMAR CORP
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1 (bases 1 to 27)
Sengu, K.Y. and Ito, S.
REPLICATION OF DNA
PAREZONA BOARD OF REGENTS
OS Artificial gene
OC Artificial sequence; Genes.
PN JP 1993103673-A/79
PD 27-APR-1993
                                                Query Match
1.2%; Score 20.4; DB 1;
Best Local Similarity 95.5%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 1;
/db_xref="taxon:32630"
. /note="synthetic construct"

    .26
    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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JP 2001503973-A/2.
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                                                                                      1 (bases 1 to 26)

Ju,J., Li,Z., Tong,A. and Russo,J.J.

Combinatorial fluorescence energy transfer tags and their
applications for multiplex genetic analyses

Patent: US 6627748-A 1 30-SEP-2003;

Location/Qualifiers
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1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 1; Indels
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1.2%; Score 20.4; DB 1;
Best Local Similarity 95.5%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 1;

    .26
/organism="synthetic construct"
/mol_type="unassigned DNA"

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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="reaxon:32630"
/note="Poly(dT)-26mer primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lin, S.L., Chuong, C.M. and Widelitz, R.B.
Gene silencing using mrna-cdna hybrids
Patent: WO 0210374-A 3 07-FEB-2002;
UNIVERSITY OF SOUTHERN CALIFORNIA (US)
Location/Qualifiers
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Sequence 53 from Patent WO02059357.
AX528804
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Sequence 3 from Patent W00210374
                                                                                                                                                                                                                                    /mol_type="genomic DNA"
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/organism="unknown"
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AR404597.1 GI:40153233
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                                                                       Unclassified.
                                 Unknown.
                                                      Unknown.
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PAT 29-SEP-1997

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db_xref="taxon:1773"
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Matches 21; Conservative
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AX355814/c
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AX104719/c
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Mycobacterium tuberculosis
Bacteria, Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterinaes; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
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Unclassified.
1 (Classified.)
1 (Dases i to 27)
Weindel, K. and Brand, J.
DNA detection by means of a strand reassociation complex
Patent: US 6410235-A 18 25-JUN-2002;
Location/Qualifiers
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/note='3'terminal fragment of ITR'
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Dna detection by a strand reassociation complex
Patent: EP 0962536.4 lg 08-DEC-1999;
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Location/Qualifiers
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/mol_type="unassigned DNA"

    .27
    ^2rganism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"

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C12N15/10,C12N15/11//C12Q1/68;
strandedness: Single;
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Sequence 18 from patent US 6410235.
AR214918 1 GI:23312859
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Sequence 18 from Patent EP0962536.
AX009609.1 GI:9996841
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/mol_type="genomic DNA"
26-AUG-1991 JP 1991240525
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AX009609/c
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                                             /note="Y means incorporation of Aminolinker-phosphoramidite subsequently estered with 3-0 carboxymethyl digoxigenin"
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munuostimulatory nucleic acids
Patent: WO 0122972-A 911 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
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'note="Phosphate linked to biotin via Aminolinker"
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backbone"
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95.5%; Pred. No. 1.6e+02;
iive 0; Mismatches 1; Indels
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UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Sequence 911 from Patent WO0122972.
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S64862S3 27 bp DNA linear PRI 17-DEC-1993 alpha 1-theta 1 globin intergenic region {3' alpha 1-Alu 1 repeat} [Hylobates sp.=gibbons, Genomic, 27 nt, segment 3 of 5].
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hylobatidae, Hylobates.

1 (Dases 1 to 27)

Bailey, A.D. and Shen, C.K.
Sequential insertion of Alu family repeats into specific genomic
                                                                                                                                                                                                                                                                                            PC C12N15/09, C07K14/47, C12N1/15, C12N1/19, C12N1/21, C12N5/10 PC ,C12P21/02, C12Q1/68, PC G01N33/15, G01N33/56, C12N15/00, C12N5/00 CC n =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 136653] from the original journal article. This sequence comes from Fig. 2A. Location/Qualifiers
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Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7205-7209 (1993)
93348242
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                                                                                                                                                       Androgen receptor complex-associated protein Patent: JP 2002262871-A 12 17-SEP-2002; VETERANS GENERAL HOSPITAL OS Artificial Sequence PN JP 2002262871-A/12 PD 17-SEP-2002 PP 28-FEB-2001 PP 2001055192 PI TAI ZHAI CHAN
 Androgen receptor complex-associated protein.
BD175131
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Best Local Similarity 95.5%; Pred. No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 1;
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Key Location/Qualifiers
misc feature (1)..(27).
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/mol_type="genomic DNA"
/db_xref="taxon:9581"
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JP 2002262871-A/12.
synthetic construct
synthetic construct
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                                                                                                      artificial sequences.
1 (bases 1 to 27)
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Best Local Similarity 95.55
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S64862S3
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|mol_type="unassigned DNA"
|db_xref="taxon:32630"
|noFe="synthetically generated primer"
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Patent: BP 1227150-A 16 31-JUL-2002;
Veterans General Hospital (TW)
Location/Qualifiers
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Best Local Similarity 95.5%; Pred. No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 1;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="texon:32630"
/noTe="Synthetic Sequence"
   Best Local Similarity 95.5%; Pred. No. 1.6e+02; Matches 21; Conservative 0; Mismatches 1
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Sequence 911 from Patent WO02053141.
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Sequence 16 from Patent EP1227150.
AX492939
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AX547772/c
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1 (bases 1 to 20) Watson,J.D. and Tan,P.L.J. Methods and compounds for the treatment of immunologically-mediated
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1 (bases 1 to 20)
Tan,P., Skinner,M. and Prestidge,R.
Compounds and methods for treatment and diagnosis of mycobacterial
infections
Patent: US 5985287-A 83 16-NOV-1999;
Location/Qualifiers
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Pitsch, S., Weiss. P.A. and Jenny, L.
Ribonucleoside-derivative and method for preparing the same Patent: US 598604.A 1 16-NOV-1999;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0;
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Patent: US 5968524-A 83 19-OCT-1999;
Location/Qualifiers
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Sequence 83 from patent US 5985287.
AR085926
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 1 from patent US 5986084.
AR087520.1 GI:10014283
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/organism="unknown"
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AR087520/c
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                                                                                       PAT 10-JAN-2003
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Patent: WO 02074988-A 3 26-SEP-2002;
THE CHANCELLOR, MASTERS AND SCHOLARS OF THE UNIVERSITY OF OXFORD
(GB)
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Sequence 83 from patent US 5968524.
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AR0800000.1 GI:10006735
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/organism="unknown"
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Sequence 5 from patent US 5849480.
AR064875.1 GI:5995091
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Sequence 3 from Patent W002074988.
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Patent: US 6160093-A 83 12-DEC-2000;
Location/Qualifiers
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Tan, P., Hiyama, J., Visser, E., Skinner, M., Scott, L. and Prestidge, R.
Mycobacterium vaccae antigens
Patent: US 60011-A 81 4-DEC-1999;
Location/Qualifiers
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Uchida,K., Uchida,T., Tanaka,Y., Matsuda,Y. and Kondo,S.
Antisense routeic acid compound targeted to VEGF
Patent: US 6150092-A 96 21-NOV-2000;
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AR121692
AR121692.1 GI:14105268
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Sequence 83 from patent US 6001361.
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/mol_type="unassigned DNA"
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/organism="unknown"
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Visser, E.
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                                                    RESULT 100
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AR118970/c
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PAT 16-MAY-2001
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1 (bases 1 to 20)
Manoharan,M. and Maier,M.A.
Compounds, processes and intermediates for synthesis of mixed backbone oligomeric compounds
Patent: US 6207819-A 1 27-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gapa
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Unclassified.
Unclassified.
1 (bases 1 to 20)
Bruice,T.C. and Dev,A.P.
Deoxynucleic alkyl thiourea compounds and uses thereof
Patent: US 6169176-A 1 02-JAN-2001;
                                                                          Length 20;
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                                                                        Query Match 1.1%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 20; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0;
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    .20
    /organism="unknown"
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Sequence 1 from patent US 6169176.
AR123335
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Sequence 1 from patent US 6207819.
AR141070 GI:14483566
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PAT 25-SEP-2002
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                                                   09-AUG-1995 JP 1995224606
MIXUGUCHI MASATSUGU, KUROSAKI NAOKO, MAKINO KEISUKE, PI
NAGI YOSHIO.
YAMAMOTO NAOKI
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                                                                                                                                                                                                              /organism='Artificial sequences'. Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
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Tan, P., Visser, E., Prestidge, R. and Watson, J.D.
                                                                                                                                                                                                                                                                                                           Query Match
1.1%; Score 20; DB 1; L.
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0;
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Sequence 16 from patent US 5605662.
136180
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                                                                                                       C07H21/04//A61K31/70;
strandedness: Single;
topology: Linear;
hypothetical: No;
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              Artificial sequences.
JP 1997052898-A/10
25-FEB-1997
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                                                                                                         Unknown.
Unclassified.
1 (bases 1 to 20)
Huang, Z. and Szostak, J.W.
Simple and efficient method to label and modify 3'-termini of RNA using DNA polymerase and a synthetic template with defined overhang nucleotides
                            PAT 08-AUG-2001
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Mizuguchi, M., Kurosaki, N., Makino, K., Koyanagi, Y. and Yamamoto, N. ANITHITLV. ANTI-SENSE OLIGONUCLEOTIDE
Patent: JP 1997052898-A 10 25-FEB-1997;
SOYAKU GIJUTSU KENKYUSHO: KK
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                             DNA
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E12676
                                                                                                                                                                                                     Patent: US 6238865-A 14 29-MAY-2001;
                          AR1S4115 20 bp 1
Seguence 14 from patent US 6238865.
AR1S4115
                                                                                                                                                                                                                                                     /mol_type="unassigned DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13 from patent US 6274321.
AR164658
AR164658.1 GI:16237754
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Matches 20; Conservative
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AR164658
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E12676/c
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PAT 10-APR-2003
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                                                                                                                                                           1 (bases 1 to 20)
Mixkin, Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
Elghanian,R. and Taton,T.A.
Nanoparticles having oligonucleotides attached thereto and uses
therefor
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1 (bases 1 to 20)

Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,

Bighanian,R. and Tacon,T.A.

Nanoparticles having oligonucleotides attached thereto and uses
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1 (bases 1 to 20)

Manoharan, L. Lonnberg, H., Salo, H. and Virta, P. Aminooxy functionalized oligomers

Patent: US 6576752-A 10 10-JUN-2003;

Location/Qualifiers
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Pred. No. 1.2e+02;
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1.1%; Score 20; DB 1; Lv
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0;
                                                 DNA
                                                                                                                                                                                                                                                         Patent: US 6506564-A 55 14-JAN-2003;
Location/Qualifiers
                                                20 bp C
Sequence 55 from patent US 6506564.
AR274394
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Sequence 55 from patent US 6582921.
AR344936
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Sequence 10 from patent US 6576752.
AR343047
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AR274394
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AR344936
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DEFINITION
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AR343047/c
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TITLE
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Compounds and methods for treatment and diagnosis of mycobacterial infections
Patent: US 6406704-A 83 18-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unknowu.
Unclassified.
1 (bases 1 to 20)
1 (bases 1 to 20)
Manoharan,M. and Maier,M.A.
Compounds, processes and intermediates for synthesis of mixed backbone oligometic compounds
backbone to 36 462184.A 1 08 -0CT-2002;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0;
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Sequence 26 from patent US 6429300.
AR222466
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Sequence 1 from patent US 6462184.
AR236083

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    /mol_type="genomic DNA"

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/organism="unknown"
/mol_type="genomic DNA"
                                              Location/Qualifiers
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Unclassified.
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AX004876 20 bp
Sequence 5 from Patent WO9910527.
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Sequence 9 from Patent WO0067023.
AX045779
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AR429653.1 GI:40189949
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Unclassified.
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AR429653
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AX045779/c
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1 (bases 1 to 20)
Watson,J.D., Tan,P.L.J. and Prestidge,R.
Methods for the treatment of immunologically-mediated skin
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1 (bases 1 to 20)
Mirkin, C.A., Letsinger, R.L., Mucic, R.C., Storhoff, J.J.,
Elghanian, R. and Taton, T.A.
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                                                                                                Query Match
1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0;
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Patent: US 6582921-A 55 24-JUN-2003;
Location/Qualifiers
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Patent: US 6328978-A 83 11-DEC-2001;
Location/Qualifiers
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Sequence 55 from patent US 6610491.
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AR365970.1 GI:34598223
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AR365970
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AR382312
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Mirkhin.C.A., Lessinger,R.L., Mucic,R.C., Storhoff,J.J.,
Elghanian,R. and Taton,T.A.
Nanoparticles having oligonucleotides attached thereto and uses
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Method for isolating anionic organic substances from aqueous systems using cationic polymer nanoparticles
Patent: WO 9910527-A 5 04-MAR-1999;
SUEDDEUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
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1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
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/note="phosphorthioate oligonucleotide"
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Location/Qualifiers
20 bp 1
Sequence 55 from patent US 6645721.
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PAT 30-APR-2001
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Immunostimulatory nucleic acids
Patent: WO 0122972-A 226 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical
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Immunostimulacory nucleic acide
Patent: WO 0122972-A 556 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
Screening for immunostimulatory dna functional modifyers
Patent: WO 0067023-A 20 09-NOV-2000;
CPG Immunopharmaceuticals GmbH (DE) ; UNIVERSITY OF IOWA RESEARCH
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
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100.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 0;
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/organism="synthetic construct"
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    /organism="synthetic construct"
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Seguence 556 from Patent WO0122972.
AX104364
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Sequence 226 from Patent WO0122972.
AX104034
                                                          FOUNDATION (US)
Location/Qualifiers
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                                 Noll, B.O., Schetter, C. and Krieg, A.M.
Screening for immunostimulatory dna functional modifyers
Screening for immunostimulatory dna functional modifyers
Batent: WO 0067023-A 9 09-NOV-2000;
CPG Immunopharmaceuticals GmbH (DE); UNIVERSITY OF IOWA RESEARCH
FOUNDATION (US)
Location/Qualifiers
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/note="synthetic oligonucleotide"
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/note="phosphorothioate backbone"

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/organism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
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Sequence 20 from Patent WO0067023.
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AX045787/c
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PAT 28-AUG-2001
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                                                                                                                                                                              Mirkin, C.A., Letsinger, R.L., Mucic, R.C., Storhoff, J.J., Blghanian, R., Taton, T.A. and Li, Z. Nanoparticles having oligonucleotides attached thereto and uses therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weiner, G. and Hartmann, G. Methods for enhancing antibody-induced cell lysis and treating
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UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
Location/Qualifiers
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/db_xref="taxon:32630"
/note="random synthetic sequence"

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    forganism="synthetic construct"
|mol_type="unassigned DNA"
|db_xref="taxon:32630"

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Nanosphere, Inc. (US)
Location/Qualifiers
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                                  AX196239 20 bp
Sequence 70 from Patent WO0151665.
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Sequence 2 from Patent WO0197843.
AX354974
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AX355810/c
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Immunostimulatory nucleic acids
Patent: WO 0122972-A 560 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
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Seguence 560 from Patent WO0122972.
AX104368
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Nanosphere, Inc. (US)
Location/Qualifiers
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Mirkin, C.A., Letsinger, R.L., Mucic, R.C., Storhoff, J.J., Elghanian, R., Taton, T.A., Park, S.J. and Li, Z. Nanoparticles having oligonucleotides attached thereto and uses
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100.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 0; Indels
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// Organism="synthetic construct"
// Mol_type="unassigned DNA"
// db_xref="taxon:32630"
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Nanosphere, Inc. (US)
Location/Qualifiers
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Nanosphere, Inc. (US)
Location/Qualifiers
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Sequence 55 from Patent WO0218643.
AX465311
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Sequence 70 from Patent WO0173123.
AX440140
                   Location/Qualifiers
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 Nanosphere, Inc. (US)
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AX465311
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AX440140
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                                                        Weiner, G. and Hartmann, G. Methods for enll lysis and treating Methods for enhancing antibody-induced cell lysis and treating
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/db_xref="taxon:32630"
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                                                                                                       Patent: WO 0197843-A 838 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
LOCATION/Qualifiers
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Sequence 839 from Patent WO0197843.
AX355811
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Sequence 55 from Patent W00173123.
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Inhibition of angiogenesis by nucleic acids
Patent: WO 02053141-A 556 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
Location/Qualifiers
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Inhibition of angiogenesis by nucleic acids
Patent: WO 02053141-A 560 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0;
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                                               Sequence 556 from Patent W002053141.
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Query Match
1.1%; Score 20; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0;
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/mol_type="unassigned DNA"
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Sequence 70 from Patent WO0218643.
AX465326
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Location/Qualifiers
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Patent: WO 03027328-A 14 03-APR-2003;
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Nucleic acid separation using immobilized metal affinity
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/note="Synthetic Oligonucleotide Sequence"
                                                                        /note="Synthetic Oligonucleotide Sequence"
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/organism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
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Patent: WO 0246398-A 6 13-JUN-2002;
The University of Houston System (US)
Location/Qualifiers
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Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
Elghanian,R., Taton,T.A., Garimella,V., Li,Z. and Park,S.J.
Nanoparticles having oligonucleotides attached thereto and uses
therefor
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Nucleic acid separation using immobilized metal affinity
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="texon:32630"
/note="random synthetic sequence"
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Similarity 100.0%; Pred. No. 1.2e+02;
00; Conservative 0; Mismatches 0;
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Pred. No. 1.2e+02;
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Patent: WO 0246398-A 5 13-JUN-2002;
The University of Houston System (US)
Location/Qualifiers
                                                                                      Patent: WO 0246472-A 55 13-JUN-2002;
Nanosphere, Inc. (US)
Location/Qualifiers
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Sequence 70 from Patent WO0246472.
AXS56139
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Location/Qualifiers
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Ribonucleoside-derivative and method for preparing the same.
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JP 2001515007 "."
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Method of detecting single base polymorphism.
BD107450
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artificial sequences.
1 (bases 1 to 20)
Segawa, M., Takarada, H., Aono, T. and Yoshiga, S.
Method of detecting single base polymorphism
Patent: 19 2002034599-A 9 05-FEB-2002;
TOYOBO CO LID
OS Artificial Sequence
/organism='Unidentified'
Location/Qualifiers
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100.0%; Pred. No. 1.2e+02;
ive 0; Mismatches 0;
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100.0%; Pred. No. 1.2e+02.
iive 0; Mismatches 0

    .20
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|mol_type="genomic RNA"
|db_xref="taxon:32630"

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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Best Local Similarity 100.0%
Matches 20; Conservative
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BD080522/c
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BD107450/c
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="texcon:32630"
/note="Description of Combined DNA/RNA Molecule:Synthetic
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Tan, P., Hiyama, J., Visser, E.S., Skinner, M.A., Scott, L.M. and Prestidge, R.L.
Compounds and methods for treatment and diagnosis of Mycobacterial
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Methods, kits and compositions pertaining to the suppression of detectable probe binding to randomly distributed repeat sequences in genomic nucleic acid aring paramic nucleic acid patent: WO 03027328-A 26 03-APR-2003;
Boston Probes, Inc. (US); DakoCytomation Denmark A/S (DK)
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ROSS L PRESTIDGE
A61K39/04,A61K35/74,C07K14/35,C12N15/63
Strandedness: Single;
Topology: Linear;
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              100.0%; Pred. No. 1.2e+02;
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Sequence 26 from Patent W003027328.
AX741052
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JP 2001503969-A/26.
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PAT 01-SEP-2000
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1 (bases 1 to 21)
Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
Oligonucleotide repeat arrays
Patent: US 5981185-A 10 09-NOV-1999;
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1 (bases 1 to 21)

1 (bases 1 to 20)

1 (bases 1 to 20)

1 (bases 1 to 20)

1 (baseon, R.S., Coassin, P.J., Rampal, J.B. and Caskey, C.Thomas. Oligonucleotide repeat arrays

Patent: US 5981185-A 13 09-NOV-1999;
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                                                                                                                                                                                                         Unclassified.

1 (bases 1 to 21)
Watson,M.A. and Fleming,T.P.
Wammaglobin, a mammary-specific breast cancer protein
Patent: US 5968754-A 13 19-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                    Length 21;
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                                                                                        21 bp | Sequence 13 from patent US 5968754.
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Sequence 10 from patent US 5981185.
AR084521
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AR084524
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/organism="unknown"
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/organism="unknown"
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PN JP 2002034599-A/9
PD 05-FEB-2002
PP 26-JUL-2000 UP 2000225354
PF 26-JUL-2000 UP 2000225354
PF MASYA SEGAWA, HIROSHI TAKARADA, TOSHIYA AONO, SATOKO YOSHIGA PC C12Q1/68,C12N15/09,C12N15/00
CC Description of Artificial Sequence:primer C Description of Artificial Sequence:primer FT source Location/Qualifiers
FT source /organism='Artificial Sequence'.
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C12N15/09, A61K31/711, A61K39/04, A61K48/00, A61P11/00, A61P11/06,
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A61P17/06,A61P31/00,A61P31/06,A61P37/04,C07K14/35,C07K16/12,
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PF 23-DEC-1998 JP 2000525553
PF 23-DEC-1997 US 08/997362, 23-DEC-1997 US 08/99708
23-DEC-1997 US 08/99664,11-UUN-1998 US 09/095855 PR
17-SEP-1998 US 09/156181,04-DEC-1998 US 09/205426 PI
TAN, JAMES WATSON, ELIZABETH S VISSER, MARGOT A SKINNER, ROSS
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100.0%; Pred. No. 1.2e+02;
ative 0; Mismatches 0;
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GENESIS RESEARCH AND DEVELOPMENT CORP LTD
OS Artificial Sequence
PN JP 2002514385-A/26
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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    /organism="synthetic construct"

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/db_xref="taxon:32630"
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Bynthetic construct
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1 (bases 1 to 20)
Tan, P. Watson, J. Vist
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Unknown.
Unclassified.
1 (bases 1 to 21)
Heller,M.J. and Tu,E.
Active programmable electronic devices for molecular biological
analysis and diagnostics
Patent: US 5605662-A 2 25-FEB-1997;
Patent: US 5605662-A 2 25-FEB-1997;
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1 (bases 1 to 21)
Watson,M.A. and Fleming,T.P.
Polynucleotides encoding mammaglobin, a mammary-specific breast cancer protein
Patent: US 566867-A 13 16-SEP-1997;
Location/Qualifiers
                                                                                                               Unknown.
Unclassified.
Unclassified.
1 (bases 1 to 21)
Heller,M.J., Tu,E., Evans,G.A. and Sosnowski,R.G.
Methods for transport in molecular biological analysis and
diagnostics
diagnostics
Patent: US 6238624-A 2 29-MAY-2001;
Location/Qualifiers
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100.0%; Pred. No. 1.30+02;
Live 0; Mismatches 0; Indels
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/mol_type="unassigned DNA"
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Sequence 13 from patent US 5668267.
           Sequence 2 from patent US 6238624. AR153849
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Sequence 2 from patent US 5605662.
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Watson,M.A. and Fleming,T.P.
Watson,M.A. and Fleming,T.P.
Machod for detecting the presence of breast cancer by detecting an increase in mammaglobin mRNA expression
Patent: US 6004756-A 13 21-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                          Unknown...
Unknown...
Unclassified.
1 (bases 1 to 21)
Bergan, R. and Neckers, L.
Inhibition of protein kinase activity by aptameric action of oligonucleotides
Patent: US 5996596-A 12 07-DEC-1999;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0;
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Sequence 12 from patent US 5998596.
AR093143
              1. .21
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Location/Qualifiers
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Matches 20; Conservative
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AR095412/c
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TITLE JOURNAL

RESULT 156 AX104720/c LOCUS

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AUTHORS TITLE JOURNAL

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REFERENCE

RESULT 157

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Weiner, G. and Hartmann, G.
Methods for enhancing antibody-induced cell lysis and treating
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/organism="synthetic construct"
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Inhibition of angiogenesis by nucleic acids
Patent: WO 02053141-A 912 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                  Patent: WO 0197843-A 840 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
Location/Qualifiers
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Sequence 912 from Patent W002053141.
AX547773
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Sequence 30 from Patent WO03072818.
AX825132
AX825132.1 GI:39750861
                  21 bp 1
Sequence 840 from Patent WO0197843.
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AX355812.1 GI:18620480
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AXS47773/c
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AX825132/c
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muniostimulatory nucleic acids
Patent: WO 0122972-A 912 05-APP-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
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Watson, M.A. and Fleming, T.P.
Mammaglobin, a secreted mammary-specific breast cancer protein
Patent: US 6566072-A 13 20-MAY-2003;
Location/Qualifiers
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tive 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0;
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1.1%; Score 20; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0;

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AR322245
AR322245.1 GI:33707814
1. .21
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Seguence 912 from Patent WO0122972.
AX104720
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PAT 11-DEC-2003

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Query Match 1.1%; Score 20; DB 1; Length 21; Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 20; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.3e+02;
tive 0; Mismatches 0; Indels
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Method for sorting single-stranded nucleic acids
Patent: Wo 03072818-A 32 04-SEP-2003;
Degussa Bioactives GmbH (DE)
Location/Qualifiers
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Sequenz:Capture-Oligonukleotid"
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Sequence 32 from Patent WO03072818.
AX825134
AX825134.1 GI:39750863
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AX825134/c
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                               Boekenkamp, D., Dieck, T.H. and Hoppe, H.U. Method for sorting single-erranded nucleic acids Patent: WO 03072818-A 30 04-SEP-2003; Degussa Bloactives GmbH (DE)
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Method for sorting single-stranded nucleic acids
Patent: WO 03072818-A 31 04-SEP-2003;
Degussa Bioactives GmbH (DE)
                                                                                                                        1. .21
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Sequenz:Capture-Oligonukleotid"
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Sequence 31 from Patent WO03072818.
AX825133
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Sequenz: Capture-Oligonukleotid"  modified_base   Jound_moiety="Biotin"   modified_base   Jound_moiety="Biotin"   modified_base   Jound_moiety="Biotin"   modified_base   Jound="LNA-T (Locked Nucleic Acid)"   modified_base   Jound="Locked N	SOURCE SOURCE SOURCE SOURCE SOURCE SURGANISM synthetic construct attificial sequences.  AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U. TITLE Method for sorting single-stranded nucleic acids JOURNAL Patent: WO 3072818-A 55 04-SEP-2003; FEATURES Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers  Inote-"Examon: Spanne" synthetic construct" Adb Xref="taxon: 2560" Anote-"Examon: Capture-Oligonukleotid"  Mod_Lype="unart (Locked Nucleic Acid)" Anote-"LNA-T (Locked N
21 bp DNP  21 bp DNP  34  1. H. and Hoppe, H.  53 04-5EP-2003;  Mi (DE)	modified_base   Modes = Land   Modes = CTHER    Query Match   1.1%   Score 20; DB 1; Length 21; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy   1735 CAAAAAAAAAAAAAA   1  RESULT 163  AX825156/C LOCUS   AX825156   AX82516   AX8

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PAT 11-DEC-2003
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
Boekenkamp, D., Dieck, T.H. and Hoppe, H.U. Method for sorting single-stranded nucleic acids Parent: WO 03072818-A 63 04-SEP-2003; Degussa Bloactives GmbH (DE)
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Method for sorting single-stranded nucleic acids
Patent: WO 03072818-A 64 04-SEP-2003;
Degussa Bioactives GmbH (DE)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db xref="taxon:32630"
/noTe="Beschreibung der kuenstlichen Sequenz:Capture-Oligonukleotid"
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Sequenz:Capture-Oligonukleotid"
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Sequence 64 from Patent W003072818.
AX825166
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                                                                    Location/Qualifiers
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Method for sorting single-stranded nucleic acids
Patent: WO 03072818-A 61 04-SEP-2003;
Degussa Bioactives GmbH (DE)
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Sequenz:Capture-Oligonukleotid"
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/mod_base=OTHER
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/mod_base=OTHER
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/mod_base=OTHER
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mod_base=OTHER
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/mod_base=OTHER
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/mod_base=OTHER
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1.3e+02;
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Sequence 63 from Patent WO03072818.
AX825165
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Sequence 61 from Patent WO03072818.
AX825163. GI:39750892
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Best Local Similarity 100.
Matches 20; Conservative
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AX825165/c
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AX825163/c
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SATISTICAL SEQUENCE

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PD 11-DEC-2001

PP 01-DEC-2001

PP 01-DEC-2001
JP 2001525193-A/2.
synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 21)
Sosnowski, R.G., Butler, W.F., Tu, E., Nerenberg, M.I., Heller, M.J. and
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Mammaglobin, breast cancer secretory protein specific to mamma.
BD224108
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CC Description of Artificial Sequence:Synthetic FH Key Location/Qualifiers 1.21
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JP 2002525098-A/10.
synthetic construct
synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 21)
Watson, M.A. and Fleming, T.P.
Mammaglobin, breast cancer secretory protein specific to mamma
Patent: JP 2002525098-A 10 13-AUG-2002;
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/organism='Artificial Sequence'.
Location/Qualifiers
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    ^2parthetic construct"
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MARK A WATSON, TIMOTHY P FLEMING
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29-SEP-1999 JP 2000572241
29-SEP-1998 US 09/1626
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18-SEP-1997 US 08/933149
MARK WATSON, TIMOTHY P FLEMING
C12N15/09, A61K35/26, A61K39/00, A61K39/00, A61K39/395, A61K39/395,
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unidentified
unclassified.
1 (bases 1 to 21)
Watson, M.A. and Fleming, T.P.
Watson, M.A. and recreted mammary specific breast cancer protein
Patent: JP 201515(559-A 10 02-OCT-2001;
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Mammaglobin, a secreted mammary specific breast cancer protein.
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/mod_base=OTHER
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1.1%; Score 20; DB 1; Le Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 20; Conservative 0; Mismatches 0;
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/organism="unidentified"
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Strandedness: Single;
Topology: Linear;
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02-OCT-2001
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JP 2001516569-A/10.
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RESULT 168 BD080832/c LOCUS

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Query Match 1.1%; Score 19.4; DB 1; Length 21; Best Local Similarity 95.2%; Pred. No. 1.6e+02; Matches 20; Conservative 0; Mismatches 1; Indels
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/noTe="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
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Sequence 13 from Patent WO03072818.
AX825115
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1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
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Sequence 8 from Patent WO03072818.
AX825110
AX825110.1 GI:39750839
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Sequence 1 from Patent WO03072818.
AX825103
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Method for sorting single-stranded nucleic acids
Patent: WO 03072818-A.I. 04-SEP-2003;
Degussa Bioactives GmbH (DE)
Location/Qualifiers
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Method for sorting single-stranded nucleic acids
Patent: WO 03072818-A 21 04-SEP-2003;
Degussa Bloactives GmbH (DE)
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/note="meachreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
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Sequence 17 from Patent WO03072818.
AX825119
XX825119.1 GI:39750848
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Sequence 21 from Patent WO03072818.
AX825123
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/db xref="taxon:32650"
/noTe="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
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/mod_base=OTHER
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/note="LNA-T (Locked Nucleic Acid)"
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/mod_base=OTHER
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                                                           /note="LNA-T (Locked Nucleic Acid)
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/organism="synthetic construct"

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1.1%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels
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Method for sorting single-stranded nucleic acids
Patent: WO 03072818-A 25 04-SEP-2003;
Degussa Bloactives GmbH (DE)
Location/Qualifiers
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                                                                ch 1.1%; Score 19.4; DB 1; 18 Similarity 95.2%; Pred. No. 1.6e+02; 20; Conservative 0; Mismatches 1;
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AX825142
AX825142.1 GI:39750871
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Sequence 25 from Patent WO03072818.
AX825127
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AX825127/c
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AX825142/c
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Method for sorting single-stranded nucleic acids
Patent: WO 03072818-A 24 04-SEP-2003;
Degussa Bioactives GmbH (DE)
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Sequence 24 from Patent WO03072818.
AX825126
                                                                                   'bound_moiety="Biotin"
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1.1%; Score 19.4; DB 1; Length
Best Local Similarity 95.2%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels
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Sequenz:Capture-Oligonukleotid"
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AX825148
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                                                  Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
Method for sorting single-stranded nucleic acids
Patent: WO 03072818-A 40 04-SEP-2003;
Degusea Bloactives GmbH (DE)
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                                                                                                                                                         /organism="synthetic construct"
/mol_type="unassigned DNA"
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/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
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/db xref="taxon:32650"
/noTe="Beschreibung der kuenstlichen
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/mod_base=OTHER
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/mod_base=OTHER
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/mod_base=OTHER
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Length 21;
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Method for sorting single-stranded nucleic acids
Patent: Wo 03072818-A 52 04-SEP-2003;
Degussa Bioactives GmbH (DE)
Location/Qualifiers
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/organism="synthetic construct"
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/db_xref="taxon:32630"
/noTe="Beschreibung der kuenstlichen
             /noTe="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
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/mod_base=OTHER
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/mod_base=OTHER
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'mod_base=OTHER
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/mod_base=OTHER
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'mod_base=OTHER
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/mod_base=OTHER
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95.2%; Pred. No. 1.6e+02;
tive 0; Mismatches 1;
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'db_xref="taxon:32630"
                                                                  'bound_moiety="Biotin"
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Best Local Similarity 95.2
Matches 20, Conservative
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AX825154/c
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Method for sorting single-stranded nucleic acids
Patent: Wo 03072818-A 49 04-SEP-2003;
Degussa Bloactives GmbH (DE)
Location/Qualifiers
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Method for sorting single-stranded nucleic acids
Patent: Wo 03072818-A 50 04-SEP-2003;
Degussa Bloactives GmbH (DE)
Location/Qualifiers
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/note="Beschreibung der kuenstlichen
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1.1%; Score 19.4; DB 1;
Best Local Similarity 95.2%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 1;

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/organism="synthetic construct"
/mol_type="unassigned DNA"

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Sequence 50 from Patent WO03072818.
AX825152
AX825152.1 GI:39750881
                                                                21 bp
Sequence 49 from Patent WO03072818.
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AX825152/c
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PAT 11-DEC-2003

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RESULT 185

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REFERENCE AUTHORS JOURNAL PEATURES

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1. (bases 1 to 24)
Kanbara, H., Okano, K. and Uematsu, K.
ANALYSIS OR DETECTION OF NUCLEIC ACID AND ANALYSER OR INSPECTION
DEVICE OF NUCLEIC ACID
Patent: JP 1997149799-A 1 10-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OC Artificial sequences.
PN JP 1997149799-A/1
PD 10-JUN-1997
PN JP 1997149799-A/1
PD 10-JUN-1997
PF 30-NOV-1995
PI KANBARA HIDEKI, OKANO KAZUNOBU, UEMATSU KAZUMUNE PC C12Q1/68, C07H21/04, C12M1/00, C12N15/09, C12Q1/44, C12Q1/48, PC G1N27/447, G01N37/50;
CC Strandedness: Single;
CC Strandedness: Single;
CC Ctopology: Linear;
FH Key
FH
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                               Boekenkamp, D., Dieck, T.H. and Hoppe, H.U. Method for sorting single-stranded nucleic acids Patent: WO 03072818-A 60 04-SEP-2003; Degussa Bioactives GmbH (DE) Location/Qualifiers
                                                                                                                   1. .21
/organism="synthetic construct"
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Sequenz:Capture-Oligonukleotid"
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E13209/c
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                                                    Length 21;
                                                                                                                                                                                                                                      linear
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                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. 21
/organism="synthetic construct"
/organism="synthetic construct"
/mol_type="unassigned DNA"
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/noTe="Beschreibung der kuenstlichen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="LNA-T (Locked Nucleic Acid)"
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/mod_base=OTHER
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/mod_base=OTHER
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/mod_base=OTHER
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mod_base=OTHER
                                                  Query Match
Best Local Similarity 95.2%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 1;
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Sequence 60 from Patent WO03072818.
AX825162
AX825162.1 GI:39750891
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Sequence 58 from Patent WO03072818.
AX825160
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PAT 27-APR-1998

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Unclassified.
1 (bases 1 to 24)
Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,
Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and
Imbach,J.Louis.
Oligonucleotides having a conserved G4 core sequence
Patent: US 5952490-A 35 14-SEP-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 24)
Hancack,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,
Hancack,J.C., Anderson,K.P., Uickers,T.A., Wyatt,J.R. and
Imbach,J.Louis.
Oligonuclectides having a conserved G4 core sequence
Patent: US 5952490.A 43 14-SEP-1999;
Location/Qualifiers
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                                   th 1.1%; Score 19.4; DB 1; Length 25; Similarity 87.0%; Pred. No. 1.9e+02; 20; Conservative 0; Mismatches 3; Indels
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/organism="unknown"
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/organism="unknown"
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Best Local Similarity 87.5°
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AR074235
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Means and methods for identifying genes and proteins involved in the prevention and/or repair of a replication error Patent: WO 02095071-A 30 28-NOV-2002;
Koninklijke Nederlandse Akademie van Wetenschappen (NL)
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/nofe="sequence to demonstrate the principle of how to detect somatic repeat instability~##N# stands for any number of nucleotides selected from A, C, T or G#"
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/note="sequence to demonstrate the principle of how to
detect somatic repeat instability-##N# stands for any
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 /organism='Artificial sequences'.
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                                                                                                                              Length 24;
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1.1%; Score 19.4; DB 1;
Best Local Similarity 95.2%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 1;
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Sequence 31 from Patent W002095071.
AX708815.1 GI:29564542
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Sequence 30 from Patent WO02095071.
AX708814
                                     1. .24
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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/organism="unknown"
/mol_type="unassigned DNA"
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                                                                                          Unclassified.

1 (bases 1 to 24)

1 (bases 1 to 24)

Hancak, R.C., Anderson, K.P., Bennett, C.Frank., Chiang, M.-Y.,

Brown-Driver, V.L., Ecker, D.J., Vickers, T.A., Wyatt, J.R. and

Imbach, J.Louis.
Oligonucleotides having a conserved G4 core sequence

Patent: US 5922490-A 109 14-SEP-1999;

Location/Qualifiers
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Hancak, R.C., Anderson, K.P., Bennett, C. Frank., Chiang, M.-Y.,
Brown-Driver, V.L., Ecker, D.J., Vickers, T.A., Wyatt, J.R. and
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Hardin, C.C., Brown, B.A. II, Roberts, J.F. and Pelsue, S.C.
Antibodies that selectively bind quadruplex nucleic acids
Patent: US 6001657-A 3 14-DEC-1999;
Location/Qualifiers
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Oligonucleotides having a conserved G4 core sequence
Patent: US 5952490-A 116 14-SEP-1999;
Location/Qualiflers
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Pred. No. 2e+02;
0; Mismatches 3; Indels
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Seguence 116 from patent US 5952490.
AR074308.1 GI:10001063
AR074301
Sequence 109 from patent US 5952490.
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/organism="unknown"
/mol_type="unassigned DNA"
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 3 from patent US 6001657.
AR094555 GI:10021587
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1 (bases 1 to 24)

Draper, K.G., Crooke, S.T., Mirabelli, C.K., Ecker, D.J., Hanecak, R.C.,
Anderson, K.P., Brown-Driver, V.L. and Wyatt, J.R.

Algonucleotide therapies for modulating the effects of herpes viruses
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Pred. No. 2e+02;
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Score 19.2; DB 1; Length 24;
Pred. No. 2e+02;
0; Mismatches 3; Indels
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Sequence 29 from patent US 6551774.
AR307272
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Sequence 52 from patent US 5514577.
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/wol_type="genomic DNA"
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PAT 20-SEP-2000

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Imbach,J.L., Brown-Driver,V.L., Vickers,T.A., Ecker,D.J.,
Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
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Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
                Oligonucleotides having a conserved 94 core sequence Patent: EP 1016715-9 35 05-UJL-2000; ISIS PHARMACEUTICALS INC (US) Location/Qualifiers
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Pred. No. 2e+02;
0; Mismatches 3; Indels
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Patent: EP 1015/15-A 33 05-UTL-2000;
ISIS PHARMCEUTICALS INC (US)
Location/Qualifiers
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Sequence 43 from Patent EP1016715.
AX032597
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/mol_type="unassigned DN?
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West, M.D. Harley, C.B., Weinrich, S.L., Strahl, C.M., McBachern, M.J.,
Shay, J., Wright, W.E., Blackburn, B.H., Kim, N.W. and Vaziri, H.
Diagnostic methods for conditions associated with elevated cellular
levels of telomerase activity
Patent: US 6551774-A 32 22-APR-2003;
Location/Qualifiers
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West,M.D., Harley,C.B., Weinrich,S.L., Strahl,C.M., McEachern,M.J.,
Shay,J., Wright,W.E., Blackburn,E.H., Kim,N.W. and Vaziri,H.
Diagnostic methods for conditions associated with elevated cellular
levels of telomerase activity
Patent: US 6551774-A 34 22-APR-2003;
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Bennett, C.F., Chiang, M.Y., Anderson, K.P., Hanecak, R.C. and
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1.1%; Score 19.2; DB 1;
Best Local Similarity 87.5%; Pred. No. 2e+02;
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Sequence 32 from patent US 6551774.
AR307275.1 GI:31697802
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Sequence 34 from patent US 6551774.
AR307277
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Sequence 35 from Patent BP1016715.
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/wol_type="genomic DNA"
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    /organism="unknown"

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AR307277
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PAT 20-SEP-2000

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PAT 28-AUG-2000

linear

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25 bp | Sequence 34 from patent US 5952490.
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Hanccak, R.C., Anderson, K.P., Bennett, C.Frank., Chiang, M.-Y.,
Brown-Driver, V.L., Ecker, D.J., Vickers, T.A., Wyatt, J.R. and
Imbach, J.Louis.
Oligonucleotides having a conserved G4 core sequence
Patent: US 5952490-A 33 14-SEP-1999;
Location/Qualifiers
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Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
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Patent: EP 1016715-A 116 05-JUL-2000;
ISIS PHARMACEUTICALS INC (US)
Location/Qualifiers
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                                                                                                                                                                             Sequence 116 from Patent EP1016715. AX032670

    .24
/organism="unidentified"
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/db_xref="taxon:32644"

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AR074225
AR074225.1 GI:10000980
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/organism="unknown"
/mol_type="unassigned DNA"
                                                                          1019 TTGGGGATGGGGCTGGGGTTGTGG 1042
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De244664.1 GI:33054634

Sputhetic construct
synthetic construct
synthetic construct
artificial sequences.

I (bases 1 to 25)
Sputhetic primer capable of making the non-specific double strand formation unstable primer. Jp. 2002532063-A 9 02-OCT-2002;
MGGILL UNIVERSITY
OS Artificial Sequence
PN 19 2002532063-A/9
PN 19 2002532063-A/9
PN 07-OCT-1999 JP 2000574722
PR 06-OCT-1999 JP 2000574722
PR 06-OCT-1999 JP 2000574722
PR 06-OCT-1999 JP 2000574722
PR 06-OCT-1999 JP 2000574722
PR 06-OCT-2002
PR 06-OCT-2004
PR 06-OCT-2004
PR 06-OCT-2007
PR 06-OCT-2007
PR 06-OCT-2007
PR 06-OCT-2008
PR 06-OC
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07-OCT-1998 CA 2246623
JERRY PELLETER, MANJULA DAS
CI2NIS/09, CI201/68, C12NIS/00
Description of Artificial Sequence: synthetic oligonucleotide
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Unknown.
Unclassified.
1 (bases 1 to 25)
Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,
Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and
Imbach,J.Louis.
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Location/Qualifiers
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Location/Qualifiers
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    .25
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|mol_type="genomic DNA"
|db_xref="taxon:32630"

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    .25
    /organism="unknown"
    /mol_type="unassigned DNA"

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RESULT 206

RESULT 204

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artificial sequences.
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Best Local Similarity 87.5
Matches 21; Conservative
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Oligonucleotides having a conserved g4 core sequence Patent: EP 1016715-A 33 05-JUL-2000;
ISIS PHARMACEUTICALS INC (US)
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Bennett, C.F., Chiang, M.Y., Anderson, K.P., Hanecak, R.C. and
Myatt, J.R.
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Best Local Similarity 87.5%; Pred. No. 2.1e+02;
Matches 21; Conservative 0; Mismatches 3; Indels
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    /mol_type="unassigned DNA"
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Sequence 503 from Patent WO006508B.
AX042937
AX042937.1 GI:11341545
      AX032587 25 bp
Sequence 33 from Patent EP1016715.
AX032587
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Seguence 34 from Patent BP1016715.
AX032588 GI:10279526
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Ulfendahl,P.J. and Wong,K.C.
Primers for identifying typing or classifying nucleic acids
Patent: WO 0065088-A 503 02-NOV-2000;
Amersham Pharmacia_Blotech AB (SE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ulfendahl, P.J. and Wong, K.C.
Primers for identifying typing or classifying nucleic acids
Patent: WO 0665088-A 680 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)
Amersham Pharmacia Biotech AB (SE)
Location/Qualifiers
1. 25
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/mol_type="unassigned DNA"
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/note="DPA1 Heterozygote Primer Sequence"
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Collingwood, S.P., Moser, H.E., Altmann, K. and Douglas, M.E.
INTERMEDIATES FOR OLIGONUCLECTIDE SYNTHESIS
Patent: WO 9747636-A 4 18-DEC-1997;
CIBA GRIGY AG (CH)
Location/Qualifiers
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                                                                                                                                 1..25
/organism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
/note="16S rRNA Homozygote Primer Sequence"
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Sequence 680 from Patent WO0065088.
AXO43114
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/db_xref="taxon:32644"
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RESULT 211 AR048767/c LOCUS

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Unclassified.

I (bases 1 to 19)

S Cook, P. Dan., Manoharan, M. and Kawasaki, A. Mamoru.

S 2'-O-aminooxy-modified oligonucleotides

AL Patent: US 6127533-A 22 03-OCT-2000;
Location/Qualifiers
                                                                                                                                                                           1.1%; Score 19; DB 1; Length 19;
100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0; Indels
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1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unclassified.
Unclassified.
1 (bases 1 to 19)
Cook, P. Dan., Manoharan, M. and Kawasaki, A. Mamoru.
2'-O-aminooxy-modified oligonucleotides
Patent: US 6127533-A 21 03-OCT-2000;
Location/Qualifiers
                            1 (bases 1 to 19)
Cook, P. Dan., Mancharan, M. and Kawasaki, A. Mamoru. 2'-0-aminoxy-modified oligonucleotides
Patent: US 6127533-A 20 03-OCT-2000;
Location/Qualifiers
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Sequence 21 from patent US 6127533.
AR111947.1 GI:12828795
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/mol_type="unassigned DNA"
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Sequence 22 from patent US 6127533.
AR111948.1 GI:12828796
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/wol_type="unassigned DNA"
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/mol_type="unassigned DNA"
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Best Local Similarity 100.0
Matches 19, Conservative
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AR111947/c
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Leclerc, G. and Martel, R.
Radiolabeled DNA oligonucleotide and method of preparation
Patent: US 5821354-A 1 13-OCT-1998;
Location/Qualifiers
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Query Match
1.1%; Score 19; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1.6e+02;
ative 0; Mismatches 0;
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100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0;
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Sequence 20 from patent US 6127533.
AR111946.1 GI:12828794

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1 (bases 1 to 19)
Leeds,J.M. and Cummins,L.L.
Fluorescence based nuclease assay
Patent: US 6127124-A 1 03-OCT-2000;
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                          Sequence 1 from patent US 5821354.
AR048767
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Best Local Similarity 100.
Matches 19; Conservative
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Best Local Similarity 100.
Matches 19; Conservative
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AR111371/c LOCUS DEFINITION

RESULT 212

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ACCESSION VERSION KEYWORDS SOURCE

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RESULT 213
AR111946/c
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PAT 14-FEB-2001
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Unclassified.
1 (bases 1 to 19)
Cook, P.Dan., Manoharan, M. and Kawasaki, A.Mamoru.
2'-O-aninooxy-modified oligonucleotides
Patent: US 6127533-A 27 03-OCT-2000;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 19)
Cook, P.Dan., Mancharan, M. and Kawasaki, A. Mamoru. 2'-O-aminooxy-medified oligonuclectides
Patent: US 6127533-A 26 03-OCT-2000;
Location/Qualifiers
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1.1%; Score 19; DB 1; L
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0;
                                                                      1.1%; Score 19; DB 1; I
100.0%; Pred. No. 1.6e+02;
cive 0; Mismatches 0;
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1.1%; Score 19; DB 1; L
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0;
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    19 /organism="unknown"
/mol_type="unassigned DNA"

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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 27 from patent US 6127533.
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/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                          Sequence 26 from patent US 6127533.
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Location/Qualifiers
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AR111952.1 GI:12828800
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Best Local Similarity 100.0
Matches 19; Conservative
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Unclassified.
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AR111957/c
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AR111952/c
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Cook, P.Dan., Mancharan, M. and Kawasaki, A.Mamoru. 2'-0-aminoxy-modified oligonucleotides
Patent: US 6127533-A 23 03-CCT-2000;
Location/Qualifiers
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1 (bases 1 to 19)
Cook, P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
2'-O-aminooxy-modified oligonucleotides
Patent: US 6127533-A 25 03-OCT-2000;
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Unclassified.
Unclassified.
1 (bases 1 to 19)
Cook.P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
2'-O-aminooxy-modified oligonuclectides
Patent: US 6127533-A 24 03-OCT-2000;
Location/Qualifiers
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1.1%; Score 19; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0;
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Pred. No. 1.6e+02;
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Matches 19; Conservative 0; Mismatches
                                                                      AR111949 19 bp | C
Sequence 23 from patent US 6127533.
AR111949
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Sequence 24 from patent US 6127533.
AR111950.1 GI:12828798
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Sequence 25 from patent US 6127533.
AR111951
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Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
Aminooxy-modified oligonucleotides and methods for making same
Patent: US 6172209 A 20 09-JAN-2001;
Location/Qualifiers
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Cook.P.Dan., Mancharan, M. and Kawasaki, A.Mamoru. 2'-O-aminooxy-modified oligonucleotides
Patent: US 6127533-A 44 03-OCT-2000;
Location/Qualifiers
   Pred. No. 1.6e+02;
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   Best Local Similarity 100.0%; Pred. No. 1.6
Matches 19; Conservative 0; Mismatches
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Seguence 44 from patent US 6127533.
AR111970
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AR124844

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    /mol_type="unassigned DNA"

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/wol_type="unassigned DNA"
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AR111970/c
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AR124843/c
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Cook, P.Dan., Mancharan, M. and Kawasaki, A.Mamoru. 2'-O-aminoxy-modified oligonuclectides
Patent: US 6127533-A 33 03-OCT-2000;
Location/Qualifiers
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Cook, P.Dan., Mancharan, M. and Kawasaki, A.Mamoru. 2'-O-aminoxy-modified oligonucleotides
Patent: US 6127533-A 34 03-OCT-2000;
Location/Qualifiers
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Cook, P.Dan., Mancharan, M. and Kawasaki, A.Mamoru.
2'-O-aminoxy-modified oligonuclectides
Patent: US 6127533-A 31 03-OCT-2000;
Location/Qualifiers
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AR111960.1 GI:12828808
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Sequence 33 from patent US 6127533.
AR111959
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/mol_type="unassigned DNA"
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Sequence 31 from patent US 6127533.
AR111957
AR111957.1 GI:12828805
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AR111959/c
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1 (Dases I to 19)
Manoharan, M., Cook, P. Dan., Prakash, T. P. and Kawasaki, A. M.
Aminooxy-modified oligomucleotides and methods for making same
Patent: US 6172209-A 24 09-JAN-2001;
Location/Qualifiers
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Manoharan, M., Cook, P. Dan., Prakash, T.P. and Kawasaki, A.M.
Aminooxy-modified oligonucleotides and methods for making same
Patent: US 6172209-A 25 09-JAN-2001;
Location/Qualifiers
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Manoharan, M., Cook, P. Dan., Prakash, T.P. and Kawasaki, A.M.
Aminooxy-modified oligonucleotides and methods for making same
Patent: US 6172209-A 26 09-JAN-2001;
Location/Qualifiers
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tive 0; Mismatches 0; Indels
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AR124849.1 GI:14110210
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/mol_type="unassigned DNA"
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Sequence 24 from patent US 6172209.
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AR124848.1 GI:14110209
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AR124847/c
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AR124849/c
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             1 (bases 1 to 19)
Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
Aminooxy-modified oligonucleotides and methods for making same
Patent: US 6172209-A 21 09-2NN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 19)
Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
Aminooxy-modified oligonucleotides and methods for making same
Patent: US 6172209-A 22 09-DAN-2001;
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Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
Aminooxy-modified oligonucleotides and methods for making same
Patent: US 6172209-A 23 09-0AN-2001;
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1.1%; Score 19; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0;
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Pred. No. 1.6e+02;
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100.0%; Pred. No. ...
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/organism="unknown"
/mol_type="unassigned DNA"
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/organism="unknown"
/wol_type="unassigned DNA"
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/organism="unknown"
/wol_type="unassigned DNA"
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AR124846
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Sequence 22 from patent US 6172209.
AR124845
AR124845.1 GI:14110206
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AR124846/c
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AR124856.1 GI:14110217
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AR124857/c
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AR124867/c
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1 (bases 1 to 19)
Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
Mannooxy-modified oligonucleotides and methods for making same
Patent: US 6172209-A 27 09-JAN-2001;
Location/Qualifiers
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1 (bases 1 to 19)
Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
Manoharan,M., Oligonuclectides and methods for making same
Patent: US 6172209-A 31 09-JAN-2001;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0;
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 27 from patent US 6172209.
AR124850 GI:14110211
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 31 from patent US 6172209.
AR124854 GI:14110215
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DEFINITION Sequence 33 from patent US 6172209.
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AR124850/c
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Manoharan, M., Cook, P. Dan., Prakash, T. P. and Kawasaki, A. M. Aminooxy-modified oligonucleotides and methods for making same Patent: US 6172209-A 34 09-JAN-2001;
Location/Qualifiers
1 (bases 1 to 19)
Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
Aminooxy-modified oligonucleotides and methods for making same
Patent: US 6172209-A 33 09-JAN-2001;
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1 (bases 1 to 19)

Manoharan,M., Cook, P.Dan., Prakash,T.P. and Kawasaki,A.M.
Aminooxy-modified oligonucleotides and methods for making same
Patent: US 6172209-A 44 09-JAN-2001;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.6
Matches 19; Conservative 0; Mismatches
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/organism="unknown"
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Sequence 44 from patent US 6172209.
AR124867
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AR124857
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/organism="unknown"
/mol_type="unassigned DNA"
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PAT 16-MAY-2001

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I (bases 1 to 19)
Cook, P. Dan., Manoharan, M. and Kawasaki, A. Mamoru.
Aminooxy-modified oligonucleotide synthetic intermediates
Patent: US 6194598-A 23 27-FEB-2001;
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1 (bases 1 to 19)
1 (bases 1 to 19)
2 (cok, P.Dan., Manoharan, M. and Kawasaki, A.Mamoru.
Aminoovy-modified oligonuclectide synthetic intermediates
Patent: US 6194598-A 24 27-FEB-2001;
Location/Qualifiers
1 (bases 1 to 19)
Cook, P. Dan., Mancharan, M. and Kawasaki, A. Mamoru.
Aminooxy-modified oligonucleotide synthetic intermediates
Patent: US 6194598-A 22 27-PEB-2001;
Location/Qualifiers
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tive 0; Mismatches 0;
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/wol_type="unassigned DNA"
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/mol_type="unassigned DNA"
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Cook, P. Dan., Mancharan, M. and Kawasaki, A. Mamoru.
Aminooxy-modified oligonucleotide synthetic intermediates
Patent: US 6194598-A 20 27-FEB-2001;
Location/Qualifiers
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1 (bases 1 to 19)

Cook, P. Dan., Manoharan, M. and Kawasaki, A. Mamoru.
Aminooxy-modified oligonucleotide synthetic intermediates
Patent: US 6194598-A 21 27-FEB-2001;
Location/Qualifiers
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Pred. No. 1.6e+02;
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/mol_type="unassigned DNA"
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Best Local Similarity 100.0%; Pred. No. 1.6
Matches 19; Conservative 0; Mismatches
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/mol_type="unassigned DNA"
 0; Mismatches
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AR135291
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AR135292
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AR135293/c
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AR135291/c
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AR135292/c
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[ (bases 1 to 19)
Cook, P. Dan., Mancharan, M. and Kawasaki, A. Mamoru.
Aminooxy-modified oligonucleotide synthetic intermediates
Patent: US 6194598-A 33 27-FEB-2001;
Location/Qualifiers
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Cook, P.Dan., Manoharan, M. and Kawasaki, A.Mamoru.
Aminooxy-modified oligonucleotide synthetic intermediates
Patent: US 6194599-A 31 27-PEB-2001;
                                      Query Match 1.1%; Score 19; DB 1; Length 19; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 19; Conservative 0; Mismatches 0; Indels
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/mol_type="unassigned DNA"
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 33 from patent US 6194598.
AR135304
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Sequence 34 from patent US 6194598.
AR135305
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Sequence 31 from patent US 6194598.
AR135302
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/organism="unknown"
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AR135302/c
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AR135305/c
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AR135304/c
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Cook, P.Dan., Manoharan, M. and Kawasaki, A. Mamoru.
Aminooxy-modified oligonucleotide synthetic intermediates
Patent: US 6194589-A 27 27-EBS-2001;
Location/Qualifiers
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Cook, P.Dan., Manoharan, M. and Kawasaki, A. Mamoru.
Aminoxy-modified oligonucleotide synthetic intermediates
Patent: 18 6194589-A 25 27-FEB-2001;
Location/Qualifiers
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Cook P.Dan., Manoharan, M. and Kawasaki, A. Mamoru.
Aminooxy-modified oligonucleotide synthetic intermediates
Patent: 18 6194598-A 26 27-FEB-2001;
Location/Qualifiers
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100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0;
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Sequence 27 from patent US 6194598.
AR135298.1 GI:14124203
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Sequence 26 from patent US 6194598.
AR135297.1 GI:14124202
                                     Sequence 25 from patent US 6194598.
                                                                                                                                                                                                                                                /organism="unknown"
/mol_type="unassigned DNA"
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/organism="unknown"
/mol_type="unassigned DNA"
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Matches 19; Conservative
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AR135297/c
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AR135298/c
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AR135296/c
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REFERENCE AUTHORS

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1 (bases 1 to 19)
Manoharan, M., Mohan, V. and Boswell, H.
RNA targeted 2'-modified oligonucleotides that are conformationally
preorganized
                                                                                                                                           PAT 08-AUG-2001
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Unclassified.
Unclassified.
1 (bases 1.0.19)
Heller,M.J., Tu,E., Evans,G.A. and Sosnowski,R.G.
Methods for transport in molecular biological analysis and
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100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0; Indels
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diagnostics
Patent: US 6238624-A 16 29-MAY-2001,
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                      Sequence 16 from patent US 6238624.
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/mol_type="unassigned DNA"
 0; Mismatches
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Location/Qualifiers
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Sequence 6 from patent US 6271358.
AR164173 GI:16235162
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BD274438
BD274438.1 GI:33084206
JP 2002543215-A/15.
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BD274438/c
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AR153863/c
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                                                     University
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Unclassified.
Unclassified.
I (bases 1 to 19)
Cook, P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
Aminooxy-modified oligonucleotide synthetic intermediates
Patent: US 6194598-A 44 27-FEB-2001;
Location/Qualifiers
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Unclassified.
Unclassified.
I (bases 1 to 19)
Manoharan,M., Kawasaki,A.M., Cook,P.Dan., Fraser,A.S. and Prakash,T.P.
2'-O-acetamido modified monomers and oligomers
Patent: US 6147200-A 4 14-NOV-2000;
Location/Qualifiers
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100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0; Indels
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Sequence 44 from patent US 6194598.
AR135315.1 GI:14124220
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Sequence 4 from patent US 6147200.
AR141898
AR141898.1 GI:15101414
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Matches 19; Conservative
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Matches 19; Conserv
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RESULT 248 AR135315/c

8 g KEYWORDS SOURCE ORGANISM

source

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REFERENCE AUTHORS

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RESULT 249
AR141898/c
LOCUS
DEFINITION
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REFERENCE AUTHORS

JOURNAL FEATURES

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S B02744401
B027444040
B02744401
B12744401
Synthetic construct
synthetic construct
artificial sequences.

CE 1 (bases 1 to 19)
RS Manoharan, M. and Mohan, V.
Oligonucleotides having A-DNA form and B-DNA form confirmational
geometry
AL Patent: JP 200254315-A 17 17-DEC-2002;
ISTS PRAWACEUTICALS INC
OS Artificial Sequence
PN D 70-2002
PF 03-MAY-1999 US 09/30358
PR 03-MAY-2000 JP 2000615638
PR 03-MAY-1099 US 09/30358
PR 03-MAY-1099 US 09/3
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BD274441
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1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels
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/db_xref="taxon:32630"

    .19
        Organism="synthetic construct"
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        /db_xref="taxon:32630"

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misc_feature (18) . (1)
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BD274440/c
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I (basel 1 to 19)

Mancharan, M. and Mohan, V.
Oligonucleotides having A-DNA form and B-DNA form confirmational geometry

Artificial Sequence
PN JP 2002543215-A 16 17-DEC-2002;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002543215-A/16
PN JP 2002543215
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                                                                                                                                                                                              Parent: JP 2002543215-A 15 17-DEC-2002;

ISIS PHARMACEUTICALS INC

S Artificial Sequence

N JP 2002543215-A/15

PD 17-DEC-2002

PP 03-MAY-2000 JP 2000615638

PR 03-MAY-1999 US 09/303586

PI MUTHIAH MANOHARAN, VENKATRAMAN MOHAN

PC COTALLY/02, A61K48/00, A61P93/00, C12N15/09,
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Oligonucleotides having A-DNA form and B-DNA form confirmational
                              synthetic construct
artificial sequences.
1 (bases 1 to 19)
Manobaran,M. and Mohan,V.
Oligonuclectides having A-DNA form and B-DNA form confirmational
geometry
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100.0%; Pred. No. 1.6e+02;
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    19
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Best Local Similarity 100.0%; Pred. No. ...
Matches 19; Conservative 0; Mismatches
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(17)..(18)
(18)..(19).
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2' - O-MOE linkage
2' - O-MOE linkage
2' - O-MOE linkage
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Oligonucleotide
3' - O-MOE linkage
3' - O-MOE linkage
3' - O-MOE linkage
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JP 2002543215-A/16.
Bynthetic construct
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misc_feature
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BD274439/c
LOCUS
DEFINITION
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SOURCE
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AUTHORS
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AUTHORS
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PAT 20-JUN-2002
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Manoharan,M. and Mohan,V.
Oligonucleotides having A-DNA form and B-DNA form conformational
geometry
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Manoharan,M. and Mohan,V.
Oligonucleotides having A-DNA form and B-DNA form conformational
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100.0%; Pred. No. 1.6e+02;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.6e+02;
iive 0; Mismatches 0; Indels
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                                             Location/Qualifiers
                                                                                                                                  1. .19
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Patent: US 6369209-A 16 09-APR-2002;
Location/Qualifiers
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Sequence 15 from patent US 6369209.
AR205798
AR205798.1 GI:21503472
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Location/Qualifiers
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Sequence 16 from patent US 6369209.
AR205799
AR205799.1 GI:21503473

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2'-modified T linkage
2'-modified T linkage
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AR205799/c
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AR205798/c
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ISIS PHARMACEUTICALS INC
OS Artificial Sequence
NO JF-DEC-2002
PP 03-MAY-2000 JP 200615638
PF 03-MAY-2000 JP 200615638
PF 03-MAY-1999 US 09/303586
PI MOTHIAH MANOHARN VENKATRAMAN MOHAN
PC CO7H21/02,A61K48/00,A61P35/00,A61P35/02,A61P43/00,C12N15/09,CC 011gonuclectide
CC 2'-modified T linkage
                                                                                                                                                                                                                      03-MAY-1999 US 09/303586,
MUTHIAH MANOHARAN, VENKATRAMAN MOHAN
C07H21/02,A61K48/00,A61P35/00,A61P35/02,A61P43/00,C12N15/09,
                                                        artificial sequences.

1 (bases 1 to 19)
Manoharan,M. and Mohan,V.
Oligonucleotides having A-DNA form and B-DNA form confirmational
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synthetic construct
artificial sequences.
1 (bases 1 to 19)
Manoharan,M. and Mohan,V.
Oligonucleotides having A-DNA form and B-DNA form confirmational
geometry
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1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels
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(19). (19).
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                                                                                                                            Patent: JP 2002543215-A 18 17-DEC-2002; ISIS PHARMACEUTICALS INC OS Artificial Sequence PD 17-200543215-A/18 PD 17-DEC-2002 PP 03-MAY-2000 JP 2000615638 PR 03-MAY-1999 US 09/303586.
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 BD274441.1 GI:33084209
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Manoharan, M. and Mohan, V.
Oligonucleotides having A-DNA form and B-DNA form conformational geometry
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Kawasaki, A.M., Fraser, A.S., Manoharan, M., Cook, P.D. and
Prakash, T.P.
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1 (bases 1 to 19)
Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
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                                                                                                                  Patent: US 6369209-A 26 09-APR-2002;
Location/Qualifiers
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Sequence 1 from patent US 6403779.
AR213490.1 GI:23310721
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Sequence 2 from patent US 6403779.
AR213491.1 GI:23310722
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Unclassified.

1 (bases 1 to 19)
Manoharan,M. and Mohan,V.
Oligonucleotides having A-DNA form and B-DNA form conformational geometry
Patent: US 6369209-A 18 09-APR-2002;
Location/Qualifiers
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Manoharan, M. and Mohan, V.
Oligonucleotides having A-DNA form and B-DNA form conformational
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Patent: US 6369209-A 17 09-APR-2002;
Location/Qualifiers
1. .19
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Best Local Similarity 100.0%; Pred. No. 1.6
Matches 19; Conservative 0; Mismatches
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Sequence 26 from patent US 6369209.
AR205809 1 GI:21503486
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Sequence 17 from patent US 6369209.
AR205800
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AR205801.1 GI:21503476
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RESULT 260

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Kawasaki, A.M., Fraser, A.S., Mancharan, M., Cook, P.D. and
Prakash, T.P.
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Kawasaki, A.M., Fraser, A.S., Manoharan, M., Cook, P.D. and Prakash, T.P.
Regioselective synthesis of 2'-0-modified nucleosides Patent: US 6403799-A 7 11-UNN-2002;
Location/Qualifiers
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Kawasaki, A.M., Fraser, A.S., Manoharan, M., Cook, P.D. and
                                                                         Regioselective synthesis of 2'-0-modified nucleosides Patent: US 6403779-A 5 11-JUN-2002; Location/Qualifiers
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1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels
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Sequence 7 from patent US 6403779.
AR213496
AR213496.1 GI:23310727
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Sequence 6 from patent US 6403779.
AR213495. GI:23310726
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                                                           Prakash, T.P.
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AR213496/c
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I (bases 1 to 19)
Kawaski,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
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Kawasaki, A.M., Fraser, A.S., Manoharan, M., Cook, P.D. and
Prakash, T.P.
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Sequence 5 from patent US 6403779.
AR213494.1 GI:23310725
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Sequence 3 from patent US 6403779.
AR213492. GI:23310723
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Sequence 4 from patent US 6403779.
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AR213493.1 GI:23310724
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            1 (bases 1 to 19)

Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.

Regioselective synthesis of 2'-O-modified nucleosides Patent: US 6403779-A 14 11-JUN-2002;

Location/Qualifiers
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1 (bases 1 to 19)
Kawasaki, A.M., Fraser, A.S., Manoharan, M., Cook, P.D. and Prakash, T.P.
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Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
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Regioselective synthesis of 2'-O-modified nucleosides
Patent: 18 6403779-A 25 11-JUN-2002;
Location/Qualifiers
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Sequence 15 from patent US 6403779.
AR213503
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AR213512.1 GI:23310743
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AR213503/c
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Kawasaki, A.M., Fraser, A.S., Manoharan, M., Cook, P.D. and
Prakash, T.P.
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Kawasaki, A.M., Fraser, A.S., Manoharan, M., Cook, P.D. and
                                                                                                                                                                                                                                                                                                    Prakash,T.P.
Regioselective synthesis of 2'-0-modified nucleosides
Patent: US 64037/9-A 8 11-UUN-2002;
Location/Qualifiers
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Patent: US 6403779-A 12 11-JUN-2002;
Location/Qualifiers
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AR213501
AR213501.1 GI:23310732
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Ravikumar, V.T., Manoharan, M., Capaldi, D.C., Krotz, A., Cole, D.L. and
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Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels
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Patent: US 6465628-A 1 15-OCT-2002;
Location/Qualifiers
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Kurz, M., Lohse, P. and Wagner, R.

Peptide acceptor ligation methods

Patent: US 6429300-A 25 06-AUG-2002,
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Sequence 10 from patent US 6562960.
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Sequence 25 from patent US 6429300.
AR222465
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Sequence 1 from patent US 6465628.
AR237463.
AR237463.1 GI:27282213
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Unclassified.
1 (bases 1 to 19)
Manoharan,M., Cook,P.D., Prakash,T.P. and Mohan,V.
Guanidinium functionalized nucleotides and precursors thereof
Patent: US 6593466-A 4 15-JUL-2003;
Location/Qualifiers
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Manoharan, M., Cook, P.D., Prakash, T.P. and Mohan, V.
Guanidinium functionalized nucleotides and precursors thereof
Patent: US 6593466.A 3 15-UUL-2003;
Location/Qualifiers
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Baxter,A.D., Collingwood,S.P., Douglas,M.E. and Taylor,R.J.
Oligonuclectide analogues
Patent: US 6562960-A 10 13-MAY-2003;
Location/Qualifiers
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100.0%; Pred. No. 1.6e+02;
live 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.6e+02;
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Seguence 3 from patent US 6593466.
AR359804
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AR359805.1 GI:33766603
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Crooke, S.T., Lima, W.F., Wu, H. and Monoharan, M.
Human Rnase H1 and Oligonucleotide compositions thereof
Patent: NGS 61742-A 18 09-SEP-2003;
Location/Qualifiers
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Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
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Patent: US 6624294-A 1 23-SEP-2003;
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1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.6e+02;
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                             Score 19; DB 1; Length 19;
Pred. No. 1.6e+02;
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Sequence 2 from patent US 6624294.
AR403602
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AR399178/c
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AR403601/c
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AR403602/c
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                                                                                                                                               1 (bases 1 to 19)
Manoharan, M., Cook, P.D., Prakash, T.P. and Mohan, V.
Guanidinium functionalized nucleotides and precursors thereof
Patent: US 6593466.A 5 15-UUL-2003;
Location/Qualifiers
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Collingwood, S.P., Moser, H.E., Altmann, K.-H. and Douglas, M.E. Intermediates for Oligonucleotide synthesis
Patent: 18 6329519-A 4 11-DEC-2001;
Location/Qualifiers
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Crooke,S.T., Lima,W.F., Wu,H. and Monoharan,M.
Human Rnase H1 and oligonuclectide compositions thereof
Patent: US 661742-A 17 09-SEP-2003;
Location/Qualifiers
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100.0%; Pred. No. 1.6e+02;
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Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0;
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                        Sequence 5 from patent US 6593466. AR359806

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/mol_type="genomic DNA"
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AR399177/c
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Unclassified.
1 (bases 1 to 19)
Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
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Kawasaki, A.M., Fraser, A.S., Manoharan, M., Cook, P.D. and
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Regioselective synthesis of 2'-O-modified nucleosides
Patent: US 624294-A 6 23-SEP-2003;
Location/Qualifiers
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Regioselective synthesis of 2'-O-modified nucleosides
Patent: US 6624294-A 5 23-SEP-2003;
Location/Qualifiers
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100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0; Indels
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1.1%; Score 19; DB 1; Length 19; 100.0%; Pred. No. 1.6e+02; tive 0; Mismatches 0; Indels
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Sequence 5 from patent US 6624294.
AR403605.
AR403605.1 GI:40151191
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Sequence 6 from patent US 6624294.
AR403606
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Sequence 7 from patent US 6624294.
AR403607.1 GI:40151193
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/mol_type="genomic DNA"
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Best Local Similarity 100.0°
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                 Best Local Similarity 100.0
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AR403607/c
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AR403605/c
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Unclassified.
1 (Dases 1 to 19)
Kawaseki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
Regioselective synthesis of 2'-O-modified nucleosides
Patent: US 6624294-A 4 23-SEP-2003;
Location/Qualifiers
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Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
                                                                           1 (bases 1 to 19)
Kawasaki, A.M., Fraser, A.S., Manoharan, M., Cook, P.D. and
Prakash, T.P.
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Patent: US 6624294-A 3 23-SEP-2003;
Location/Qualifiers
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Patent: US 6624294-A 2 23-SEP-2003;
Location/Qualifiers
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AR403604
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Sequence 3 from patent US 6624294.
AR403603
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/mol_type="genomic DNA"

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    /organism="unknown"
    /mol_type="genomic DNA"

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1 (bases 1 to 19)
Kawasaki, A.M., Fraser, A.S., Manoharan, M., Cook, P.D. and Prakash, T.P.
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1 (bases 1 to 19)
Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
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Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0;
 Pred. No. 1.6e+02;
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Sequence 25 from patent US 6624294.
AR401623. GI:40151209
Best Local Similarity 100.0%; Pred. No. 1.6
Matches 19; Conservative 0; Mismatches
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AR403613/c
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                                                          1 (bases 1 to 19)
Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
Regioselective synthesis of 2'-0-modified nucleosides
Patent: US 6624294-A 7 23-SEP-2003;
Location/Qualifiers
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1 (bases 1 to 19)
Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
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1 (bases 1 to 19)
Kawasaki, A.M., Fraser, A.S., Manoharan, M., Cook, P.D. and Prakash, T.P.
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Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0;
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Sequence 12 from patent US 6624294.
AR403612
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Sequence 8 from patent US 6624294.
AR403608
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PAT 06-FEB-2002

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Genman, C.F.

Self-assembling microelectronic integration system capable of designating self address, compartment device, mechanism, method and operation for molecular biological analysis and diagnosis patent: JP 200125193-A 16 11-DEC-2001;

NANOGEN INC

Sold Artificial Sequence
PN JP 2001525193-A/16

PD 11-DEC-2001

PP 01-DEC-1999 JP 200524303

PR 05-DEC-1997 US

O8/986065

PR NO-NALD G SOSNOWSKI, WILLIAM F BUTLER, EUGENE TU, MICHAEL I PI

NERENBERG,
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Self-assembling microelectronic integration system capable of designating self address, compartment device, mechanism, method and operation for molecular biological analysis and diagnosis.
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synthetic construct
artificial sequences.
1 (bases 1 to 19)
Sosnowski,R.G., Butler,W.F., Tu,E., Nerenberg,M.I., Heller,M.J. and
                                                                                                                                                                                                                                                                                     Bickel, R., Ehricht, R., Ellinger, T., Ermantraut, E., Kaiser, T., Schulz, T. and Wagner, G.
Method for qualitative and/or quantitative detecting of molecular interactions on probe arrays
Patent: WO 0202810-A 31 10-JAN-2002;
Clondiag Chip Technologies GmbH (DE)
Location/Qualifiers
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100.0%; Pred. No. 1.6e+02;
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PC C12Q1/68, C12N15/09, C12N15/00
CC Description of Artificial Sequence: Amine
conjugate to provide
CC reactivity
CC with dyes Location/Qualifiers
FF Key Location, Public Reserved
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/db xref="texon:32630"
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Sequence 33 from Patent W00202810.
AX349249
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BD087505.1 GI:22633115
JP 2001525193-A/16.
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AX349249/c
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BD087505/c
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Cook, P.D., Manoharan, M., Maier, M. and An, H.
C3'-methylene hydrogen phosphonate oligomers and related compounds
Patent: US 6639061-A 1 28-OCT-2003;
Location/Qualifiers
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                                              I Chaeses I to 19)

Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.

Regioselective synthesis of 2'-0-modified nucleosides
Patent: US 6624294-A 25 23-SEP-2003;

Location/Qualifiers
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1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels
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Manoharan M., Cook, P.D. and Guinosso, C.J.
Modified oligonucleotides
Patent: US 6653458-A 6 25-NOV-2003;
Location/Qualifiers
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Sequence 1 from patent US 6639061.
AR412338.1 GI:40167448
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Sequence 6 from patent US 6653458.
AR432616
AR432616.1 GI:40195149
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/organism="unknown"
/mol_type="genomic DNA"
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/organism="unknown"
/mol_type="genomic DNA"
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/mol_type="genomic DNA"
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Best Local Similarity 100.0
Matches 19; Conservative
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AR432616/c
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AR412338/c
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AR140279/c
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AR140557/c
LOCUS
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1 (bases 1 to 19)

Cohen,D., Blumenfeld,M., Chumakov,I. and Bougueleret,L.

Prostatic cancer gene
Patent: JP 2002516657-A 489 11-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OS Homo sapiens (human)
PN JP 2002516657-A/489
PD 11-UUN-2002
PF 22-DEC-1998 JP 200525562
PF 22-DEC-1999 US 60/099658 PI
DANIEL COHEN, MARTA BLUMENPELD, ILYA CHUMAKOV, LYDIE BOUGUELERET PC
C12N1/19.
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CC Dotential microsequencing oligo for 4-4-187.mis2 FH Key Location/Qualifiers
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Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
/organism='Artificial Sequence'. Location/Qualifiers
                                                                                                                                                                                                                                                                              linear
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                                                                                                           Length 19;
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1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels

    19
    forganism="synthetic construct"
|mol type="genomic DNA"
|db_xrefe="taxon:32630"

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Sequence 32 from patent US 6207417.
AR139960
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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JP 2002516657-A/489.
Homo sapiens (human)
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AR139960/c
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1 (bases 1 to 20)

Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.

Method for enhancing the efficiency of gene transfer with stem cell factor (SCF) polypeptide

Patent: US 6207454-A 32 27-MAR-2001;
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1 (bases 1 to 20)
2sebo, K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
Stem cell factor and compositions
Patent: US 6207802-A 32 27-MAR-2001;
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Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1.7e+02;
tive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0;
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DNA encoding stem cell factor
Patent: US 6207417-A 32 27-MAR-2001;
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 32 from patent US 6207802.
AR140557
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/mol_type="unassigned DNA"

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    /organism="unknown"
    /mol_type="unassigned DNA"

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Best Local Similarity 100.
Matches 19; Conservative
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PAT 11-DEC-2003
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/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
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/mol_type="unassigned DNA"
/db_txrefe="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
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/mod_base=OTHER
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/mod_base=OTHER
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/mod_base=OTHER
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/mod_base=OTHER
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/mod_base=OTHER
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/mod_base=OTHER
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Sequence 19 from Patent W003072818.
AX825121. GI:39750850
                                                                                                'bound_moiety="Biotin"
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Brenner,S.
Massively parallel sequencing of sorted polynucleotides
Patent: US 5695334-A 23 09-DEC-1997;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels
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Compositions for sorting polynucleotides
Patent: US 6140489-A 23 31-0CT-2000,
Location/Qualifiers
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Sequence 23 from patent US 5695934.
184433
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Sequence 18 from Patent WO03072818.
AX825120
                                   AR118155 21 bp
Sequence 23 from patent US 6140489.
AR118155
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Method for sorting single-stranded nucleic acids
Patent: WO 03072818-A 22 04-SEP-2003;
Degussa Bloactives GmbH (DE)
Location/Qualifiers
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Sequenz:Capture-Oligonukleotid"
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Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0;
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Sequence 23 from Patent WO03072818.
AX825125
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Method for sorting single-stranded nucleic acids
Patent: WO 03072818-A 20 04-SEP-2003;
Degussa Bloactives GmbH (DE)
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Sequenz:Capture-Oligonukleotid"
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Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0;
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Sequence 22 from Patent W003072818.
AX825124. GI:39750853
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Method for sorting single-stranded nucleic acids
Patent: WO 03072818-A 27 04-SEP-2003;
Degussa Bioactives GmbH (DE)
Location/Qualifiers
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Sequence 28 from Patent WO03072818.
AX825130
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Sequence 27 from Patent WO03072818.
AX825129
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              19 CAAAAAAAAAAAAAA 1
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AX825129/c
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AX825130/c
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/db xref="taxon:32650"
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Sequenz:Capture-Oligonukleotid"
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18
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/mod_base=OTHER
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/mod_base=OTHER
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/mod_base=OTHER
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Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels
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Sequenz:Capture-Oligonukleotid"
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Sequence 57 from Patent W003072818.
AX825159.
AX825159.1 GI:39750888
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Sequence 59 from Patent WO03072818.
AX825161. GI:39750890
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AX825159/c
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AX825161/c
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/organism="synthetic construct"
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/note="Beschreibung der kuenstlichen
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/nore="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
                                                                                                              /note="LNA-T (Locked Nucleic Acid)"
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|mod_base=OTHER
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/mod_base=OTHER
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                                                                                  'bound_moiety="Biotin"
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artificial sequences.

I (bases 1 to 23)

S Hartwich, G. and Heller, A.

Batchich, G. and Heller, A.

Method of electrochemically detecting nucleic acid

Patent: JP 2002532386-A 16 02-0CT-2002;

FRIZ BIOCHEM GNBH

OS Artificial Sequence

PD 02-0CT-2002

PP 19-NOV-1999 JP 2000583928

PR 23-NOV-1999 BD 198 53 957.6,29-APR-1999 DE 199 21 940.0 PI

GERHARD HARTWICH, ADAM HELLER

PC 1077421/00, C077421/02, C077421/04, C12N15/09, C12Q1/68, G01N27/12, PC
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1 (bases 1 to 24)
Vaisberg, E.A., Adams, C.L., Sabry, J.H. and Crompton, A.M.
Database system including computer code for predictive cellular bioinformatics
Patent: US 6651008-A 6 18-NOV-2003;
                                                                                                                Gaps
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                                                                         1.1%; Score 19; DB 1; Length 22;
100.0%; Pred. No. 1.9e+02;
tive 0; Mismatches 0; Indels
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    ...23
    forganism="synthetic construct"
|mol_type="genomic DNA"
|db_xref="taxon:32630"

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Sequence 6 from patent US 6651008.
AR431312.1 GI:40193280
/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"
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JP 2002532386-A/16.
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synthetic construct
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 22)

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UNITECH CO LID
OS Homo sapiens (human)
N JP 2001333800-A/1
PD 04-DEC-2001
PP 30-MAY-2000 JP 2000160324
PI KARRI SHIMADA
PC C12Q1/68,C12N15/09
CC Method of comparison and detection of RNA amount and DNA C
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KAORI SHIMADA
C12Q1/68,C12N15/09,G01N33/50,C12N15/00
Method of comparison and detection of RNA amount
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Location/Qualifiers
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100.0%; Pred. No. 1.8e+02;
tive 0; Mismatches 0; Indels
                                                  Boekenkamp, D., Dieck, T.H. and Hoppe, H.U. Method for sorting single-stranded nucleic acids Patent: WO 03072818-A 59 04-SEP-2003; Degussa Bioactives GmbH (DE) Location/Qualifiers
                                                                                                                                                                 /organism="synthetic construct"
/mol type="unassigned DNA"
/db xref="taxon:32630"
/noTe="Beschreibung der kuenstlichen
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/mod_base=OTHER
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/mod_base=OTHER
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/mod_base=OTHER
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/mod_base=OTHER
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/mod_base=OTHER
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/mod_base=OTHER
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               artificial sequences.
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                                                      AUTHORS
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Datent: JP 2002191369-A 8 09-JUL-2002;
TOYO KOHAN CO LTD, KOJIRO TAKAHASHI
OS Artificial Sequence
PN JP 2002191369-A/8
PD 09-JUL-2002
PP 27-DEC-2000
PP 200-200
PP 20
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Nucleic acid molecules and other molecules associated with soybean
cyst nematode resistance
Patent: WO 0151627-A 686 19-JUL-2001;
MONSANTO COMPANY (US)
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/db_xref="taxon:3847"
/note="Seq ID:
318013_region_A3__151839__17_Reverse_Primer_Seq"
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Location/Qualifiers
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Pred. No. 2.2e+02;
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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100.0%; Pred. No. a...
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Sequence 686 from Patent WO0151627.
AX196979
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Sequence 2 from patent.US 6651008.
AR431308
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artificial sequences.
1 (base 1 to 24)
Tanga,M., Okamura,H. and Takahashi,K.
Method for carrying out thermal cycle of PCR using DNA-immobilized
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Support for immobilizing nucleotide and process for producing
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1 (bases 1 to 24)
Tanga,M., Okamura,H., Takagi,K. and Takahashi,K.
Support for immobilizing nucleotide and process for producing the Patent: WO 0153355-A 1 02-AUG-2001;
TOYO KOHAN CO LTD,MICHIFUMI TANGA,HIROSHI OKAMURA,KENICHI TAKAGI,KOJIRO TAKAHASHI
                                                                                                                                                                                Gaps
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27-JAN-2000 JP 00P 019301
MICHIFUMI TANGA, HIROSHI OKAMURA, KENICHI TAKAGI, KOJIRO
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100.0%; Pred. No. 2.1e+02;
ative 0; Mismatches 0;
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Pred. No. 2.1e+02;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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                               1. .24
/organism="unknown"
/mol_type="genomic DNA"
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WO 0155365-A/1
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BD161931.1 GI:27867689
JP 2002191369-A/8.
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WO 0155365-A/1.
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PP 02-AU
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BD097127/c
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Zsebo, K.M., Bosselman, R.A., Suggs, S.V. and Martin, F.H.
Zsebo, K.M., Bosselman, R.A., Suggs, S.V. and Martin, F.H.
Eachod for enhancing the efficiency of gene transfer with stem cell
factor (SCF) polypeptide
Patent: US 6207454-A 33 27-MAR-2001;
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Unclassified.
1 (bases 1 to 20)
2 sebo. K.W. Bosselman, R.A., Suggs, S.V. and Martin, F.H.
DNA encoding stem cell factor
Patent: US 6207417-A 34 27-MAR-2001;
Location/Qualifiers
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Matches 19; Conservative 0; Mismatches 1; Indels
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Sequence 34 from patent US 6207454.
AR140281
AR140281.1 GI:14482777
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Sequence 34 from patent US 6207417.
AR139962
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/organism="unknown"
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/organism="unknown"
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AR139962/c
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AR140280/c
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AR140281/c
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                          Unclassified.
1 (bases 1 to 24)
1 (bases 1 to 24)
Vaisberg E.A., Adams, C.L., Sabry, J.H. and Crompton, A.M.
Vaisberg Es.A., Adams, C.L., Sabry, J.H. and Crompton, A.M.
Database system including computer code for predictive cellular bioinformatics
Patent: US 6651008-A 2 18-NOV-2003;
Location/Qualifiers
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Primers for identifying typing or classifying nucleic acids
Patent: WO 0065088-A 685 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)
Location/Qualifiers
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1 (bases 1 to 20)
2sebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
DNA encoding stem cell factor
Patent: US 6207417-A 33 27-MAR-2001;
                                                                                                                                                                                                            Length 24;
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/roganism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
/note="DPA1 Heterozygote Primer Sequence"
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90.9%; Pred. No. 2.2e+02;
tive 0; Mismatches 2;
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Sequence 33 from patent US 6207417.
AR139961
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/mol_type="unassigned DNA"
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/organism="unknown"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                       Protection of partial complementary nucleic acid fragment using a electroconductive chip and intercalator Patent: US 6399305-A 5 04-JUN-2002; Location/Qualifiers
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Patent: WO 0100669-A 57 04-JAN-2001;
GENSET (FR)
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Makino,Y., Abe,Y., Takagi,M., Takenaka,S., Yamashita,K.
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    /organism="synthetic" construct"
    /mol_type="unassigned DNA"
    /db xref="taxon:32630"
    /noTe="oligonucleotide BAP28polyTcourt"

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/organism="unknown"
/wol_type="unassigned DNA"
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Sequence 5 from patent US 6399305.
AR211367.1 GI:21514670
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Sequence 57 from Patent W00100669.
AX067205. GI:12544870
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Sequence 5 from Patent EP1065278.
AX136903
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Matches 19; Conserva
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AX067205/c
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AR211367/c
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        Unclassified.
Unclassified.
1 (bases 1 to 20)
Zeebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
Zeebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
Method for enhancing the effciency of gene transfer with stem cell
factor (SCF) polypeptide
Patent: US 6207454-A 34 27-MAR-2001;
Location/Qualifiers
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(Dassel to 20)
Zeebo, K.M.; Bosselman, R.A., Suggs, S.V. and Martin, F.H. Stem cell factor and compositions
Patent: US 6207802-A 33 27-MAR-2001;
Location/Qualifiers
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Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
Stem cell factor and compositions
Patent: 18 6207802-A 34 27-MAR-2001;
Location/Qualifiers
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1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels
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AR140559
AR140559.1 GI:14483055
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AR140558.1 GI:14483054
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Method for sorting single-stranded nucleic acids
Patent: Wo 03072818-A 3 04-SEP-2003;
Degussa Bioactives GmbH (DE)
Location/Qualifiers
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Sequenz:Capture-Oligonukleotid"
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/mod_base=OTHER
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/mod_base=OTHER
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/mod_base=OTHER
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/mod_base=OTHER
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/mod_base=OTHER
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/mod_base=OTHER
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   Sequenz:Capture-Oligonukleotid"
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Sequence 3 from Patent WO03072818.
AX825105
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                                                                Yamashita, K.
Detection of partly complementary nucleic acid fragment
Patent: EP 1065278-A 5 03 JAN-2001;
FUJI PHOTO FILM CO., LID. (JP)
Location/Qualifiers
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                                                  Makino, Y., Abe, Y., Ogawa, M., Takagi, M., Takenaka, S. and
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Garner, H.R., Wren, J.D., Minna, J.D. and Fondon, J.W. III.
Polymorphic repeats in human genes
Patent: US 6472154-A 119 29-OCT-2002;
Location/Qualifiers
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Method for sorting single-stranded nucleic acids
Patent: WO 03072818-A 2 04-SEP-2003,
Degussa Bioactives GmbH (DE)
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/noTe="sample nucleic acid fragment"
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Organism="synthetic construct"
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Sequence 119 from patent US 6472154.
AR241831. GI:27287643
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Sequence 2 from Patent WO03072818.
AX825104
AX825104.1 GI:39750833
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Boekenkamp, D., Dieck, T.H. and Hoppe, H.U. Method for sorting single-stranded nucleic acids Patent: WO 03072818.A 5 04-SEP-2003; Degussa Bioactives GmbH (DE)
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Method for sorting single-stranded nucleic acids
Patent: WO 03072818-A 6 04-SEP-2003;
Degussa Bioactives GmbH (DE)
Location/Qualifiers
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Sequenz:Capture-Oligonukleotid"
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Sequence 6 from Patent WO03072818.
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Matches 19; Conservative 0; Mismatches 1;
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Sequence 7 from Patent WO03072818.
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Method for sorting single-stranded nucleic acids
Patent: WO 03072818-A 15 04-SEP-2003;
Degussa Bioactives GmbH (DE)
Location/Qualifiers
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Method for sorting single-stranded nucleic acids
Patent: WO 03072818-A 16 04-SEP-2003;
Degussa Bioactives GmbH (DE)
Location/Qualifiers
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95.0%; Pred. No. 2.1e+02;
tive 0; Mismatches 1;
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Sequence 38 from Patent WO03072818.
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Best Local Similarity 95.0°
Matches 19; Conservative
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Method for sorting single-stranded nucleic acids
Patent: Wo 03072818-A 37 04-SEP-2003;
Degussa Bloactives GmbH (DE)
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
                                                                                                                                   /note="LNA-T (Locked Nucleic Acid)"
/nod_base=OTHER
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'mod_base=OTHER
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/mod_base=OTHER
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/mod_base=OTHER
                                           /note="LNA-T (Locked Nucleic Acid)"
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mod_base=OTHER
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/mod_base=OTHER
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/mod_base=OTHER
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                  bound_moiety="Biotin"
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Method for sorting single-stranded nucleic acids
Patent: Wo 03072818-A 48 04-SEP-2003;
Degussa Bioactives GmbH (DE)
Location/Qualifiers
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   /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
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/mod_base=OTHER
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/mod_base=OTHER
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1.0%; Score 18.4; DB 1;
Best Local Similarity 95.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 1;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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AX825150
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AX478523/c
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Method for sorting single-stranded nucleic acids Patent: WO 03073818-A 3 04-SEP-2003; Degussa Bioactives GmbH (DE)
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/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
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/mod_base=OTHER
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/mod_base=OTHER
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/mod_base=OTHER
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1.0%; Score 18.4; DB 1;
Best Local Similarity 95.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 1;
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Sequence 47 from Patent WO03072818.
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BD24665.1 GI:33054635

BD24665.1 GI:33054635

Synthetic construct

SM synthetic construct

artificial sequences.

E 1 (bases 1 to 23)

S Pelletier, J. and Das, M.

Oligonuclectide primer capable of making the non-specific double strand formation unstable

L patent: JP 2002532063-A 10 02-OCT-2002;

MCGILL UNIVERSITY

OS Artificial Sequence

PN JP 2002532063-A/10

PD 02-OCT-2002

PP 06-OCT-1999 JP 2000574722

PR 07-OCT-1999 CA 2246623
                                    23 bp DNA linear PAT 17-JUL-2003 Oligonucleotide primer capable of making the non-specific double strand formation unstable.
                                                                                                                                                                                                                                                                                                                                                                                                                          JERRY PELLETIER, MANJULA DAS
C12N15/09,C12Q1/68,C12N15/00
Description of Artificial Sequence: synthetic oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pignot, M.
Detection system for analyzing molecular interactions, production and utilization thereof and utilization thereof Patent: WO 0071749-A 17 30-NOV-2000;
Patent: WO 0071749-A 17 30-NOV-2000;
Aventis Research & Technology GmbH & Co. KG. (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boekenkamp, D., Hoppe, H.U., Burgstaller, P., Konz, D., Woelk, U. and
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Best Local Similarity 86.4%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 3;
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modified base (8)
modified base (18).
Location/Qualifiers
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synthetic construct
artificial sequences.
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N = inosine
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Best Local Similarity
Matches 19; Conserv
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                   RESULT 349
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AX053001/c
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 PAT 12-AUG-2002
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JP 2005532063-A/8
02-0CT-2003
06-0CT-1999 JP 2000574722
07-0CT-1998 CA 2246623
JERRY PELLETIER, MANJULA DAS
C12N15/09, C12Q1/68, C12N15/00
Description of Artificial Sequence: synthetic oligonucleotide
N = 3-Nitropyrrole
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synthetic construct
synthetic construct
synthetic construct
artificial sequences.
1 (basea 1 to 23)
Pelletier,J. and Das,M.
Oligonucleotide primer capable of making the non-specific double
Barrand formation unstable
Patent: JP 2002532063-A 8 02-OCT-2002;
MCGILL UNIVERSITY
                                                                                                                                                            Presnell, S.R., Xu, W., Novak, J.B., Whitmore, T.E. and Grant, F.J. Cytokine receptor zcytor19
Patent: WO 0244209-A 27 06-JUN-2002;
ZymoGenetics, Inc. (US)
Location/Qualifiers
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   linear
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/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Oligonucleotide primer ZC37681"
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/organism="synthetic construct"
/mol_type="genomic DNA"
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22 bp
Sequence 27 from Patent WO0244209.
AX478523
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JP 2002532063-A/8.
                                                                                                                               artificial sequences.
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Matches 19; Conserv
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VERSION KEYWORDS SOURCE ORGANISM

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PAT 12-JAN-2001

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PAT 29-SEP-1999
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                                                                                                  OS Unidentified

PN JP 199196874-A/9

PN JP 199196874-A/9

PD 27-JUL-1999

PF 14-JAN-1998 JP 1998005399

PR HIDEKI KAMIBARA, SENSHU UEMATSU

PC C12N15/09, C12Q1/69, G01N27/447, C12N15/00, G01N27/26 CC

Strandedness: Single;

CC Topology: Linear;

FH Key Location/Qualifiers

FT Source /organism='Unidentified'.
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Chatelain, F. and Kumarev, V.
Process for preparing polynucleotides on a solid support in tightly packed bed Patent: US 5869641-A 12 09-FEB-1999;
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/organism='Unidentified'.
Location/Qualifiers
            1 (bases 1 to 20)
Hideki, K. and Senshu, U.
Method for analyzing DNA fragment
Matchod for analyzing DNA fragment
Patent: JP 1999196874-A 9 27-JUL-1999;
HITACHI LTD
OS Unidentified
PN JP 1999196874-A/9
PD 27-JUL-1999
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1 (bases 1 to 18)
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AR034896/c
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AR034899
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                                                                                                                                                                                                                                                                                  1 (bases 1 to 19)
Croteau, R. Bruce., Lupien, S. Lee. and Karp, F.
Recombinant materials and methods for the production of limonene hydroxylases
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1 (bases 1 to 19)

Croteau, R.Bruce., Lupien, S.Lee. and Karp, F.

Recombinant materials and methods for production of limonene
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1.0%; Score 18.2; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 2e+02;
Matches 18; Conservative 1; Mismatches 0; Indels
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1.0%; Score 18.2; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 2e+02;
Matches 18; Conservative 1; Mismatches 0; Indels
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Patent: US 6194185-A 18 27-FEB-2001;
Location/Qualifiers
1. .19
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                        Patent: US 6083731-A 18 04-JUL-2000;
Location/Qualifiers
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AR134802
AR134802.1 GI:14123707
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AR102020
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                                      20 ACAAGAAAAAAAAAAAA 1
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E28098.1 GI:13018323
JP 1999196874-A/9.
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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E28098/c LOCUS

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18 bp DNA linear PAT 18-JUN-2001
Method for labeling oligonucleotide and utilization thereof.
E28535
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Kenichi, H., Hiroshi, Y. and Masahide, N.
Method for labeling oligonucleotide and utilization thereof
Patent: JP 1999075880-A 2 23.MAR-1999;
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Location/Qualifiers
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Pred. No. 2e+02;
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Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                    1 (bases 1 to 18)
Keeling,P. and Guan,H.
Starch encapsulation
Patent: US 6107060-A 30 22-AUG-2000;
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                                                                                18 bp i Sequence 30 from patent US 6107060.
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    .18
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    /mol_type="genomic DNA"
    /db_xref="taxon:32644"

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De Rose,R., Douce,R., Duval,M., Job,C. and Job,D.
Seed specific blotinylated protein, SBP65, from leguminous plants
Patent: US 5837820-A 317-NOV-1998;
Location/Qualifiers
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Unclassified.
1 (bases 1 to 18)
Lin,C.-I.Patsy., Wallace,R.Bruce., Cossman,J. and French,C.
Lin,C.-I.Patsy., Wallace,R.Bruce., Cossman,J. and French,C.
Lin,C.-I.Patsy., Wallace,R.Bruce., Cossman,J. and French,C.
Disperserve RNA and DNA contained in cells for use in molecular
biology experiments
Disperserve RNA and DNA contained in cells for use in molecular
biology experiments
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Chatelain, F. and Kumarev, V.
Process for preparing polynucleotides on a solid support in tightly packed bed
Patent: US 5869643-A 18 09-FEB-1999;
Location/Qualifiers
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/organism="unknown"
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Sequence 3 from patent US 5837820.
AR058305 GI:5983882
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Sequence 6 from patent US 6383754.
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AR208426.1 GI:21509577
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Kenichi, H., Hiroshi, Y. and Masahide, N.
Method for labeling oligonucleotide and utilization thereof
Patent: 7P 199075880-A 3 23 MAR-1999;
CHEMO SERO THERAPEUT RES INST
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                                                                                                                                                                                                                                                                                                              /organism='Unidentified'
Location/Qualifiers
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Sequence 16 from patent US 5707807.
179509.1 GI:3207799
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RESULT 360
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AR208426/c
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179509/c
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PAT 25-SEP-2002
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Unclassified.
1 (bases 1 to 18)
Lin,C.-I.P., Wallace,R.B., Cossman,J. and French,C.
Lin,C.-I.P., Wallace,R.B., Cossman,J. and Prench,C.
Ein,C.-I.P., Wallace,R.B., Cossman,J. and Prench,C.
preserve RNA and DNA contained in cells for use in molecular biology experiments
biology experiments
Patent: US 6410321-A 9 25-JUN-2002;
Location/Qualifiers
Unknown.
Unclassified.
Unclassified.
1 (bassified.
1 (bassified.
1 Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
Binary encoded sequence tags
Binary encoded sequence tags
Patent: US 6383754-A 6 07-MAY-2002;
Location/Qualifiers
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Sequence 24 from patent US 6429300.
AR222464
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Sequence 9 from patent US 6410321.
AR215435
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Borkow,G.
Antisense oligonucleotide constructs based on beta -arabinofuranose
and its analogues
and its 42 29-DEC-1999;
Patent: WO 9967378-A 2 29-DEC-1999;
DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER
(CA); UNIV. W.CILL (CA); ARION DOMINIQUE (CA); NOROWHA ANNE M (CA);
  PAT 24-AUG-2000
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                                                                                                                                                                                                                                         Method for isolating anionic organic substances from aqueous systems using cationic polymer nanoparticles
L Patent: WO 9910527-A 8 04-WAR-1999;
SUEDDEUTSCHE KALKSTOFF (DE); BAVER ERNST (DE)
Location/Qualifiers
1. .18
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//db_aref="taxon:32630"
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Use as an oligomer"
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Best Local Similarity 100.0%; Pred. No. 2e+02;
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Sequence 3 from Patent WO9967378.
AX008118 GI:9995743
Sequence 8 from Patent WO9910527.
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Manoharan,M., Cook,P.D., Prakash,T.P. and Kawasaki,A.M.
Maninoxy-modified nucleosidic compounds and oligomeric compounds
prepared therefrom
Patent: US 6639062-A 14 28-OCT-2003;
Location/Qualifiers
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Method for isolating anionic organic substances from aqueous systems using cationic polymer nanoparticles
Patent: WO 9910527-A 4 04-MAR-1999;
SUEDDEUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
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100.0%; Pred. No. 2e+02;
trive 0; Mismatches 0; Indels
                       1.0%; Score 18; DB 1; Length 18;
100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
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1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels
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/db_xref="taxon:33630"
/note="3' palmityl oligonucleotide"
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Sequence 14 from patent US 6639062.
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    /organism="unknown"
    /mol_type="genomic DNA"

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AXO04875/c
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AR412363/c
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AX004879/c
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REFERENCE AUTHORS JOURNAL

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Antisense oligonucleotide constructs based on beta -arabinofuranose and its analogues
Patent: WO 9967378-A 8 29-DEC-1999;
DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER GA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NOROWHA ANNE M (CA);
LOCATION/QUALIFIERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear PAT 24-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PACENT: WO 9732023-A 29 04-SEP-1997;
FLORIGENE LIMITED (AU); BRUGLIERA FILIPPA (AU); HOLTON TIMOTHY
ALBERT (AU); MICHAEL MICHAEL ZENON (AU)
LOCATION/QUAILIFIERS
                                      Damha, M.J., Parniak, M.A., Wilds, C., Arion, D., Noronha, A.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brugliera, F., Holton, T.A. and Michael, M.Z.
Genetic sequences encoding flavonoid pathway enzymes and uses
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/organism="synthetic construct"
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/note="Use as an oligomer"
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/db_xref="texon:32630"
/note="Oligonucleotide"
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Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches (
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Sequence 21 from Patent WO0068422.
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Patent: WO 9967378-A 3 29-DEC-1999,
DAWHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER
GCA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA);
BORKOW GADI (IL)
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Antibense oligonucleotide constructs based on beta -arabinofuranose
and its analogues
Patent: WO 9967378-A 7 29-DEC-1999;
DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER
GCA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NOROWHA ANNE M (CA);
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                                                                                                Damha, M.J., Parniak, M.A., Wilds, C., Arion, D., Noronha, A.M. and
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Sequence 8 from Patent W09967378.
AX008123 GI:9995748
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RESULT 370
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                 Score 18; DB 1;
Pred. No. 2e+02;
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                 Query Match
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Best Local Similarity 100.0%; Pred. No. 2e+
Matches 18; Conservative 0; Mismatches
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AX104747
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AX104747/c
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Gumblowski, K. and Zulauf, M.
High density labeling of dna with modified or chromophore carrying nucleotides and dna polymerases used
Patent: WO 006842-A 316-NOV-2000;
Roche Diagnostics GmbH (DE)
Location/Qualifiers
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Patent: WO 0112855-8 6 22-FEB-2001;
YALE UNIVERSITY (US)
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1.0%; Score 18; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0;

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    Organism="synthetic construct"
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Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0
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nucleotides and dna polymerases used
Patent: WO 0068422-A 21 16-NOV-2000;
Roche Diagnostics GmbH (DE)
Location/Qualifiers
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Sequence 23 from Patent WO0068422.
AX047273
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AX085252/c
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Krieg,A.M., Schetter,C. and Vollmer,J.C.
muniostimulacory nucleic acids
Patent: WO 0122972-A 31 05-APK-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
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munuostimulacory nuclei acids
Patent: WO 0122972-A 919 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical
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                                                  Location/Qualifiers
1. .18
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ive 0; Mismatches 0; Indels
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Inhibition of angiogenesis by nucleic acids
Patent: WO 02053141-A 913 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
Location/Qualifiers
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UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0
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Sequence 913 from Patent WO02053141.
AXS47774
Secreted factors
Patent: WO 0174901-A 84 11-OCT-2001;
Scios Inc. (US)
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AX355809
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                      DNA
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Patent: WO 0123564-A 10 05-APR-2001;
Scios Inc. (US)
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Differentially expressed genes
Patent: WO 0123419-A 10 05-APR-2001;
SCIOS INC. (US)
                  AX105651 18 bp
Sequence 10 from Patent WO0123564.
AX105651
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Sequence 10 from Patent WO0123419.
AX108642
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Sequence 84 from Patent WO0174901.
AX268883
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                                                                                                                                                                             Stanton, L.W. and Kapoun, A.M.
                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                      AX105651.1 GI:13921674
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RESULT 379
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RESULT 383 AX547800/c LOCUS

PAT 05-DEC-2003

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Oligonucleotides comprising alternating segments and uses thereof Patent: WO 03064441-A 8 07-AUG-2003; MCGILL UNIVERSITY (CA)
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/note="Residues 1, 3, 5, 7, 9, 11, 13, 15
2'-0-methyl-D-uridi ne"
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100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
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                 linear

    .15
/note="Residues 1-3, 7-9, and 13-15 are
2'-O-methyl-D-uridine"

                                                                                                                                                                                                                                                                                        /organism="synthetic construct"
/mol_type="unassigned DNA"
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Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches (
                 DNA
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               18 bp
Sequence 8 from Patent WO03064441.
AX814723
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Sequence 9 from Patent WO03064441.
AX814724
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                                                                                                                                                                               Damha, M.J. and Parniak, M.A.
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AX814724/c
AX814723/c
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Patent: WO 0306441-A 1 07-AUG-2003;
McGILL UNIVERSITY (CA)
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               Score 18; DB 1; Length 18;
Pred. No. 2e+02;
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100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
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Inhibition of angiogenesis by nucleic acids
Patent: WO 20051141-A 939 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="synthetic construct"
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               Query Match 1.0%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 2e+ Matches 18; Conservative 0; Mismatches
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Sequence 1 from Patent WO03064441.
AX814716
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE JOURNAL REFERENCE

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RESULT 384 AX814716/c LOCUS DEFINITION

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СО7H19/167, СО7H19/067, СО7H19/10, СО7H19/20, СО7H21/02, C12N15/00,
C12N15/00
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07-AUG-1998 US 09/130973
MUTHIAH MANOHARAN, PHILIP DAN COOK, THAZHA P PRAKASH, ANDREW M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SM synthetic construct
artificial sequences.

E 1 (basea to 18)
S Manoharan, M. Cook, P.D., Prakash, T.P. and Kawasaki, A.M.
Aminooxy-modified nucleoside compound and oligomer compound produced therefrom
D produced therefrom
ISIS PHARMACEUTICALS INC
OS Artificial sequence
PN JP 2002522447-A/14
PD 23-JUL-2002
                                                                    30-MAY-2000 JP 2000160324
XAORI SHIMADA
C1201/68,C12N15/09,G01N33/50,C12N15/00
Method of comparison and detection of RNA amount and DNA
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/organism='Homo sapiens (human)'.
Location/Qualifiers
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Location/Qualifiers
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                                                                                                                                                          Location/Qualifiers

    .18
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                                                                                                                                                                                                                              l. .18
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JP 2001333800-A/2
04-DEC-2001
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JP 2002522447-A/14.
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UNITECH CO LTD
OS Home sapies
PN JP 20013331
PD 04-DEC-2001
PF 30-MAY-2001
PC C12Q1/68,CC
CC C12Q1/68,CC
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BD222596/c
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AUTHORS
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Digonucleotides comprising alternating segments and uses thereof
Patent: WO 03064441-A. 21 07-AUG-2003;
MCGILL UNIVERSITY (CA)
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                                                                                                        alternating segments and uses thereof
                                                                                                                                                                                                                                                                               /note="Residues 1-6 and 13-18 are 2'-O-methyl-D-uridine"
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/organism="synthetic construct"
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/db_tref="taxon:32630"
/noTe="Target RNA oligonucleotide"
                                                                                                                                                                       1. .18
/organism="synthetic construct"
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"
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                                                                                  Damha,M.J. and Parniak,M.A.
Oligonucleotides comprising alternation
Patent: WO 03064441-A 10 07-AUG-2003;
MCGILL UNIVERSITY (CA)
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                                                                                                                                                        Location/Qualifiers
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PAT 30-MAR-2001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                     Lander, E.S., Gargill, M., Ireland, J.S., Bolk, S., Daley, G.Q. and Mccarthy, J.J.
Single nucleotide polymorphisms in genes
Patent: WO 0118250-A 477 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); Millennium
Pharmaceuticals, Inc. (US)
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Single nucleotide polymorphisms in genes
Patent: WO 0118250-A 481 15-WAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); Millennium
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Sequence 481 from Patent W00118250.
AX095303
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 Sequence 477 from Patent WO0118250.
AX095299
AX095299.1 GI:13511502
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AX825111/c
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Protein skeleton of antibody mimetics and other binding proteins.
BD234126
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C12N1S/09, C07K1/04, C07K14/78, C07K16/46, C07K17/00, C07K19/00, PC
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Patent: JP 2002532072-A 14 02-OCT-2002;
PHYLOS INC
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Manoharan,M., Cook,P.D. and Guinosso,C.J.
Modified oligonucleotides
Patent: US 6651458-A 7 25-NOV-2003;
Location/Qualifiers
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1.0%; Score 18; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 0;
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                       DNA
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                Sequence 7 from patent US 6653458.
AR432617
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10-DEC-1998 US 60/1117
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JP 2002532072-A/14
02-OCT-2002
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JP 2002532072-A/14.
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Method for sorting single-stranded nucleic acids
Patent: WO 03072818-A 11 04-SEP-2003;
Degussa Bioactives GmbH (DE)
Location/Qualifiers
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Sequenz:Capture-Oligonukleotid"
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Sequence 11 from Patent WO03072818.
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AX825113/c
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                           Boekenkamp, D., Dieck, T.H. and Hoppe, H.U. Method for sorting single-stranded nucleic acids Patent: WO 03072818-A 9 04-SEP-2003; Degussa Bioactives GmbH (DE)
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                                                                                                                 1. .21
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Sequence 10 from Patent W003072818.
AX825112.
AX825112.1 GI:39750841
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Sequenz:Capture-Oligonukleotid"
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Sequenz:Capture-Oligonukleotid"
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Sequence 34 from Patent WO03072818.
AX825136
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Method for sorting single-stranded nucleic acids
Patent: WO 03072818-A 12 04-SEP-2003;
Degussa Bioactives GmbH (DE)
Location/Qualifiers
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|mol_type="unassigned DNA"
|dD_xref="taxon:32630"

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Sequence 33 from Patent W003072818.
AX825135
                                 21 bp 1 Sequence 12 from Patent W003072818.
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Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels
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Boekenkamp, D., Dieck, T.H. and Hoppe, H.U. Method for sorting single-stranded nucleic acids Patent: WO 03072818-A 36 04-SEP-2003; Degussa Bioactives GmbH (DE)
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Sequence 41 from Patent WO03072818.
AX825143
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/mod_base=OTHER
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Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0;
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Sequence 35 from Patent WO03072818.
AX825137
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                   linear
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Method for sorting single-stranded nucleic acids
Patent: WO 03072818.A 44 04 SEP-2003;
Degussa Bioactives GmbH (DE)
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/noce="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
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/mol type="unassigned DNA"
/db_Xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
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/mod_base=OTHER
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/mod_base=OTHER
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/mod_base=OTHER
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100.0%; Pred. No. 2.4e+02;
tive 0; Mismatches 0;
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Sequence 43 from Patent WO03072818.
AX825145
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Sequence 44 from Patent WO03072818.
AX825146.1 GI:39750875
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Method for sorting single-stranded nucleic acids
Patent: WO 03072318-A 4 2 04-SEP-2003;
Degussa Bioactives GmbH (DE)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/noTe="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
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/mod_base=OTHER
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Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0;
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Sequence 42 from Patent WO03072818.
AX825144
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Torrence, P., Silverman, R., Maitra, R. and Lesiak, K. Method of cleaving specific strands of RNA
Patent: US 5583032-A 1 10-DEC-1996;
Location/Qualifiers
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Torrence, P., Silverman, R., Maitra, R. and Lesiak, K. Method of Cleaving specific strands of RNA
Patent: US 558303-A 2 10-DEC-1996;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels
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Sequence 1 from patent US 5583032.
131810.
131810.1 GI:1822601
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Sequence 2 from patent US 5583032.
131811
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DEFINITION Sequence 1 from patent US 5677289.
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/organism="unknown"
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I31811/c
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I69407/c
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1 (bases 1 to 22)
Torrence,P.F., Silverman,R.H., Maitra,R.K. and Lesiak,K.
Chimeric molecules targeted to viral RNAs
Patent: US 6271369-A 2 07-AUG-2001;
Location/Qualifiers
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Torrence, P.F., Silverman, R.H., Maitra, R.K. and Lesiak, K. Chimeric molecules targeted to viral RNAs
Patent: US 6271369-A 1 07-AUG-2001;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels
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Sequence 1 from patent US 6271369.
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ARE64319
ARE64319.1 GI:16235434
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18 AAAAAAAAAAAAAAA 1
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AR164318.1 GI:16235432
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AR164319/c
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AR164318/c
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PR 23-NOV-1998 DE 198 53 957.6,29-APR-1999 DE 199 21 940.0 PI GERHARD HARTWICH, ADAM HELLER PC CO7121/00,C07H21/02,C07H21/04,C12N15/09,C12Q1/68,G01N27/12, PC G01N27/30,
                                                                         PC
G01N27/416,G01N27/48,G01N33/483,G01N33/50,G01N33/566,C12N15/00, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pignot, M.

Pignot, M.

Detection system for analyzing molecular interactions, production and utilization thereof

Patent: WO 0071749-A 9 30-NOV-2000;

Patent: WO 0071749-A 9 10-NOV-2000;

Aventis Research & Technology GmbH & Co. KG. (DB)

Location/Qualifiers
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Detection system for analyzing molecular interactions, production
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                                                                                                                           Method of electrochemically detecting nucleic acid FH Location/Qualifiers
                                                                                                                                                                     rce 1..23
/organism='Artificial Sequence'
Location/Qualifiers
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Matches 18; Conservative 0; Mismatches 0;
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/note="Komponente (b)-2"
                                                                                                                                                                                                                                         /organism="synthetic construct"
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/db_xref="taxon:32630"
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Sequence 18 from Patent WO0071749.
AX053002
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AX052993
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artificial sequences.
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AX053002/c
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AX052993/c
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Torrence,P., Silverman,R., Maitra,R. and Lesiak,K.
Method of cleaving specific strands of RNA and medical treatments
                                                                                                            1 (bases 1 to 22)
Torrence, P., Silverman, R., Maitra, R. and Lesiak, K.
Method of cleaving specific strands of RNA and medical treatments
thereby
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artificial screening nucleic acid
Harwich, G. and Heller, A.
Method of electrochemically detecting nucleic acid
Patent: JP 2002532386-A 24 02-0CT-2002;
FRIZ BIOCHEM GMBH
OS Artificial Sequence
PN JP 2002532386-A/24
PD 02-0CT-2002
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Method of electrochemically detecting nucleic acid.
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Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                  Patent: US 5677289-A 1 14-OCT-1997;
Location/Qualifiers
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Location/Qualifiers
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Sequence 2 from patent US 5677289.
169408
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   I69407
I69407.1 GI:2831529
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                                                                           Unknown.
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I69408/c
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1 (bases 1 to 20)
Holton, T.Albert., Cornish, E.Cecily., Kovacic, F., Tanaka, Y. and
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Genetic sequences encoding flavonoid pathway enzymes and uses
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94.7%; Pred. No. 2.8e+02;
tive 0; Mismatches 1; Indels
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100.0%; Pred. No. 2.8e+02;
tive 0; Mismatches 0; Indels
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="probes to target sequences"
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Location/Qualifiers
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AR030917
                                                                                                                                                                                                                                                      Wobler, P.K. and Delenstarr, G.C.
Calibration of molecular array data
Patent: EP 1186673-A 7 13-MAR-2002;
Agilent Technologies Inc (US)
Location/Qualifiers
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                                                                                                           Sequence 7 from Patent EP1186673. AX394609
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1736 AAAAAAAAAAAAAAAA 1753
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                              24 AAAAAAAAAAAAAAAAA
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Matches 18; Conservative
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Best Local Similarity 100.
Matches 18; Conservative
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AR030917/c
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AX394609
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I28309/c
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Unknown.
Unclassified.
1 (bases 1 to 24)
2 purr,N.K., Gray,I.C. and Stewart,L.M.
Diagnosis of susceptibility to cancer and treatment thereof
Patent: US 6287854-A 82 11-SEP-2001;
Location/Qualifiers
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1.0%; Score 18; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels
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          Patent: WO 0071749-A 18 30-NOV-2000;
Aventis Research & Technology GmbH & Co. KG. (DE)
Location/Qualifiers
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/organism="synthetic construct"
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/noTe="probes to target sequences"
                                                            1. .23
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="texon:32630"
/note="Komponente (b)-5"
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Sequence 82 from patent US 6287854.
AR168453.1 GI:17904379
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Calibration of molecular array data
Patent: EP 1186673-A 5 13-MAR-2002,
Agilent Technologies Inc. (US)
                                                                                                                                                                                                                                                                                                                                     Sequence 5 from Patent EP1186673. AX394607
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and utilization thereof
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synthetic construct
artificial sequences.
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AX394607
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PAT 29-SEP-1999

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PAT 06-FEB-1997

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Synthetic construct
SM synthetic construct
artificial sequences.

I (bases 1 to 23)
Hartwich,G. and Heller,A.
Method of electrochemically detecting nucleic acid
Method of electrochemically detecting nucleic acid
Datactic JP 2002532366-A 20 02-OCT-2002;
FRIZ BIOCHEM GMBH
OS Artificial Sequence
PN JP 2002532386-A/20
PD 02-OCT-2002
PP 19-NOV-1999 JP 2000583928
PR 23-NOV-1999 DE 198 53 957.6,29-APR-1999 DE 199 21 940.0 PI
GERHARD HARTWICH,ADAM HELLER
PC CO7H21/00,CO7H21/02,CO7H21/04,C12N15/09,C12Q1/68,G01N27/12, PC
GG1N27/30,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PC
G01N27/416,G01N27/48,G01N33/483,G01N33/50,G01N33/566,C12N15/00,
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PN JP 200253286-A/28
PD 02-OCT-2002
PF 19-NOV-1999 JP 2000583928
PR 23-NOV-1999 DE 199 53 957.6,29-APR-1999 DE 199 21 940.0 PI
GERHARD HARTWICH,ADAM HELLER
PC C07H21/00.C07H21/n.
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SM synthetic construct
artificial sequences.
3 Har bases 1 to 23)
5 Har bases 1 to 23)
6 Har bases 23)
7 Patent: JP 2002532386-A 28 02-OCT-2002;
7 FRIZ BIOCHEM GMBH
OS Artificial Sequence
PN JP 2002532386-A/28
PD 02-OCT-2002
PF 19-NOV-1999 JP 2000583928
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                                                                                                                                 BD245234 23 bp DNA linear Method of electrochemically detecting nucleic acid. BD245234

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|mol type="genomic DNA"
|db_xref="taxon:32630"

                 1736 AAAAAAAAAAAAAAAA 1754
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                                                 1 AAAAAAAAAAAAAA 19
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JP 2002532386-A/20.
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BD245234
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                                               1 (bases 1 to 20)
Holton, T.A., Cornish, E.C., Kovacic, F., Tanaka, Y. and Lester, D.R.
Genetic sequences encoding flavonoid pathway enzymes and uses
therefor
Patent: US 5569832-A 20 29-OCT-1996;
Location/Qualifiers
1. 20
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                        Gapa
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Holton, T.Albert., Cornish, E.Cecily. and Tanaka, Y.
Genetic sequences encoding flavonoid pathway enzymes and uses
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94.7%; Pred. No. 2.8e+02;
tive 0; Mismatches 1; Indels
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Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
Peptide nucleic acids
Patent: US 6395474.A 4 28-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
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Location/Qualifiers
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147310
147310.1 GI:2471275
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Sequence 4 from patent US 6395474.
AR371268.1 GI:34608200
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Best Local Similarity 94.77
Matches 18; Conservative
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Best Local Similarity 94.7
Matches 18; Conservative
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Matches 18, Conservative
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PAT 29-SEP-1997

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/organism='Artificial sequences' Location/Qualifiers
                             ch 1.0%; Score 17.2; DB 1; Length 19; 1 Similarity 94.4%; Pred. No. 2.8e+02; 17; Conservative 1; Mismatches 0; Indels
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1 (bases 1 to 20)

Takagi,S. and Kamioka,S.

DETERMINATION OF CDNA
Patent: JP 1994303997-A 3 01-NOV-1994;
NIPPON TELEGR & TELEPH CORP <NTT>
OS None
OC Artificial Reminance
                                                                                                                                                                                                                                                                                                                                              Takadi,S. and Kamioka,S.
DETERMINATION OF CDNA
PATENTION OF CDNA
PATENTION OF CDNA
PATENTION OF CDNA
NIPPON TELEGR & TELEPH CORP <NTT>
OS None
C Artificial sequences.
PN JP 199430397-A/2
PD 01-NOV-1994
PF 199430397-A/2
PD 01-NOV-1994
PF 16-APR-1993 JP 1993112515
PT TAKAGI SHIGERU, KAMIOKA SUKEYUKI
PC (1201/68,C12N15/10)
CC Strandedness: Single;
CC topology: Linear;
CC anti-sense: 'Yes,
CC anti-sense: 'Yes,
FH Key
FT source //organism='Artificia
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/mol_type="unassigned DNA"

    .19
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Reverse transcription primer.
E08331
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JP 1994303997-A/2.
unidentified
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JP 1994303997-A/3.
unidentified
unidentified
                                Query Match
Best Local Similarity
Matches 17; Conserva
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               PC
GOIN27/416, GOIN27/48, GOIN33/483, GOIN33/50, GOIN33/566, C12N15/00, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Unknown.
Unclassified.
Unclassified.
I (bases 1 to 19)
Weinstein, J.N. and Buolamwini, J.
Restriction display (RD-PCR) of differentially expressed mRNAs
Restriction display (RD-PCR) of aliferentially expressed mRNAs
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tuijnder,M., Telerman,A., Amson,R. and Susini,L. Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
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                               Method of electrochemically detecting nucleic acid FH Location/Qualifiers
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                                                                                                           /organism='Artificial Sequence'
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1.0%; Score 17.4; DB 1; Length 23;
Best Local Similarity 94.7%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels
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Pred. No. 3.3e+02;
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                                                                                                                                                 1. .23
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parent: WO 02059256-A 1869 01-AUG-2002;
MOLECULAR ENGINES LAB (FR)
Location/Qualifiers
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85.7%; Pred. No. s.c.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1 from patent US 6270966.
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Best Local Similarity 85.7%
Matches 18; Conservative
G01N27/30,
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PAT 29-SEP-1997

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1 (Dases 1 to 22)
Hancak, R.C., Anderson, K.P., Bennett, C.Frank., Chiang, M.-Y.,
Brown-Driver, V.L., Ecker, D.J., Vickers, T.A., Wyatt, J.R. and
Imbach, J.Louis.
Oligonucleorides having a conserved G4 core sequence
Patent: US 5952490.A 44 14-SEP-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unknown.
Unclassified.
1 (bases 1 to 22)
Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,
Brown-briver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and
                                                                                                                                                        1 (bases 1 to 22)
Hanecak, R.C., Anderson, K.P., Bennett, C.Frank., Chiang, M.-Y.,
Brown-Driver, V.L., Ecker, D.J., Vickers, T.A., Wyatt, J.R. and
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Oligonucleotides having a conserved G4 core sequence
Patent: US 5952490-A 36 14-SEP-1999;
Location/Qualifiers
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Sequence 110 from patent US 5952490.
AR074302.
AR074302.1 GI:10001057
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Sequence 44 from patent US 5952490.
AR074236
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/organism="unknown"
/mol_type="unassigned DNA"
                               22 bp i
Sequence 36 from patent US 5952490.
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/mol_type="unassigned DNA"
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ARO74228.1 GI:10000983
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RESULT 430
AR07428
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/organism='Artificial sequences'.
Location/Qualifiers
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1.0%; Score 17.2; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.9e+02;
Matches 17; Conservative 1; Mismatches 0; Indels
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                           16-APR-1993 JP 1993112515
TAKAGI SHIGGERU, KAMIOKA SUKEYUKI
C1201/68, C12N15/10;
Etrandedness: Single;
topology: Linear;
hypothetical: No;
anti-sense: Yes;
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DETERMINATION OF CDNA
DETERMINATION OF CDNA
NIPPON TELEGR & TELEPH CORP <NTT>
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JP 1994303997-A/4
01-NOV-1994
16-APR-1993 JP 1993112515
TAKAGI SHIGERU, KAMIOKA SUKEYUKI
C12Q1/68,C12N15/10;

    .20
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/db_xref="taxon:32644"

    .21
    /organism="unidentified"
    /mol_type="genomic DNA"
    /db_xref="taxon:32644"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reverse transcription primer.
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topology: Linear;
hypothetical: No;
anti-sense: Yes;
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01-NOV-1994
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Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Imbach,J.L., Brown-Driver,V.L., Vickers,T.A., Ecker,D.J.,
Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
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                                                                                                                                                                                                                                                                                                                       Weatt.J.R.
Oligonucleotides having a conserved g4 core sequence
Digonucleotides having a conserved g4 core sequence
Patent: EP 1016/15-A 44 05-JUL-2000;
ISIS PHARMACEUTICALS INC (US)
Location/Qualiflers
Location/Qualiflers
//organism="unidentified"
//mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Oligonucleotides having a conserved g4 core sequence
Digonucleotides having a conserved g4 core sequence
Patent: EP 1016715-A 110 05-JUL-2000;
ISIS PHARMACEUTICALS INC (US)
Location/Qualifiers
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86.4%; Pred. No. 3.3e+02;
tive 0; Mismatches 3; Indels
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86.4%; Pred. No. 3.3e+02;
tive 0; Mismatches 3; Indels
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Sequence 44 from Patent EP1016715.
AX032598
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Best Local Similarity 86.4
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Matches 19; Conservative
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unidentified
unclassified
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AX032671
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AX032598
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Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,
Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and
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Bennett, C.F., Chiang, M.Y., Anderson, K.P., Hanecak, R.C. and
Wyatt, J.R.
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              Oligonucleotides having a conserved G4 core sequence
Patent: US 5952490-A 110 14-SEP-1999;
Location/Qualifiers
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Oligonucleotides having a conserved G4 core sequence
Patent: US 5952490-A 117 14-SEP-1999;
Location/Qualifiers
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Patent: EP 1016715-A 36 05-JUL-2000;
ISIS PHARMACEUTICALS INC (US)
Location/Qualifiers
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1.0%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 3.3e+02;
Matches 19; Conservative 0; Mismatches 3; Indels
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86.4%; Pred. No. 3.3e+02;
tive 0; Mismatches 3;
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1.0%; Score 17.2; DB 1;
Best Local Similarity 86.4%; Pred. No. 3.3e+02;
Matches 19; Conservative 0; Mismatches 3;
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Sequence 117 from patent US 5952490.
AR074309
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                                                                                /organism="unknown"
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Sequence 36 from Patent EP1016715.
AX032590
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Best Local Similarity 86.43
Matches 19; Conservative
Imbach, J. Louis
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Page 115

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Gaps

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PAT 01-MAR-2003

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synthetic construct
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artificial sequences.
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Holton, T.A., Cornish, E.C., Kovacic, F., Tanaka, Y. and Lester, D.R.
Genetic sequences encoding flavonoid pathway enzymes and uses
                                                                                                                                                                                           Length 22;
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Inhibition of angiogenesis by nucleic acids
Patent: WO 02053141-A 61 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
Location/Qualifiers
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INTERNATIONAL FLOWER DEVELOPMENTS Pty. Ltd
Location/Qualifiers
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1.0%; Score 17.2; DB 1;
Best Local Similarity 86.4%; Pred. No. 3.3e+02;
Matches 19; Conservative 0; Mismatches 3;
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86.4%; Pred. No. 3.3e+02;
tive 0; Mismatches 3;
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/db_xref="taxon:32630"
/note="Synthetic Sequence"
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/noTe="Primer"

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primer sequence 4 from patent EP0522880.
A28997
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    Patent: WO 0231186-A 21 18-APR-2002;
Epigenomics AG (DE)
Location/Qualifiers
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Sequence 61 from Patent WO02053141.
AX546922
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Best Local Similarity 86.4%
Matches 19; Conservative
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AX546922/c
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munuostimulatory nucleic acids
Patent: WO 0122972-A 6.1 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
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Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
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Oligonucleotides having a conserved g4 core sequence
Patent: EP 1016715-A 117 05-JUL-2000;
ISIS PHARMACEUTICALS INC (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                         1.0%; Score 17.2; DB 1; Length 22;
86.4%; Pred. No. 3.3e+02;
tive 0; Mismatches 3; Indels
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Method for the detection of cytosine methylations
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Local Similarity 86.4%; Pred. No. 3.3e+02;
les 19; Conservative 0; Mismatches 3;
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Sequence 117 from Patent EP1016715.
AX032671
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Sequence 61 from Patent W00122972.
AX103869
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Sequence 21 from Patent W00231186.
AX457060
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AX103869/c
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Manoharan, M. and Maier, M.A.
Compounds, processes and intermediates for synthesis of mixed backbone oligomeric compounds
Patent: US 6462184-A 5 08-OCT-2002;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 0;
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1.0%; Score 17; DB 1; Lo
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 0;
                                         Telomerase
Patent: US 6309867-A 132 30-OCT-2001;
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                                                                                                                                                                                                                                                                                                           Sequence 23 from patent US 6429300.
                                                                                       1. .17
/organism≂"unknown"
/mol_type="unassigned DNA"
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    17
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    /mol_type="genomic DNA"

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/mol_type="genomic DNA"
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Cech, T.R. and Nakamura, T.
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Compounds, processes and intermediates for synthesis of mixed backbone oligomeric compounds

Patent: US 6207819-A 5 27-MAR-2001,

Location/Qualifiers
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Matches 17; Conservative 0; Mismatches 0; Indels
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Patent: US 6093809-A 132 25-JUL-2000;
Location/Qualifiers
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Sequence 132 from patent US 6309867.
AR175846.1 GI:17917145
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Sequence 5 from patent US 6207819.
AR141074
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Cech, T.R. and Lingner, J.
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AR104585/c
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E32454 18-JUN-2001
Mammal-derived tissue specific physiologically active protein.
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                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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JP 2000037190-A/14.
Synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 18)
Jun,N. Yusuke,N. and Toshihiro,T.
Mammal-derived tissue specific physiologically active protein
Patent: JP 2000037190-A 14 08-FEB-2000;
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                                                                                                                      Telerman, A., Amson, R. and Tuijnder, M.
Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
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100.0%; Pred. No. 2.6e+02;
tive 0; Mismatches 0; Indels
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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 AX758974.1 GI:32253590
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                                                                                        PAT 31-MAR-2003
                                                                                                                                                                                                                                                                  Shannon, M., Gu, Y. and Nguyen, C.T. Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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1.0%; Score 17; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 0;
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1.0%; Score 17; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 0;
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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                                                                                      AX692526
Sequence 5258 from Patent EP1281758.
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AX728616
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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 17 AAAAAAAAAAAAAA
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PAT 24-NOV-2000

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FLORICENE LIMITED (AU); BRUGLIERA FILIPPA (AU); HOLTON TIMOTHY ALBERT (AU); MICHAEL MICHAEL ZENON (AU)
Location/Qualifiers
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FLORIGENE LIMITED (AU); BRUGLIERA FILIPPA (AU); HOLTON TIMOTHY
ALBERT (AU); MICHAEL ZENON (AU)
Location/Qualifiers
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Binary encoded sequence tags
Patent: WO 0112855-A 5 22-FEB-2001;
YALB UNIVERSITY (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brugliera, F., Holton, T.A. and Michael, M.Z. Genetic sequences encoding flavonoid pathway enzymes and uses
                                                                                                                                              . Match 1.0%; Score 17; DB 1; Length 18; Local Similarity 100.0%; Pred. No. 2.8e+02; les 17; Conservative 0; Mismatches 0; Indels
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/organism="synthetic construct"
/nol type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"
                                               1. 18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="reaxon:32630"
/note="01igonucleotide"
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="taxon:32630"
/noTe="Primer"
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Sequence 28 from Patent WO9732023.
AX028844
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                                                                                                                                            CI2P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
C12N15/00,
                                                                                              JUN NISHIU, YUSUKE NAKAMURA, TOSHIHIRO TANAKA
CI2N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 18)
Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
Binary encoded sequence tags
Patent: US 6333754-A 5 07-WAY-2002;
Location/Qualifiers
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Genetic sequences encoding flavonoid pathway enzymes and uses
therefor
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100.0%; Pred. No. 2.8e+02;
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primer_bind (1). (18).
Location/Qualifiers
1. 18
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/mol_type="unassigned DNA"
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AR208425
AR208425.1 GI:21509576
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AX028843
                                                                23-JUL-1998 JP 1998225228
               Artificial Sequence
JP 2000037190-A/14
08-FEB-2000
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AR208425/c
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AX028843/c
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JP 2002191169-A/1.
synthetic construct
artificial sequences.
1 (bases 1 to 20)
Tanga, M., Okamura, H. and Takahashi, K.
Method for carrying out thermal cycle of PCR using DNA-immobilized substrate
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PI MICHIFUMI TANGA,HIROSHI OKAMURA,KOJIRO TAKAHASHI PC
C12N15/09,C12N15/09,C12Q1/68,C12N15/00,C12N15/00 CC Method for
carrying out thermal cycle of PCR using DNA- CC
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Location/Qualifiers
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     Length 19;
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                                         Indels
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Emrich, T., Leylig, H., Hinzpeter, M. and Karl, G. ethod of detecting telomerase activity
Patent: US 6221584-A 6 24-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
1.0%; Score 17; DB 1; L.
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 0;
   1.0%; Score 17; DB 1; L
100.0%; Pred. No. 2.9e+02;
tive 0; Mismatches 0;
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/db_xref="taxon:32630"
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TOYO KOHAN CO LTD, KOJIRO TAKAHASHI
OS Artificial Sequence
PN JP 2002191369-A/1
PD 09-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="unknown"
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Sequence 6 from patent US 6221584.
AR147331
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                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae.
1 (bases 1 to 18)
                                                                                                                                                                                                                                                                                                                                                                              Jacobs, K., Mccoy, J.M., Lavallie, E.R., Racie, L.A., Merberg, D.,
Treacy, M., Spaulding, V. and Agostino, M.J.

Treacy, M., Spaulding, V. and Agostino, M.J.

Bacretory proteins and polynucleotides encoding the same
Patent: JP 2002515753-A 12 28-MAY-2002;

GENETICS INSTITUTE INC

PN JP 2002515753-A/12

PP 28-MAY-2002

PP 10-007-1997 JP 1998521609

PR 01-NOV-1996 US 08/724973

PR NINNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE,
                                           Gaps
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E l (bases 1 to 19)
S Emrich, T. and Leying, H.
METHOD OF DETECTING TELOMERASE ACTIVITY
L Patent: WO 9720069-A 6 05-JUN-1997;
BOEHRINGER MANNHEIM GMBH (DE); EMRICH THOMAS (DE)
Location/Qualifiers
     Length 18;
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   1.0%; Score 17; DB 1; Le
100.0%; Pred. No. 2.8e+02;
ative 0; Mismatches 0;
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1.0%; Score 17; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 0;
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Topology: Linear;
Location/Qualifiers.

    .19
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"

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Sequence 6 from Patent WO9720069.
A79657
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/db_xref="taxon:10114"
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/organism="Rattus"
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JP 2002515753-A/12.
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1 (bases 1 to 20)

Hanecak, R.C., Anderson, K.P., Bennett, C.Frank., Chiang, M.-Y.,
Brown-Driver, V.L., Ecker, D.J., Vickers, T.A., Wyatt, J.R. and
                                                                                         Tanccak, R.C., Anderson, K.P., Bennett, C.Frank., Chiang, M.-Y., Brown-Driver, V.L., Ecker, D.J., Vickers, T.A., Wyatt, J.R. and Imbach, J.Louis.
Oligonucleotideotide having a conserved G4 core sequence Patent: US 5952490-A 114 14-SEP-1999;
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Oligonucleotides having a conserved G4 core sequence
Patent: US 5952490-A 118 14-SEP-1999;
                                                                                                                                                                                                                                                        1.0%; Score 16.8; DB 1; Length 20; llarity 90.0%; Pred. No. 3.3e+02; Conservative 0; Mismatches 2; Indels
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Dean,N.M. and Cowsert,L.M.
Antisense modulation of daxx expression
Patent: US 6180353-A 68 30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                 AR074310 20 bp DN
Sequence 118 from patent US 5952490.
                                                                                                                                                                                                           /organism="unknown"
/mol_type="unassigned DNA"
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AR126639
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/organism="unknown"
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/organism="unknown"
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AR126639/c
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Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,
Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and
Imbach,J.Louis.
Oligonucleotides having a conserved G4 core sequence
Patent: US 5952490-A 37 14-SEP-1999;
Location/Qualifiers
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Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,
Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and
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Oligonuclectides having a conserved G4 core sequence
Patent: US 5952490-A 45 14-SEP-1999;
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Pred. No. 3.3e+02;
Best Local Similarity 100.0%; Pred. No. 3.1e+02; Matches 17; Conservative 0; Mismatches 0;
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Sequence 45 from patent US 5952490.
AR074237
AR074237.1 GI:10000992
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/organism="unknown"
/mol_type="unassigned DNA"
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Draper, K.G., Crooke, S.T., Mirabelli, C.K., Ecker, D.J., Hanecak, R.C.,
Anderson, K.P., Brown-Driver, V.L. and Wyatt, J.R.
Oligonucleotide therapies for modulating the effects of herpes
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Bennett, C.F., Chiang, M.Y., Anderson, K.P., Hanecak, R.C. and
Wyatt, J.R.
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Sequence 55 from patent US 5514577.
120476
120476.1 GI:1600831
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Location/Qualifiers
  0; Mismatches
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/mol_type="unassigned DNA"

    .20
    /organism="unidentified"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"

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Sequence 37 from Patent EP1016715.
AX032591 GI:10279529
AX032591.1 GI:10279529
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Kambara, H. and Uematsu, C.
DNA fragment preparation method for gene expression profiling
Patent: US 2019898.A 7 20-MAR-2001;
Location/Qualifiers
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PR HIDEKI KAMIBARA, SENSHU UEMATSU
PC C12N15/09, C12Q1/68, G01N27/447, C12N15/00, G01N27/26 CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source Location="Topology" | Location="Topolo
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                     Query Match
1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels
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Location/Qualifiers
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1.0%; Score 16.8; DB 1;
Best Local Similarity 90.0%; Pred. No. 3.38+02;
Matches 18; Conservative 0; Mismatches 2;
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Hideki,K. and Senshu,U.
Method for analyzing DNA fragment
Patent: JP 1999196874-A 7 27-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .20
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                     20 bp
Sequence 7 from patent US 6203988.
AR142677
AR142677.1 GI:15103963
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Method for analyzing DNA fragment.
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JP 1999196874-A/7
27-JUL-1999
14-JAN-1998 JP 1998005399
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JP 1999196874-A/7.
unidentified
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Best Local Similarity
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PAT 15-FEB-2002
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antisense therapy for hormone-regulated tumors
Patent: WO 105435-A 15 25-JAN-2001;
THE UNIVERSITY OF BRITISH COLUMBIA (CA); Miyake, Hideaki (JP)
Location/Qualifiers
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A method and an algorithm for mrna expression analysis
Patent: WO 0208461-A 18 31-JAN-2002;
Global Genomics AB (SE)
                Oligonuclectides having a conserved 94 core sequence Patent: EP 1016715-A 118 05-JUL-2000; ISIS PHARMACEUTICALS INC (US)
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/organism="synthetic construct"
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/noTe="Double-stranded product DNA"
                                                                                                                                                                              1.0%; Score 16.8; DB 1;
90.0%; Pred. No. 3.3e+02;
tive 0; Mismatches 2;
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"

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    /organism="Homo sapiens"
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Sequence 15 from Patent WO0105435.
AX078001
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Best Local Similarity 90.0°
Matches 18; Conservative
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Best Local Similarity 90.0
Matches 18; Conservative
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ACCESSION
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AX078001/c
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Bennett, C.F., Chiang, M.Y., Anderson, K.P., Hanecak, R.C. and
Wyatt, J.R.
Wjatt, J.R.
Oligonucleotides having a conserved g4 core sequence
Patent: EP 1016715-A 45 05-JUL-2000;
ISIS PHARMACEUTICALS INC (US)
Location/Qualifiers
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Bennett,C.P., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
Wyatt,J.R.
Oligonucleotides having a conserved g4 core sequence
Patent: EP 1016715-A 114 05-JUL-2000;
ISIS PHARMACETICALS INC (US)
Location/Qualifiers
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Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
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1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels
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90.0%; Pred. No. 3.38+02;
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    .20
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    /db_xref="taxon:32644"

    .20
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    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"

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Sequence 114 from Patent EP1016715.
AX032668
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AX032599.1 GI:10279537
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Griffais, R., Hoiseth, S.K., Zagursky, R.J., Metcalf, B.J., Sankaran, B. and Fletcher, L.D.
Chlamydia pneumoniae polymucleotides and uses thereof Patent: US 6559294-A 2140 06-MAY-2003;
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   Length 20;
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1 (bases 1 to 21)
S Brysch, W. and Schlingensiepen, K.
AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
L Patent: WO 9833904-A 263 06-AUG-1998;
BIOGNOSTIK GES (DB); BRYSCH WOLFGANG (DE)
Location/Qualifiers
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ch 0.9%; Score 16.4; DB 1; 1 Similarity 94.4%; Pred. No. 3.8e+02; 17; Conservative 0; Mismatches 1;
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85.7%; Pred. No. 4.2e+02;
iive 0; Mismatches 3;
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Sequence 2140 from patent US 6559294.

    .21
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Sequence 263 from Patent EP0856579.
A90082
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A88115
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Best Local Similarity 85.7
Matches 18; Conservative
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              Best Local Similarity
Matches 17; Conserv
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A90082
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/organism="synthetic construct"
/organism="synthetic construct"
/ml_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: Double-stranded product DNA"
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Location/Qualifiers
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                                                                                                                                                           linear
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                   1; Indels
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Patent: WO 03064691-A 18 07-AUG-2003;
Global Genomics AB (SE)
Location/Qualifiers
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JP 2000342265-A/9.
synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 20)
Hirose, K. and Yoshida, T.
Method for purifying oligonucleotide
Patent: JP 2000342265-A/9
TOAGOSEI CHEM IND CO LTD
OS Artificial Sequence
PN JP 2000342265-A/9
PD 12-DEC-2000
    Pred. No. 3.3e+02;
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/mol_type="genomic DNA"
    /db_xref="taxon:32630"

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                 0; Mismatches
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C12N15/09, B01D15/08, C12N15/00
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Best Local Similarity 94.4%;
Matches 17; Conservative
 Best Local Similarity 94.4 Matches 17; Conservative
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E59328
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Sequence 131 from patent US
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1 (bases 1 to 16)
Cech, T.R. and Lingner, J.
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AR037355.1 GI:5955211
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Best Local Similarity 100.0
Matches 16; Conservative
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1 (bases 1 to 21)
Schlingenslepen, K.H. and Brysch, W.
An antisense oligonucleotide preparation method
Patent: JP 201511000-A 263 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
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JP 2001511000-A/263
JP 2001511000-A/263
30-7AN-1998 JP 1998512533
31-JAN-1997 EP 97101531.8
KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
C12115/11, C077121/04, A61K31/70
C12115/11, C077121/04, A61K31/70
Location/Qualifiers
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BD065628
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                                                              1 (bases 1 to 21)
Brysch, W.D. and Schlingensiepen, K.D.
An antisense oligonuclectide preparation method
Patent: EP 0856579-A 263 05-AUG-1998;
BIOGNOSTIK GES (DE)
                                                                                                                                                                                                            0.9%; Score 16.2; DB 1;
ilarity 85.7%; Pred. No. 4.2e+02;
Conservative 0; Mismatches 3;
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    .21
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Sequence 15 from patent US 5856435.
AR027678.
AR027678.1 GI:5938498
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JP 2001511000-A/263.
A90082.1 GI:6738596
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AR027678/c
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Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
Covalently linked oligonucleotide minor grove binder conjugates
Patent: US 5801155-A 2 01-SEP-1998;
Location/Qualifiers
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Unknown.
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Unclassified.
I (bases I to 16)
Bazile, D., Emile, C., Helene, C. and Spenlehauer, G.
Bazile, D. & Emile, C., Helene, C. and Spenlehauer, G.
Bazile, D. & Said-containing composition, its preparation and use Patent: US 5856435-A 15 05-JAN-1999;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 3.3e+02
tive 0; Mismatches 0
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Patent: US 6093809-A 131 25-JUL-2000;
Location/Qualifiers
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/mol_type="unassigned DNA"
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/organism="unknown"
/mol_type="unassigned DNA"
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/organism="unknown"
/mol_type="unassigned DNA"
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Gaps

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TITLE JOURNAL FEATURES

REFERENCE AUTHORS

RESULT 483 AR175845 LOCUS DEFINITION

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PAT 13-MAY-1997
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Kutyavin, I.V., Lukhtanov, E.A., Gamper, H.B. and Meyer, R.B. Jr.
Covalently linked oligonucleotide minor groove binder conjugates
Patent: US 6426408-A 2 30-UUL-2002;
Location/Qualifiers
Nuclease resistant, pyrimidine modified oligonucleotides that detect and modulate gene expression Patent: US 5614617-A 42 25-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 16)
Cook, P. D. and Sanghvi, Y. S.
Nuclease resistant, pyrimidine modified oligonucleotides that
detect and modulate gene expression
Patent: US 5614617-A 60 25-MAR-1997;
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Sequence 60 from patent US 5614617.
138700
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Sequence 2 from patent US 6426408.
AR221692.
AR221692.1 GI:23328764
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Unclassified.
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AR221692/c
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Cook, P.D. and Sanghvi, Y.S.
Nuclease resistant, pyrimidine modified oligonucleotides that
detect and modulate gene expression
Patent: uS 5614617-A 36 25-MAR-1997;
Location/Qualifiers
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Cech, T.R. and Nakamura, T.
Telomerase
Patent: US 6309867-A 131 30-OCT-2001;
Location/Qualifiers
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Seguence 131 from patent US 6309867.
AR175845
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Sequence 36 from patent US 5614617.
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Cook, P.D. and Sanghvi, Y.S.
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DEFINITION ACCESSION

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RESULT 484 I38676/c

VERSION KEYWORDS SOURCE ORGANISM

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AUTHORS TITLE

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RESULT 485 138682/c LOCUS

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DEFINITION ACCESSION VERSION KEYWORDS

SOURCE ORGANISM

REFERENCE AUTHORS

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Gaps

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PAT 11-SEP-2001

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unidentified
unclassified.
unclassified.
unclassified.
1 (bases 1 to 16)
Surface-roughened slide glass and method of analyzing biological
substance using the same
substance using the same
LT 2002211954-A 1 31-JUL-2002;
TOYO KOHAN CO LTD
OS Artificial Sequence
PN JP 2002211954-A/1
PD 31-JUL-2002
PP 30-OCT-2001 JP 2001332778
PI HIROSHI OKAMURA, MICHIFUMI TANGA, MITSUYOSHI OBA, KAORU YAWAKAWA,
PI KENICHI TAKAGI
PC C03C15/00,C03C17/245,C12M1/00,C12N11/14,C12N15/09,C12N15/09,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Surface-roughened slide glass and method of analyzing biological abbience using the same.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cuzin,M., Peltie,P., Fontecave,M., Decout,J.L. and Dueymes,C. Analysis of biological targets using a biochip comprising a fluorescent marker Patent: WO 013282-A 9 30-AUG-2001; COMMISSARIAT A L'ENERGIE ATOMIQUE (FR) LOCATION/Qualifiers
                                                                                                                  Query Match 0.9%; Score 16; DB 1; Length 16; Best Local Similarity 100.0%; Pred. No. 3.3e+02; Matches 16; Conservative 0; Mismatches 0; Indels
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              1..16
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/note="Oligonucleotid"
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Sequence 9 from Patent WO0163282.
AX235176
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JP 2002211954-A/1.
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synthetic construct
artificial sequences.
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AX235176/c
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Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
Covalently linked oligonuclectide minor groove binder conjugates
Patent: US 6486308-A 2 26-NOV-2002;
Location/Qualifiers
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Nucleoside derivatives with photo-unstable protective groups
Patent: WO 0061594-A 2 19-OCT-2000;
DEUTSCHES KREBSFORSCH (DE) ; BEIER MARKUS (DE) ; HOHEISEL JOERG (DE)
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                                                                                                                                                               Unclassified.

1 (bases 1 to 16)

Rurz,M., Lohse,P. and Wagner,R.
Peptide acceptor ligation methods
Patent: US 6429300-A 22 06-AUG-2002;
Location/Qualifiers
                                              16 bp 1
Sequence 22 from patent US 6429300.
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Sequence 2 from patent US 6486308.
AR257437
AR257437.1 GI:27307448
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Sequence 2 from Patent WO0061594.
AX039049.1 GI:11228345
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AR222462
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Indels

Length 17;

PAT 17-DEC-2001

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artificial sequences.

E 1 (bases 1 to 17)
S Nagasu.T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
S Nagasu.T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., No,N. and Ogawa,K.
Pollinosis-associated gene
L Patent: MP 2000106879-A 4 18-APR-2000;
GENOX RESEARCH INC
OS Artificial Sequence
PN JP 2000106879-A/4
PD 18-APR-2000
PF 06-OCT-1998 JP 1998284610
PR
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Unclassified.

(bases 1 to 17)
Scelonge, C.J. and Bidney, D.L.
Gene encoding oxelate decarboxylase from aspergillus phoenices
Patent: US 6303846-A 30 16-QCT-2001,
Location/Qualifiers
                                                                                                                                                 1 (bases 1 to 17)
Scelonge, C. J. and Bidney, D. L.
Gene encoding oxalate decarboxylase from aspergillus phoenices
Patent: US 6297425-A 30 02-OCT-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                              0.9%; Score 16; DB 1; Lv 100.0%; Pred. No. 3.5e+02; tive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 0;
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AR173367
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/organism="unknown"
/mol_type="unassigned DNA"
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/organism="unknown"
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                            AR172076.1 GI:17911026
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JP 2000106879-A/4.
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Matches 16; Conservative
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HIROSHI OBA,KAORU YAMAKAWA,
KENICHI TAKAGI
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Okamura, H., Tanga, M., Oba, M., Yamakawa, K. and Takagi, K.
Okamura, H., Tanga, M., Oba, M., Yamakawa, K. and Takagi, K.
Subrface-roughened slide glass and method of analyzing biological substance using the same Patent: JP 2002211954-A 2 31-JUL-2002;
TOYO KOHAN CO LID
OS Artificial Sequence
PD 31-JUL-2002
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PN JP 200211954-A/2
PN JP 200211954-A/2
PN 31-011-2002
PP 31-011-2003
PP 31-011-2003
PP HIROSHI OKAMURA, MICHIFUMI TANGA, MITSUYOSHI OBA, KAORU NEW KANKINI TAKAGI
PC C1201/68,
PC C1201/68,
PC G1N133/53,G01N33/53,G01N37/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C12N15/00,C1
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PC G01N33/53,G01N33/53,G01N37/00,C12N15/00,C12N15/00
Surface-roughened slide glass and method of analyzing
biological substance
CC using the same
Location/Qualifiers
FT source
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/organism='Artificial Sequence'.
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/organism='Artificial Sequence'
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100.0%; Pred. No. 3.3e+02;
tive 0; Mismatches 0; Indels
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Sequence 30 from patent US 6297425.
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    .16
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unidentified
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Length 17;

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1 (bases 1 to 17)

Muramatsu, T., Fujita, T., Kiyama, M., Irie, T. and Okano, K.

Preparation method of nucleic acid sample for rare expressed genes
and analyzing method using the prepared nucleic acid samples
                                                                                                                                                                                      1 (bases 1 to 17)
Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6346398-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unclassified.

1 (bases 1 to 17)

1 (bases 1 to 17)

2 (bases 1 to 17)

3 (bases 1 to 17)

4 (bases 1 to 17)

5 (bases 1 to 17)

7 (bases 1 to 18)

8 (bases 1 to 18)

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100.0%; Pred. No. 3.5e+02;
tive 0; Mismatches 0;
                                            Sequence 2550 from patent US 6346398.
AR187062.
AR187062.1 GI:20233027
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Sequence 2551 from patent US 6346398.
AR187063
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    .17
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Sequence 3 from patent US 6485916.
AR256849 1 GI:27306475
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Takamichi,M., Tsuyoshi,F., Masaharu,K., Takashi,I. and Kazunori,O.
Method for preparing nucleic acid sample for analyzing minor gene,
nucleic acid sample thus prepared and method for analyzing nucleic
acid sample by using the same, and reagent kit and analysis service
for using the same
Patent: JP 2000037193-A 3 08-FEB-2000;
HITACHI LTD
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TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
NING NO,
                                                 KAORU OGAWA
C12N15/09,A61K31/00,A61K39/36,A61K45/00,C12Q1/68,C12N15/00 CC
                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                    organism='Artificial Sequence'
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iive 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels
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                                                                                                    Location/Qualifiers
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/organism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Strandedness: Single;
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JP 2000037193-A/3
08-FEB-2000
19-MAY-1999 JP 1999138051
                                                                                                                                                    Location/Qualifiers
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JP 2000037193-A/3.
unidentified
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PAT 15-FEB-2002
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                       1 (bases 1 to 17)
Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6566127-A 1075 20-MAY-2003;
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A method and an algorithm for mrna expression analysis
Patent: WO 0208461-A 24 31-JAN-2002;
Global Genomics AB (SE)
Location/Qualifiers
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                                    linear
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Double-stranded product DNA"
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                                AR323673 17 bp RNA Sequence 1075 from patent US 6566127.
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                                                                                                                                                                                                                                                                                                            /mol_type="unassigned RNA"
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Sequence 24 from Patent WO0208461.
AX361606
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                                                                                                                                                                                                                                                                               1. .17
/organism="unknown"
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                                                                    AR323673.1 GI:33709481
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synthetic construct
artificial sequences.
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                                                                                                                                                       Unclassified.
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RESULT 503
AR323673/C
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AX361606/c
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AX692525/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Unclassified.

1 (bases 1 to 17)

McClelland,M., Welsh,J. and Trenkle,T.

Reduced complexity nucleic acid targets and methods of using same
Patent: US 6495319-A 64 17-DEC-2002;

Location/Qualifiers
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Unclassified.
Unclassified.
Unclassified.
I (bases I to 17)

Pavco, P., McSwiggen, J. A., Stinchcomb, D.T. and Escobedo, J.

Pavco, P., McSwiggen, Eor the treatment of diseases or conditions
method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 1074 20-MAY-2003;

Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels
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Sequence 1074 from patent US 6566127.
AR323672 GI:33709480
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Sequence 64 from patent US 6495319.
AR266626
                  Patent: US 6485916-A 3 26-NOV-2002;
Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
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/organism="unknown"
/wol_type="genomic DNA"
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WO 0065050-AAL

Synthetic construct

artificial sequences.

artificial sequences.

I (bases I to 17)

S Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,

AL (bases I to 17)

Takahashi,E. and Yokoi,A.

795, a novel gene related to pollen allergy

AL PATCHING,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,

TARAHASHI,AKIRA YOKOI

OS Artificial Sequence

PN WO 0065050-A/4

PD 02-NOV-2000

PF 26-APR-2000 WO 2000JP002734

PR 27-APR-1999 JP 99P 120494

PR 27-APR-1999 JP 99P 120499

PR 27-APR-1999 JP 99P 1
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synthetic construct
artificial sequences.
1 (Sepsel to 17)
Nagaeu, T., Sugita, Y., Kashiwabara, T., Oshida, T., Obayashi, M.,
Gunji, S., Obayashi, I., Imai, Y., Yoshida, N., Ogawa, K. and Matsui, K.
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795, a novel gene related to pollen allergy.
BD011732
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441, a novel gene related to pollen allergy.
BD091744
                                                 Query Match
0.9%; Score 16; DB 1; Lv
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 0;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xrefe="taxon:32630"
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WO 0065050-A/4.
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WO 0073435-A/4.
product DNA"
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Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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                                            Patent: EP 1281758-A 5257 05-FEB-2003;
Aeomica, Inc. (US)
Location/Qualifiers
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Sequence 5259 from Patent EP1281758.
AX692527
                                                                                                                                            /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

    .17
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Sequence 24 from Patent WO03064691.
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Location/Qualifiers
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synthetic construct
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100.0%; Pred. No. 3.5e+02;
iive 0; Mismatches 0;
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Patent: WO 0073435-A 4 07-DBC-2000;
GENOX RESEARCH INC, TAKESHI NAGASU, YUJI SUGITA, TOWOKO KASHIWABARA, TADAHIRO OSHIDA, MASAYA OBAYASHI, SHIGEMICHI GUNJ, IZUMI OBAYASHI, YUKIHO IMAI NEI YOSHIDA, KAORU OGAWA, KEIKO MATSUI

COMMENT OS ALTIficial Sequence
PN WO 0073435-A/4
PD 07-DEC-2000
PF 18-MAY-2000 WO 200019003190
PR 27-MAY-1999 JP 99P 148783
PI TAKESHI NAGASU, YUJI SUGITA "
PI NASAYA OBAYASHI, SHIGFW"
PI KAORU OGAW"
PC C12N'
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CI2N15/10, C12Q1/68, G01N33/15, G01N33/50
Description of Artificial Sequence:Artificially Synthesized CC
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27-MAY-1999 JP 99P 148783
TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,
MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI, YUKIHO IMAI,
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OS Artificial Sequence
NW 0073439-A/4
PD 07-BEC-2000
PF 18-MAY-2090 JP 99P 148784
PI TAKESHI NAGASU,YUJI SUGITA, TOWOKO KASHIWABARA, TADAHIRO OSHIDA,
PI MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI, YUKIHO IMAI,
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PI TAKESHI NGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA
PI MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI, YUKIHO IMAI,
PI NEI YOSHIDA,
PI KAORU OGAWA, KEIKO MATSUI, EIKI TAKAHASHI, AKIRA YOKOI PC
C12N15/12, C12Q1/68, A61P37/08, A61K39/36, A61K45/00 CC Description
of Artificial Sequence: Artificially Synthesized CC Primer
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to pollen allergy.
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Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 0;
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/db_xref="taxon:32630"
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/mol_type="genomic DNA"
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KEYWORDS
SOURCE
ORGANISM
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BD091752/c
LOCUS
DEFINITION
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S BOUSTA'S LANGE CONSTRUCT

SYNTHETIC CONSTRUCT

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SYNTHETIC CONSTRUCT

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NN WO 0073440-A/4
PD 07-BCC-2000
NO 2000JP003192
PF 18-MAY-2000 WO 2000JP003192
PF 27-MAY-1999 JP 99P 148785
PI TAKESHIN NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,
PI MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI, YUKIHO IMAI,
PI NSAYA OBAYASHI, SEKIXO MATSUI, EIKI TAKAHASHI, AKIRA YOKOI PC
PI KAORU OGAWA, KEKIXO MATSUI, EIKI TAKAHASHI, AKIRA YOKOI PC
C12N15/12, C12Q1/68, C12N5/06, C07K14/415, CC Description of
Artificial Sequence: Artificially Synthesized CC Primer Sequence
FH Key
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synthetic construct
synthetic construct
synthetic construct
synthetic construct
synthetic construct
artificial sequences.

1 (bases 1 to 17)
Nagasu,T., Obsida,T., Obsyashi,I., Matsul,K. and Sait,H.
Nagasu,T., Obsida,T., Obsyashi,I., Matsul,K. and Sait,H.
Nagasu,T., Obsida,T., Obsyashi,I., Matsul,K. and Sait,H.
Nathor for examination for allergosis
patent: WO 0165259-A 7 07-SEP-2001,
GENOX RESERCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, HIROHISUN NAKAUCHI,YUTAKA
DEBVIRKI,KAZUO FUKWAN,OSANI KUDO TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI
OBAYASHI,KEIKO MATSUI, HIROHISA SAITO
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BD091775
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PAT 17-JAN-2003
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Patent: JP 2002095500-A 4 02-APR-2002;
GENOX RESEARCH INC, THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL
OS Artificial Sequence
PD 02-APR-2002
PP 25-APR-2000
PP 25-SEP-2000
PP 25-SEP-2000
PP VUJI SUGITA, RYOLCHI HASHIDDA, KAORU OGAWA. WASAYA OBAYARHT PT
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oc C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/10 PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Artificial Sequence
17 2002095500-A/4
02-BEP-2000 JP 2000291316
25-SEP-2000 JP 2000291316
YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,WASAYA OBAYASHI,
                                                          Gaps
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synthetic construct
artificial sequences.
I (bases 1 to 17)
Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
Tsujimoto,K.
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                    0.9%; Score 16; DB 1; Length 17;
100.0%; Pred. No. 3.5e+02;
iive 0; Mismatches 0; Indels
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N BD167837
N BD167837.1 G1:27873649
WO 0233122-A/4.
Synthetic construct
A synthetic construct
artificial sequences.

1 (bases 1 to 17)
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    .17
    forganism="synthetic construct"
|mol_type="genomic DNA"
|db_xref="taxon:32630"

                                                                                                                                                                                                                 BD143836 17 bp DNA Method of examining allergic disease. BD143836
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                                                                                         1735 CAAAAAAAAAAAAA 1750
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                                                                                                                            17 CAAAAAAAAAAAA 2
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                    Query Match
Best Local Similarity 100.0
Matches 16; Conservative
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ACCESSION
VERSION
KEYWORDS
SOURCE
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BD143836/c
LOCUS
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BD167837/c
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AUTHORS
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G01N33/50//C12P21/08, (C12N5/10,C12R1:91), (C12P21/02,C12R1:91)
Description of Artificial Sequence:an artificially synthesized
                                                   23-FEB-2001 WO 2001JP001372
02-MAR-2000 JP 00P 61832
TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI OBAYASHI,KEIKO MATSUI, PI
                                                                                                                                                           Description of Artificial Sequence: Artificially Synthesized CC
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                                                                                                      HIROHISA SAITO
C GO1N33/53,C12Q1/68,C12N15/12,G01N33/15,A01K67/027,A61K39/395,
C A61P37/08
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CI2N15/09, CI2NS/10, C07K14/47, C07K16/18, C12P21/02, C12Q1/02, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A01K67/027, A61K31/713, A61K45/00, A61K48/00, A61P17/00, A61P37/08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Artificial Sequence
WO 0224903-A/4
28-MAR-2002
21-SEP-2001 WO 2001JP008246
25-SEP-2000 JP 00P 291318
YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTATIONAL CHILDREN'S

synthetic construct
artificial sequences.

1 (bases 1 to 17)
Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T.,
Fujimco,G. and Takahashi,E.
Method of examining allergic disease
Patent: WO 0224903-A 4 28-MAR-2002,
GENOX RESEARCH INC, JAPPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, YUJI SUGITA,RYOICHI HASHIDA,KAORU
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'organism='Artificial Sequence'.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                            Length 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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100.0%; Pred. No. 3.5e+02;
rative 0; Mismatches 0;
                                                                                                                                                                                                Location/Qualifiers

    17
    Organism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"

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    17
    Aorganism="synthetic construct"
|mol_type="genomic DNA"
|db_xref="taxon:32630"

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Artificial Sequence
WO 0165259-A/7
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Best Local Similarity 100.0
Matches 16; Conservative
                                                                                                                                                                                Primer Sequence
                                    07-SEP-2001
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OS Artif
PN WO 02
PD 28-MAI
PF 21-SE
PR 25-SE
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PC A01K6
PC G01N3
PC G01N3
CC Descr
   PR PR
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LOCUS
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VERSION
KEYWORDS
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
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Method for examination for allergosis

Method for examination for allergosis

Match: WO 0233069-A 20 25-APR-2002;

GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF

NATIONAL CHILDREN'S HOSPITAL, TOMOYUKI FUKASAWA, CHUHEI NOJIRI, NOBUO

MATSUHASHI, KOJI NISHIZAWA, YUJI SUGITA, RYOICHI HASHIDA, KAORU

OGAWA, MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA SAITO

OS Artificial Sequence

PW 00 233069-A/20

PP 28-SEP-2001 WO 2001JP008574

PR 13-OCT-2000 JP 00P 314093
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Description of Artificial Sequence:an artificially synthesized
    Description of Artificial Sequence:an artificially synthesized
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28-SEB-2001 WO 2001JP008574
13-CCT-2000 JP 00P 314093
YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI,
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synthetic construct
artificial sequences.
1 (bases 1 to 17)
Sugita.Y., Hashida.R., Ogawa.K., Obayashi,M., Nagasu,T. and
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Location/Qualifiers
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100.0%; Pred. No. 3.5e+02;
iive 0; Mismatches 0; Indels
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    .17
    /organism="synthetic construct"
|mol_type="genomic DNA"
|db_xrefe="taxon:32630"

    1.17
    Corganism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"

                                                                               Location/Qualifiers
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WO 0233069-A/20.
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PI HIROHISA SP
PC C12N15/09,
A61K39/395,
PC C07K14/47,
CC Description
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Description of Artificial Sequence:an artificially synthesized
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C12Q1/68,C12N15/09,G01N33/53,G01N33/50,C12Q1/02,A61K48/00, PC
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Patent: WO 0226962-A 8 04-APR-2002;
GENOX RESEARCH INC. JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDEREN'S HOSPITAL, MASAKAZU ADACHI, KAZUO MIYANAGA YUJI
SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOWOKO FUJISHIMA, TAKESHI
NAGASU, HIROHISA SAITO
OS ATRIFICIAL Sequence
PN WO 0226962-A/8
PD 04-APR-2002
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Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H. and Takahashi,E. Method for examination of allergosis Patent: WO 0233122-A 4 25-ARR-2002; GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF WAITONAL, CHILDREN'S HOSPITAL, RINAKO NAKAGAMA YUJI SUGITA,RYORU HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, TAKAHASHI NAGASU, HIROHISA
                                                                                                                                                                                                  25-APR-2002
11-OCT-2001 WO 2001JP008937
13-OCT-2000 JP 00P 314093
YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
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26-SEP-2000 JP 00P 293021
YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA,
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Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and
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100.0%; Pred. No. 3.5e+02;
ttive 0; Mismatches 0;
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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BD167909/c
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E32460 E32460.1 GI:13018696
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C12N15/00,
                                                               C12P21/02, C12P21/08// (C12N5/10, C12R1:91), (C12P21/08, C12R1:91),
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CI2N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10,
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Mammal-derived tissue specific physiologically active protein.
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primer bind (1). (18).
Location/Qualifiers
1. 18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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    .18
/organism="synthetic construct"

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/db_xref="taxon:32630"
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E32457.1 GI:13018693
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PC C12P21
PC C12N15
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Method of examining allergic disease
Method of examining allergic disease
Batent: W0 0250269-A 4 27-JUN-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, MASAMICHI TAKAGI,AKINORI OTA YOSHIKO
MATSUMOTO,YUKIHO IMAI,TADAHIRO OSHIDA,YUJI SUGITA, TAKESHI NAGASU,
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CIZRAIŠ/11,CO7K16/18,A61K67/027,A61K31/711,A61K45/00,A61K48/00,
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Mammal-derived tissue specific physiologically active protein.
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Matsumoto,Y., Imai,Y., Oshida,T., Sugita,Y., Nagasu,T. and
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xrefe="taxon:32630"
                                                                               Method of examining allergic disease.
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21-DEC-2001 WO 2001JP011286
21-DEC-2000 JP 00P 389476
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JP 2000037190-A/11
08-FEB-2000
23-JUL-1998 JP 1998225228
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WO 0250269-A/4
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synthetic construct
artificial sequences.
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PAT 18-MAY-2002
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                                                                                                      Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R. Blnary encoded sequence tags
Patent: WO 0112855-A 7 22-FEB-2001;
YALE UNIVERSITY (US)
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Mol_type="unassigned DNA"
Ab Aref="taxon:32630"
/db cref="probes to target sequences"
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Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 0;

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    /organism="synthetic construct"
/mol_type="unassigned DNA"
    /db xref="taxon:32630"
    /noTe="Primer"

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Calibration of molecular array data
Patent: EP 1186673-A 1 13-MAR-2002;
Agilent Technologies Inc (US)
Location/Qualifiers
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1 (bases 1 to 21)
Rambara, H. and Uematsu, C.
DNA fragment preparation method for Patent: US 6203988-A 8 20-MAR-2001;
Location/Qualifiers
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/wol_type="unassigned DNA"
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20 bp
Sequence 1 from Patent EP1186673.
AX394603
AX394603.1 GI:21065716
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Best Local Similarity 100.'
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                                                                                                                                                                                                                                                                                                                                                                            JUN NISHIU, YUSUKE NAKAMURA, TOSHIHIRO TANAKA
C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
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1 (Dages I to 18)
Kaufman, J.C., Roth, M.B., Lizardi, P.M., Feng, L. and Latimer, D.R.
Binary encoded sequence tags
Patent: US 6383754-A 77 - MAY-2002;
Location/Qualifiers
                                                                          artificial sequences.

1 (bases 1 to 18)
Jun,N., Yusuke,N. and Toshihiro,T.
Mammal-derived tissue specific physiologically active protein
Datent: JP 2000037190-A 20 08-FEB-2000;
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0.9%; Score 16; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 0;
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0.9%; Score 16; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 0;
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/organism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"
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    .18
    /organism="unknown"
    /mol_type="unassigned DNA"

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Sequence 7 from patent US 6383754.
AR208427
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Sequence 7 from Patent WO0112855.
AX085253
AX085253.1 GI:13275311
                                                                                                                                                                                                                                        Artificial Sequence
JP 2000037190-A/20
08-FEB-2000
23-JUL-1998 JP 1998225228
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Unclassified.
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PN JP 20
PD 08-FE
PF 23-JU
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PC C12N15/02,
PC C12P2
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AUTHORS TITLE JOURNAL FEATURES

RESULT 523

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ACCESSION VERSION KEYWORDS SOURCE

RESULT 522

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PAT 18-MAY-2002
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 0.9%; Score 16; DB 1; Length 21; 88.9%; Pred. No. 4.5e+02;
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                                    1; Indels
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .21
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//nol_type="unassigned DNA"
/db_xref="taxon:32650"
/noTe="probes to target sequences"
                                                                                                                                                                                                  DNA
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Patent: WO 0130362-A 1938 03-MAY-2001;
IMMUSOL, INC. (US)
                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                        Calibration of molecular array data
Patent: EP 1186673-A 2 13-MAR-2002;
Agilent Technologies Inc (US)
Location/Qualifiers
                                                                                                                                                                                            21 bp
Sequence 2 from Patent EP1186673.
AX394604
AX394604.1 GI:21065717
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synthetic construct
artificial sequences.
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Homo sapiens
Query Match
Best Local Similarity 88.9°
Matches 16; Conservative
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AX130720
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PR HIDEKI KAMIBARA, SENSHU UEMATSU
PC C12N15/09, C12Q1/68, G01N27/447, C12N15/00, G01N27/26 CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1. 21
/organism='Unidentified'.
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   Length 21;
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Query Match
0.9%; Score 16; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels
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Human single nucleotide polymorphisms
Patent: WO 0138276-A BS 31-MAY-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
Location/Qualifiers
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/organism='Unidentified'
Location/Qualifiers
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100.0%; Pred. No. 4.5e+02;
tive 0; Mismatches 0;
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1 (bases 1 to 21)
Hideki, K. and Senshu, U.
Method for analyzing DNA fragment
Patent: JP 1999196874-A 8 27-JUL-1999;
HITACHI LTD
OS Unidentified
PN JP 1999196874-A/8
PD 27-JUL-1999
PP 14-JAN-1999 JP 1998005399
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 85 from Patent W00138576.
AX153987.1 GI:14535601
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/organism="unidentified"
/mol_type="genomic DNA"
/do_xref="taxon:32644"
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Best Local Similarity 100.(
Matches 16; Conservative
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E28097/c
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AX153987
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TITLE
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PAT 16-MAY-2001
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89.5%; Pred. No. 4.5e+02;
tive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                 Unclassified.

Unclassified.

1 (bases 1 to 20)

S Bennett, C.Frank. and Mirabelli, C.K.
Oligonucleotide inhibition of cell adhesion

AL Patent: US 6169079-A 57 02-JAN-2001;

Location/Qualifiers

Location/Qualifiers
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1 (bases 1 to 20)
Bennett, C.Frank. and Mirabelli, C.K.
011gonuclectide modulation of cell adhesion
Patent: US 5514788-A 57 07-MAY-1996;
Location/Qualifiers
                                                         Query Match 0.9%; Score 15.8; DB 1; Best Local Similarity 89.5%; Pred. No. 4.5e+02; Matches 17; Conservative 0; Mismatches 2;
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Sequence 57 from patent US 5514788.
120659 1 GI:1601014
1. .20
/organism="unknown"
/mol_type="unassigned DNA"
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Seguence 57 from patent US 6169079.
AR123244
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/mol_type="unassigned DNA"
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/mol_type="unassigned DNA"
                                                                                                                     839 CTGCTGGGGTCTCTGGCCC 857
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AR123244/c
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I20659/c
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133352/c
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FEATURES
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AUTHORS
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Bennett, C. Frank., Mirabelli, C. K. and Baker, B.
Antisense modulation of cell adhesion molecule expression and treatment of cell adhesion molecule-associated diseases
Patent: US 609672-2A 57 01-AUG-2000;
Location/Qualifiers
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89.5%; Pred. No. 4.5e+02;
ative 0; Mismatches 2; Indels
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89.5%; Pred. No. 4.5e+02;
tive 0; Mismatches 2; Indels
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Bennett, C. Frank. and Mirabelli, C.K.
Oligonucleotide modulation of cell adhesion
Patent: US 6093811-A 57 25-UUL-2000;
Location/Qualifiers
                                                                                                                                                                                               adhesion
                                                                                                                                     Unclassified.
Unclassified.
1 (bases 1 to 20)
Bennett, C. Frank. and Mirabelli, C. K.
Oligonucleotide modulation of cell adhe
Patent: US 5843738-A 57 01-DEC-1998;
Location/Qualifiers
                                            DNA
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Sequence 57 from patent US 5843738.
AR062657
AR062657.1 GI:5990348
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Sequence 57 from patent US 6096722.
AR105582.1 GI:12819179
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/organism="unknown"
/mol_type="unassigned DNA"
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/organism="unknown"
/mol_type="unassigned DNA"
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Matches 17; Conservative
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Matches 17; Conservative
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DEFINITION
ACCESSION
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KEYWORDS
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ORGANISM
           RESULT 530
AR062657/C
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AR105582/c
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Query Match 0.9%; Score 15.8; DB 1; Length 20; Best Local Similarity 89.5%; Pred. No. 4.5e+02; Matches 17; Conservative 0; Mismatches 2; Indels
   /note="Antisense oligonucleotide
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Sequence 1782 from Patent WO0142511.

    .20
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    /db_xref="taxon:9606"

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    .20
    /organism="Homo sapiens"

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Antisense oligonucleotide sequences derived from groel and groes as inhibitors of microorganisms
Patent: WO 0136625-A 16 25-MAY-2001,
GeneSense Technologies Inc. (CA)
Location/Qualifiers
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89.5%; Pred. No. 4.5e+02;
tive 0; Mismatches 2; Indels
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                                                         Unclassified.
Unclassified.
1 (bases 1 to 20)
3 Bennett, C.Frank. and Mirabelli, C.K.
Oligonucleotide modulation of cell adhesion
Location/Qualifiers
Location/Qualifiers
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Bennett, C.F. and Mirabelli, C.K.
Oligonuclectide inhibition of cell adhesion
Patent: US 6300491-A 57 09-OCT-2001;
Location/Qualifiers

    .20
    forganism="synthetic construct"
|mol type="unassigned DNA"
|db_xref="taxon:32630"

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Sequence 57 from patent US 6300491.
AR370582. GI:34607335
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Seguence 16 from Patent WO0136625.
AX148814
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/mol_type="genomic DNA"
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I33352.1 GI:1824143
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Matches 17; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Daly,M., Hudson,T.J., Lander,E.S., Rioux,J. and Siminovitch,K. Ibd-related polymorphisms
Patent: WO 0142511-A 1782 14-JUN-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); Ellipsis Biotherapeutics Corporation (CA)
Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
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MOLECULAR ENGINES LAB (FR)
Location/Qualifiers
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Topology: Linear;
Gene family encoding apoptosis-associated peptides, peptides
encoded
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No JP 2002516564-A/6

PD 04-JUN-2002

PF 24-SEP-1997 JP 1998515877

PR 24-SEP-1996 US 60/028363 PI

SAMULI UMANSKY, HOVSEP MELKONYAN

PC 021N15/12, C12N15/62, C07K14/47, C07K16/18, C12Q1/68, G01N33/53, G01N33/68,
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0159103-A 2364 16-AUG-2001;
RIBOZYME HAMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
                   1 (bases 1 to 17)
Umansky, S. and Melkonyan, H.
Gene family encoding apoptosis-associated peptides, peptides encoded thereby and method of using the same
Patent: JP 2002516564-A 6 04-JUN-2002;
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/organism="synthetic construct"
/mol_type="unassigned RNA"
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/noTe="Nucleic Acid"
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Sequence 2364 from Patent WO0159103.
AX216922
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/organism="unidentified"
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/db_xref="taxon:32644"
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AX216922
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BD217905-BD217905-1 GI:33027675
UP 2002516564-A/6.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Method for the amplification of hla class i alleles
Patent: WO 061795-A 73 19-OCT-2000;
CANCK ILSE DE (BE); ROSSAU RUDI (BE); INNOGENETICS NV (BE)
ROMBOUT ANNELIES (BE)
                                                                                                                                                                                                                        1 (bases 1 to 21)
Cohen, D., Chumakov, I. and Blumenfeld, M.
Biallelic markers for use in constructing a high density disequilibrium map of the human genome Patent: US 6537751-A 10471 25-MAR-2003, Location/Qualifiers
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0.9%; Score 15.8; DB 1;
Best Local Similarity 89.5%; Pred. No. 4.7e+02;
Matches 17; Conservative 0; Mismatches 2;
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Sequence 10471 from patent US 6537751.
AR298736
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/mol_type="genomic DNA"
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                                                                                                                                                                                                         Unclassified.
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Sequence 7 from patent US 5965403.
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                                                                                                           Aeomica, Inc. (US)
Location/Qualifiers
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Mus musculus
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AX723348/c
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AR079076
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method and reagent for the inhibition of erg
Patent: WO 0188124-A 1467 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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AX692524
                                  RNA
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Aeomica, Inc. (US)
Location/Qualifiers
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Sequence 5255 from Patent EP1281758.
                               AX423131
Sequence 1467 from Patent WO0188124.
                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="unassigned RNA"
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                       Shannon, M., Gu, Y. and Nguyen, C.T.
Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
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Unknown.
Unclassified.
1 (bases 1 to 18)
1 (bases 1 to 18)
Celeste, A.J. and Murray, B.L.
Nucleic acids encoding bone morphogenic protein-16 (BMP-16)
Patent: US 5965403-A 7 12-0CT-1999;
Patent: Location/Qualifiers
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Patent: WO 03025176-A 1035 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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                                                                                                                                                   Patent: EP 1281758-A 5256 05-FEB-2003;

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    /organism="Homo sapiens"
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/db_xref="taxon:9606"

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/db_xref="taxon:10090"
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

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RESULT 549 E32450/c LOCUS

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PAT 18-JUN-2001
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C12N15/00,
                                                                                                                                                 C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
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                                                            JUN NISHIU, YUSUKE NAKAMURA, TOSHIHIRO TANAKA
CI2N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
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CI2N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
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JP 2000037190-A/13.
Synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 18)
Jun, N., Yusuke, N. and Toshihiro, T.
Mammal-derived tissue specific physiologically active protein
patent: JP 2000037190-A 13 08-FEB-2000;
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Mammal-derived tissue specific physiologically active protein.
E32453
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Pred. No. 4.5e+02;
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Location/Qualifiers 1.18
/ organism="synthetic construct"/mol_type="genomic DNA"/db_xref="taxon:32630"
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/organism="synthetic construct"
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/db_xref="taxon:32630"
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JP 2000037190-A/13
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Matches 16; Conservative
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E32455/c
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Mammal-derived tissue specific physiologically active protein.
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Synthetic construct
Synthetic construct
artifictal sequences.

E 1 (bases 1 to 18)

Mammal-derived tissue specific physiologically active protein

I DAPAN TOBACCO INC
OS Artifictal Sequence

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NA POBO0037190-A/12

PN JP 2000037190-A/12

PD 08-FEB-2000
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UP 2000037190-A/10.
SM synthetic construct
artificial sequences.
E 1 (bases 1 to 18)
S Jun,N., Yusuke,N. and Toshihiro,T.
Mammal-derived tissue specific physiologically active protein
L Patent: JP 2000037190-A 10 08-FEB-2000;
JAPAN TOSACCO INC
OS Artificial Sequence
PD 08-FEB-2000
PD 08-FEB-2000
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CI2N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
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Mammal-derived tissue specific physiologically active protein.
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                                                               Length 18;
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0.9%; Score 15.4; DB 1;
Best Local Similarity 94.1%; Pred. No. 4.5e+02;
Matches 16; Conservative 0; Mismatches 1;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="texon:32630"
      /mol_type="unassigned DNA"
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AUTHORS TITLE REFERENCE

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Celeste, A.J. and Murray, B.L.
Bone morphogenic protein-16 (BMP-16) compositions
Patent: US 6331612-A 7 18-DEC-2001;
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Celeste, A.J. and Murray, B.L.
Bone morphogenetic protein-16 (BMP-16) antibodies
Patent: US 6623934-A 7 23-88P-2003;
                                                                  ch 0.9%; Score 15.4; DB 1; Similarity 94.1%; Pred. No. 4.5e+02; 16; Conservative 0; Mismatches 1;
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AR401428
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Sequence 21 from Patent W00063359.
AX039283
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/organism="unknown"
/wol_type="genomic DNA"
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/organism="unknown"
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Mammal-derived tissue specific physiologically active protein.
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C12N15/00,
           Manual Terrived Lissue specific physiologically active protein.
B32455.1 GI:13018691
JP 200037190-4/15.
Synthetic construct
artificial sequences.
To bases 1 to 18)
Jun, N., Yusuke, N. and Toshihiro, T.
Mammal-derived tissue specific physiologically active protein
DAPAN TOBACCO INC
OS Artificial Sequence
PR 22-00037190-4/15
PP 2200037190-4/15
PP 23-JUL-1998 JP 199825228
PP 23-JUL-1998 JP 199825228
PP 23-JUL-1998 JP 199825228
PP CI2NIS/09, CO7K14/47, CO7K16/18, CI2NI/21, CI2NS/10, PC
CI2NIS/00,
PC CI2NIS/00,
PC CI2NIS/00, CI2NIS/00, CI2NIS/10, CI2NI:91)
CC CI2NIS/00, 
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C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
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CI2N15/09, CO7K14/47, CO7K16/18, C12N1/19, C12N1/21, C12N5/10, PC
Mammal-derived tissue specific physiologically active protein.
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JP 2000037190-A/16.
synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 18)
Jun,N., Yusuke,N. and Toshihiro,T.
Patent: JP 2000037190-A 16 08-FEB-2000;
JAPAN TOBROCO INC
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/organism="synthetic construct"
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JP 2000037190-A/16
08-FEB-2000
23-JUL-1998 JP 1998225228
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E32456/c
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Kambara, H. and Okano, K.
DNA sequencing method and DNA sample preparation method
Patent: US 5985556-A 5 16-NOV-1999;
Location/Qualifiers
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Location/Qualifiers
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  Query Match 0.9%; Score 15.4; DB 1; Length 20; Best Local Similarity 94.1%; Pred. No. 5.1e+02; Matches 16; Conservative 0; Mismatches 1; Indels
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JP 1997140400-A/1
JS 1997140400-B/1
JS 5EP-1997
JS 5EP-1996
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1 (bases 1 to 20)
Okano, K. and Kanbara, H.
DETERMINATION OF BASE SEQUENCE
PATENT: JP 1997140400-A 1 03-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="unknown"
/mol_type="unassigned DNA"
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Sequence 5 from patent US 5985556.
AR086111
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Oligonucleotide.
E13187
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Unclassified.
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E13187/c
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Unknown.
Unclassified.
Unclassified.
Kambara,H. and Okano,K.
DNA sequencing method and DNA sample preparation method
Patent: US 598556-A 3 16-NOV-1999;
Location/Qualifiers
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Kambara, H. and Okano, K.
DNA sequencing method and DNA sample preparation method
Patent: US 598556-A 4 16-NOV-1999;
Location/Qualifiers
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/organism="synthetic construct"
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/note="PCR PRIMER"
                                                                                                                                                          Gene expression in eukaryotic cells
Patent: WO 0063359-A 21 26-OCT-2000,
University College London (GB)
Location/Qualifiers
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/organism="unknown"
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Sequence 3 from patent US 5985556.
AR086109
AR086109.1 GI:10012875
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5985556.
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Sequence 4 from patent US
AR086110
AR086110.1 GI:10012876
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    GI:11229388
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                                            synthetic construct
synthetic construct
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    AX039283.1
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AR086109/C
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: A61P13/12,A61P31/18,A61P37/06,C12N5/10,C12N15/02,C12N15/09, PC
C12P21/08//
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HIROKO YOSHIDA,
PI KIMIHISA ICHIKAWA,JUN OKUMA,MASAHIKO OTSUKI,AKIO SHIRAISHI, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A61K39/395, A61K39/395, A61K39/00, A61P1/16, A61P7/06, A61P9/00, PC
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Drug containing anti-Fasantila. As antiboo,
Patent: JP 2000169393-A 57 20-JUN-2000;
SANKYO CO LTD
OS ARTIFICIAL Sequence
PN JP 2000169393-A/57
PD 20-JUN-2000
PP 20-JUN-2000
PP 20-JUN-2000
PP PP 20-JUN-2000
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                                                                                        ce 1. .20
/organism='Artificial sequences'
Location/Qualifiers
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/organism='Artificial Sequence'.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                     linear
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OKANO KAZUNOBU, KANBARA HIDEKI
C12Q1/68,G01N27/447,G01N33/58//C12N15/09;
strandedness: Single;
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    .20
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|db_xref="taxon:32630"

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Drug containing anti-Fas antibody.
E40060
                                                                                                                                         1. .20
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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synthetic construct
artificial sequences.
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E40060
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/organism='Artificial sequences'.

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                                                                                                                                                        linear
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                 1; Indels
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JP 1997140400-A/2
03-JUN-1997
13-SEP-1996 UP 1996242929
18-SEP-1996 UP 5P 95P 238141
OKANUORU, KANBARA HIDEKI
C1201/68,001N27/447,001N33/58//C12N15/09;
   94.1%; Pred. No. 5.1e+02;
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                                                                                                                                                        DNA
                                                                                                                                                                                                                                                                                   Okano, K. and Kanbara, H.
DETERNINATION OF BASE SEQUENCE
PATENT: JP 1997140400-A 2 03-JUN-1997;
HITACHI LTD
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Okano, K. and Kanbara, H.
DETERMINATION OF BASE SEQUENCE
PACENT: JP 1997140400-A 3 03-JUN-1997;
HITACHI LTD
                 0; Mismatches
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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18-SEP-1995 JP 95P 2381
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JP 1997140400-A/3
03-JUN-1997
                                             1733 TACAAAAAAAAAAAA 1749
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E13188
E13188.1 GI:3251993
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unidentified
unidentified
unclassified.
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 Best Local Similarity 94.1
Matches 16; Conservative
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E13189
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E13189/c
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Length 20;
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synthetic construct
artificial sequences.

1 (bases 1 to 20)
Serizawa,N., Haruyama,H., Nakahara,K. and Tamaki,I.
Humanized anti-Fas antibody
Patent: 17 200166574-A 61 20-JUN-2000;
SANKYO CO LTD
                                                                                                                                                                                                                                                                                                                                      linear
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0.9%; Score 15.4; DB 1;
Best Local Similarity 94.1%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 1;
                   Location/Qualifiers
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E43414. GI:18627680
JP 2000166573-A/57. synthetic construct synthetic construct artificial sequences.
                                                                Location/Qualifiers
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JP 2000166574-A/61
20-JUN-2000
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C12N15/09,A61K39/00,A61K39/395,A61K39/395,A61P37/02,A61P43/00,
C07K16/18,
C12N1/21,C12N5/10,C12P21/08//(C12N1/21,C12R1:19),C12N15/00, PC
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                  PAT 31-JAN-2002
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PI KIMIHISA ICHIKAWA, JUN OKUMA, MASAHIKO OTSUKI, AKIO SHIRAISHI,
                                                                                                                                                       Serizawa, N., Haruyama, H., Takahashi, W., Yoshida, H., Ichikawa, K., Okuma, J., Otsuki, M., Shiraishi, A. and Yonehara, S. Drug containing anti-Fas antibody Patent: JP 2000169393-A 61 20-JUN-2000; SANKYO CO LTD
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JP 2000166574-A/57

SYnthetic construct
synthetic construct
artificial sequences.

I (bases 1 to 20)
Serizawa,N., Haruyama,H., Nakahara,K. and Tamaki,I.
Humanized anti-ras antibody
Patent: JP 2000166574-A 57 20-JUN-2000;
SANKYO CO LTD
OS Artificial Sequence
PN JP 2000166574-A/57
PD 20-JUN-2000
PF 29-SEP-1999 JP 1999275441
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                   linear
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Drug containing anti-Fas antibody.
E40064
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JP 2000169393-A/61
20-JUN-2000
30-SEP-1999 JP 1999278301
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Humanized anti-Fas antibody.
                                                           E40064.1 GI:18627180
JP 2000169393-A/61.
synthetic construct
synthetic construct
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1 (bases 1 to 20)
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Best Local Similarity 94.13
Matches 16; Conservative
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E40064/c
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E40868
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PAT 31-JAN-2002
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C12N1/21,C12N5/10,C12P21/08//(C12N1/21,C12R1:19),C12N15/00, PC
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C12N15/09,A61K39/00,A61K39/395,A61K39/395,A61P37/02,A61P43/00,
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1. .20
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Location/Qualifiers
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PAT 20-DEC-2002
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Egholm,M., Nielsen,P., Buchardt,O., Dueholm,K.L., Christensen,L.,
Coull,J.M., Kiely,J. and Griffith,M.
Peptide nucleic acids
Patent: US 6451968-A 49 17-SEP-2002;
Location/Qualifiers
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A61K37/02,CI2N15/00
Description of Artificial Sequence: Sequencing primer
DNA encoding
the heavy chain of a humanized anti-Fas antibody FH
Location/Qualifiers
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/organism='Artificial Sequence'.
Location/Qualifiers
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synthetic construct
artificial sequences.

1 (bases 1 to 20)
Serizawa,N., Haruyama,H., Nakahara,K. and Tamaki,I.
Parug containing humanized anti-Fas antibody
Patent: JP 2001342148-A 57 11-DEC-2001;
                                                                                                                                                               linear
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BD090597.1 GI:22636207
DP.201342148-A/57.
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88.9%; Pred. No. 5.1e+02;
tive 0; Mismatches 2;
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'organism="synthetic construct"
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   Mismatches
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JP 2001342148-A/57
11-DEC-2001
28-MAR-2001 JP 2001093106
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                                    21 TTAGGGGGGAAGAGAA 37
                                                                     18 TTTGGGGGGAAGAGAA 2
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Best Local Similarity 88.9
Matches 16; Conservative
   16; Conservative
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Unclassified.
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PC A6
A61P13/
PC A6
PC C1
PC C1
PC C0
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AR231312/c
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C12N15/09, A61K38/00, A61K39/00, A61K39/395, A61R39/395, A61P37/00, PC
A61P43/00,
PC C07K16/28, C12N1/21, C12N5/10, C12N15/00
PC C12R1:91),
PC C12N1:91),
PC C12N15/00, A61K37/02, C12N5/00, C12N15/00
CC C12N15/00, A61K37/02, C12N5/00, C12N15/00
FF Key Location/Qualifiers
FT Source /organism='Artificial Commonn'
                                                                                                                                                                 PI WATARU TAKAHASHI, HIDEYUKI HARUYAMA, NOBUKI SERIZAWA PC
C12N15/09, A61K38/00, A61K39/00, A61K39/395, A61K39/395, A61P37/00, PC
A61P43/00,
C C07K16/28, C12N1/21, C12N5/10, C12N15/00
PC C12R1:91),
PC C12R1:91),
PC C12N15/00, A61K37/02, C12N5/00, C12N15/00
CC L2N15/00, A61K37/02, C12N5/00, C12N15/00
FF Key Location/Qualifiers
FT Source /organism='Artificial Sequence'.
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Location/Qualifiers
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            Takahashi W., Haruyama, H. and Serizawa, N. Humanized anti-Fas antibody Patent: JP 200166573-A 57 20-JUN-2000; SANKYO CO LTD
OS Artificial Sequence
PD 20-JUN-2000
PF 29-SEP-1999 JP 1999275440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            artificial sequences.

1 (bases 1 to 20)
Takahashi,W., Haruyama,H. and Serizawa,N. Humanized anti-Fas antibody
Patent: JP 2000166573-A 61 20-UN-2000;
SANKYO CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.9%; Score 15.4; DB 1;
Best Local Similarity 94.1%; Pred. No. 5.1e+02;
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JP 2000166573-A/61
20-JUN-2000
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synthetic construct
synthetic construct
 (bases 1 to 20)
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E43418/c
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L Parkahashi, W., Haruyama, H. and Serizawa, N.

S Takahashi, W., Haruyama, H. and Serizawa, N.

Drug containing humanized anti-Fas antibody

L Patent: JD 2001342149-A 61 11-DEC-2001;

SANKYC CO LTD

SANKYC COLOR CO

SANKYC CO

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Description of Artificial Sequence: Sequencing primer for a
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A61P43/00//C12N15/02, C12N15/00
Description of Artificial Sequence: Sequencing primer for a Description of a humanized anti-Fas antibody FH Key Location/Qualifiers
PN JP 2001342149-A/57
PD 11-DEC-2001
PP 28-MAR-2001
PP 28-MAR-2015
PP AG1N29/395,AG1P1/16,AG1P7/06,AG1P9/00,AG1P9/10, PC AG1N39/395,AG1N39/395,AG1N39/196,AG1P1/16,AG1P7/06,AG1P9/10,PC AG1P37/09,
PC AG1P37/09,
PC AG1P37/09,
PC AG1P37/09,AG1P31/18,AG1P31/20,AG1P37/00,AG1P37/CC AG1P37/09,AG1P37/CC AG1P37/OB,ATTIFICIAL Sequence: Sequencing primer for DNA encoding
CC the heavy chain of a humanized anti-Fas antibody FH Key
                                                                                                                                                                                                                                                    DNA encoding
the heavy chain of a humanized anti-Fas antibody FH
Location/Qualifiers
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ilarity 94.1%; Pred. No. 5.1e+02;
Conservative 0; Mismatches 1; Indels
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'organism='Artificial Sequence'
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

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    ^organism="synthetic construct"
|mol_type="genomic DNA"
|db_xref="taxon:32630"

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JP 2001342149-A/61.
synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 20)
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A61K37/02,C12N15/00
Description of Artificial Sequence: Sequencing primer for DNA encoding
the heavy chain of a humanized anti-Fas antibody FH Key Location/Qualifiers
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NOBUFUSA SERIZAWA, HIDEYUKI HARUYAMA, KAORI NAKAHARA, IKUKO
                                                                                     Gaps
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JP 2001342148-A/61.
JP 2001342148-A/61.
Synthetic construct
artificial sequences.

I (bases 1 to 20)
Serizawa, N., Haruyama, H., Nakahara, K. and Tamaki, I.
Drug containing humanized anti-Fas antibody
Patent: JP 2001342148-A 61 11-DEC-2001;
                           Score 15.4; DB 1; Length 20;
Pred. No. 5.1e+02;
0; Mismatches 1; Indels
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/organism='Artificial Sequence'
Location/Qualifiers
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BD090706.
BD090706.1 GI:22636316
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Takahashi, W., Haruyama, H. and Serizawa, N.
Drug containing humanized anti-Fas antibody
Patent: JP 2001342149-A 57 11-DEC-2001;
                                                                                                                                                                                                                                                                                                           20 bp DNA Drug containing humanized anti-Fas antibody.

    .20
    forganism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"

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                              Query Match
Best Local Similarity 94.1%;
Matches 16; Conservative (
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synthetic construct
synthetic construct
artificial sequences.
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PC A61K3
A61P13/12,
PC A61P1
PC A61P1
PC A61P1
CC DB8C1
CC DB8C1
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BD090706
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PAT 27-AUG-2002

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PAT 16-MAY-2001
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Method for generation of sequence sampled maps of complex genomes Patent: US 5851760-A 253 22-DEC-1998; Location/Qualifiers
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Uchida,K., Uchida,T., Tanaka,Y., Matsuda,Y. and Kondo,S.
Antisense nucleic acid compound targeted to VEGF
Patent: US 6150092-A 10 21-NOV-2000;
Location/Qualifiers
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Bruice, T.C. and Dev, A.P.
Deoxynucleic alkyl thiourea compounds and uses thereof
Patent: US 6169176-A 2 02-JAN-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.9%; Score 15.2; DB 1; Length 20; Best Local Similarity 85.0%; Pred. No. 5.4e+02; Matches 17; Conservative 0; Mismatches 3; Indels
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                                                                                                         Length 20;
                                                                                                                                                                                                                                                                              linear
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Best Local Similarity 85.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 3;
                                              1. .20
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/mol_type="unassigned DNA"
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Sequence 10 from patent US 6150092.
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Sequence 2 from patent US 6169176.
AR123336.1 GI:14108302
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AR118884.1 GI:14100794
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Unclassified.
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AR123336
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AR118884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unclassified.
Unclassified.
1 (bases 1 to 17)
Kozian,D. and Reuner,B.
Two-color differential display as a method for detecting regulated genes
                                                                                                                                                                                                1 (bases 1 to 17)
Sociation. D. and Reuner, B.
Two-color differential display as a method for detecting regulated genes
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Best Local Similarity 93.8%; Pred. No. 4.5e+02;
Matches 15; Conservative 1; Mismatches 0;
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0.9%; Score 15.2; DB 1;
Best Local Similarity 93.8%; Pred. No. 4.5e+02;
Matches 15; Conservative 1; Mismatches 0;
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AR066905
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                                                                                                                                                                                                                                                          Patent: US 6342376-A 2 29-JAN-2002;
Location/Qualifiers
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Location/Qualifiers
                                                                 AR183909 17 bp
Sequence 2 from patent US 6342376.
AR183909
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Sequence 2 from patent US 6645741.
AR429726
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/organism="unknown"
/mol_type="genomic DNA"
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Unclassified.
1 (bases 1 to 20)
Evans, G.A. and Smith, M.W.
                                                                                                                     AR183909.1 GI:20227878
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AR429726/C
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AR066905/c
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BD267704.1 GI:33077472
JP 2002541812-A/4.
Acremonium chrysogenum
SM Acremonium chrysogenum
Eukaryota, Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreocae; Acremonium.
Hypocreocae; Acremonium.
I (bases 1 to 20)
S Alvarez,J.V., Martin,S.G., Blanco,F.J.C., Garcia,S.C., Fierro,F.F., Funte,J.L.B., Garcia,B.D. and Martin,J.F.M.
Extracellular protease of Acremonium chrysogenum having CPC acetylhydrolase activity, and use thereof in gene inactivation for synthesizing deacetylated cepharosporin C and elevating
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                  PAT 16-MAY-2001
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C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12P35/06//(C12P35/06,
                                                                                                                                 1 (bases 1 to 20)
Kwok, P.-Y. and Chen, X.
Method for nucleic acid analysis using fluorescence resonance
energy transfer
Patent: US 6177249-A 22 23-JAN-2001;
                                                                                                                                                                                                                                                                                                                   Gaps
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PR 09-ARR-1999 ES P 9900731
PI JAVIER VELASCO ALVAREZ, SANTIAGO GUTIERREZ MARTIN, PI FRANCISCO JAVIER CASQUEIRO BLANCO, SONIA CAMPOY GARCIA, PI FRANCISCO PIERRO FIERRO, JOSE LUIS BARREDO FUENTE, BRUNO DIEZ
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Location/Qualifiers
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Pred. No. 5.4e+02;
0; Mismatches 3; Indels
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Patent: JP 2002541812-A 4 10-DEC-2002;
ANTIBIOTICOS SAU
            Sequence 22 from patent US 6177249.
AR125322
AR125322.1 GI:14111384
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/organism="unknown"
/mol_type="unassigned DNA"
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BD267704
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20 bp DNA linear PAT 29-SEP-1997
Oligonucleotide specific to subtype Tr of Hepatitis C virus.
E06099
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synthetic construct
artificial sequences.
1 (bases 1 to 20)
Chayama, K. and Kumada, H.
METHOD FOR EXAMINING C TYPE HEPATITIS VIRUS AND PRIMER SET USED FOR
THE SAME
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CHAYAMA KAZUAKI, KUMADA HIROMITSU
C12Q1/68,C12N15/10,C12N15/11,C12Q1/70;
Btrandedness: Single;
/organism="Acremonium chrysogenum"
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RDS
JP 2000342265-A/15.
3 synthetic construct
artificial sequences.
ICE 1 (bases 1 to 20)
RS Hirose, R. and Yoshida, T.
Method for purifying oligonucleotide
L Patent: JP 2000342265-A 15 12-DEC-2000;
TOAGOSEI CHEM IND CO LTD
OS Artificial Sequence.
PN JP 2000342265-A
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                                                                              Query Match

0.9%; Score 15.2; DB 1;
Best Local Similarity 85.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 3;
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CHAYAMA KAZUAKI
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Artificial sequence; Genes.
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JP 1993337000-A/23
21-DEC-1993
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hypothetical: No;
anti-sense: No.
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Dattagupta, N. and Tseng, T.-C.
Methods and compositions for analyzing nucleotide sequence mismatches using RNaes a mismatches using RNaes a Patent: US 6596489-A 18 22-JUL-2003;
Location/Qualifiers
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1 (bases 1 to 20)

1 (bases 1 to 20)

Biallell (bases 1 to 20)

Biallell (markers for use in constructing a high density disequilibrium map of the human genome Patent: US 6537751-A 10187 25-MAR-2003;

Location/Qualifiers
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85.0%; Pred. No. 5.4e+02;
tive 0; Mismatches 3; Indels
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Sequence 18 from patent US 6596489.
AR360403.
AR360403.1 GI:33767433
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Sequence 18 from patent US 6596490.
AR360430.1 GI:33767460
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/wol_type="genomic DNA"
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    .20
    /organism="unknown"

                                              1014 TGTGGTTGGGGATGGGGCTG 1033
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                                                                   1 TCTGATTTGGGATGGGGCTG 20
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AR298452/c
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AR360430
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AR360403
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MCKAY,R., Freier,S.M. and Wyatt,J.
Antisense modulation of casein kinase 2-alpha prime expression
Patent: US 6455307-A 93 24-SEP-2002;
Location/Qualifiers
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Uncloses it co 20)
1 (bases 1 to 20)
Cohen,D., Chumakov,I. and Blumenfeld,M.
Biallelic markers for use in constructing a high density disequilibrium map of the human genome
Patent: US 6537751-A 6563 25-MAR-2003;
Location/Qualifiers
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85.0%; Pred. No. 5.4e+02;
tive 0; Mismatches 3; Indels
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/organism="synthetic construct"
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/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                             DNA
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Sequence 6563 from patent US 6537751.
AR294828 AR294828 GI:31682112
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Sequence 93 from patent US 6455307.
AR232303. GI:27274295
                                             KUNIHIKO HIROSE, TADAO YOSHIDA
C12N15/09, B01D15/08, C12N15/00
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/organism="unknown"
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/organism="unknown"
/mol_type="genomic DNA"
12-DEC-2000
02-JUN-1999 JP 1999154974
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PAT 02-JUL-2002
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Detection system for separating constituents of a sample and production and use of the same
Patent: WO 0071747-A 35 30-NOV-2000;
Aventis Research & Technologies GmbH & Co. KG (DE)
Location/Qualifiers
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                   3; Indels
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Nucleic acid hairpin probes and uses thereof
Patent: WO 0206531-A 18 24-JAN-2002,
Applied Gene Technologies, Inc. (US)
Location/Qualiflers
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/organism="synthetic construct"
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/db_xref="taxon.32630"
/noTe="Beschreibung der kunstlichen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.9%; Score 15.2; DB 1; Best Local Similarity 85.0%; Pred. No. 5.46+02; Matches 17; Conservative 0; Mismatches 3;

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|db_xrefe"taxon:32630"

   85.0%; Pred. No. 5.4e+02;
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                  0; Mismatches
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Sequence 18 from Patent WO0206531.
AX441514
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Matches 17; Conservative
                   17; Conservative
Best Local Similarity
Matches 17; Conserva
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AX048436/c
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Wright,J.A., Young,A.H. and Dugourd,D.
Antisense Oligonucleotide sequences as inhibitors of microorganisms
Patent: US 6610539-A 72 26-AUG-2003;
Location/Qualifiers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Method for the amplification of hla class i alleles
Patent: WO 0061795-A 36 19-OCT-2000;
CANCK ILSE DE (BE); ROSSAU RUDI (BE); INNOGENETICS NV (BE)
ROMBOUT ANNELIES (BE)
Location/Qualifiers
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85.0%; Pred. No. 5.4e+02;
tive 0; Mismatches 3; Indels
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                                                                 Dattegupta, N. Notled to the second national national national national nations and uses thereof Patent: US 6556490-A 18 22-JUL-2003; Location/Qualifiers
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Sequence 72 from patent US 6610539.
AR382832 GI:40091645
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Sequence 36 from Patent WO0061795.
AX038279
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                                                                                                                                      1. .20
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                   Unknown.
Unclassified.
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Matches 17; Conserv
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AR382832
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AX038279
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.

Enterobacteriaceae; Escherichia.

I (basea 1 to 20)

Wright, J.A., Young, A.H. and Dugourd, D.
Antisense oligonucleotide sequences as inhibitors of microorganisms
L. Patent: 19 2002514093-A 72 14-MAY-2002;
GENESENSE TECHNOLOGIES INC
OS Escherichia coli
PN JF 2002514093-A/72
PP 10-JUL-1998 JF 1999507930
PF 10-JUL-1999 JF 1999507930
PR 10-JUL-1997 US 60/052160
PI JIM A WRIGHT, AIPING H YOUNG, DOMINIQUE DUGOURD PC
C12N15/11, C12N15/31
CC Antisense oligonucleotide sequences as inhibitors of CC
                                                                             PAT 17-JUL-2003
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1 (bases 1 to 15)

1 thirschbein, B.L., Fearon, K.L., Gryaznov, S.M., McCurdy, S.N., Nelson, J.S. and Schultz, R.G.
Synthons for synthesis of Oligonucleotide N3-P5 phosphoramidates Patent: US 5859233-A 3 12-JAN-1999;
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ilarity 85.0%; Pred. No. 5.4e+02;
Conservative 0; Mismatches 3; Indels

    .20
    /organism='Escherichia coli'.

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    /db_xref="taxon:562"

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    /organism="unknown"
    /mol_type="unassigned DNA"

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Sequence 3 from patent US 5859233.
AR029402
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JP 2002514093-A/72.
Escherichia coli
Escherichia coli
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PN WO 017293-A/5
PD W4-0CT-2001
PP 02-APR-2001 WO 2001JP002869
PR 31-MAR-2000 JP 00P 356719 PR
28-MAR-2001 US 09/806158
PI SHOJI FURUSAKO, SADAO MORI, KAMON SHIRAKAWA, TOWOHIRO TAKAHASHI
PC C12NIS/00, C07K7/08, C07K14/705, C07K16/28, A61K45/00, A61P31/04,
PC A61P38/02,
PC A61P38/02,
PC A61P38/02,
PC A61P38/03, Dinding inhibitor
PC TLR/CD14 binding inhibitor
PH Rey Location/Qualifiers
FH Source / Jorganism='Artificial Sequence'.
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                   PAT 27-JAN-2003
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                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                           New polynucleotides and polypeptides of the erythropoietin gene Patent: WO 02085940-A 6 31-OCT-2002, GenOdyssee (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     synthetic construct
synthetic construct
synthetic construct
artificial sequences.

1 (bases 1 to 20)
Furusako, S., Mori, S., Shirakawa, K. and Takahashi, T.
Fur(CD14 binding inhibitor
Patent: WO 0172993-A 5 04-0CT-2001;
MOCHIDA PHARMACEUTICAL CO LID, SHOJI FURUSAKO, SADAO MORI, KAMON
SHIRAKAWA, TOWOHIRO TAKAHASHI
OS Artificial Sequence
PN WO 0172993-A/5
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    .20
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    /db_xref="taxon:32630"

                       DNA
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    20
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                 20 bp
Sequence 6 from Patent WO02085940.
AX591245
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TLR/CD14 binding inhibitor.
BD10255.
BD10255.1 GI:22648126
WO 0172993-A/5.
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Query Match

0.9%; Score 15; DB 1; L
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0;
tightly packed bed
Patent: US 5869643-A 16 09-FEB-1999;
Location/Qualifiers
                                                                                               /organism="unknown"
/mol_type="unassigned DNA"
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                                                                                                                                                                                                                                                                  Unclassified.

1 (bases 1 to 15)

1 (bases 1 to 15)

1 (bases 2 to 15)

1 (bases 3 to 15)

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4 (bases 3 
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1 (bases 1 to 15)
Chatelain, F. and Kumarev, V.
Process for preparing polynucleotides on a solid support in rightly packed bear Patent: US 5869641-A 10 09-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 15)
Chatelain, F. and Kumarev, V.
Process for preparing polynucleotides on a solid support in
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    /mol_type="unassigned DNA"

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Sequence 4 from patent US 5859233.
AR029403
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Unclassified.
Unclassified.
I (bases 1 to 15)
I trachbein, B.L., Fearon, K.L., Gryaznov, S.M., McCurdy, S.N.,
Nelson, J.S. and Schultz, R.G.
Solid phase synthesis of oligonucleotide N3'-P5' phosphoramidates
Patent: US 5824793-A 3 20-OCT-1998;
Location/Qualifiers
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                                                                                                                                               Unclassified.
Unclassified.
1 (bases 1 to 15)
Leclerc,G. and Martel,R.
Radiolabeled DNA Oligonucleotide and method of preparation
Patent: US S821384-A 2 13-OCT-1998;
Location/Qualifiers
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AR048768 15 bp
Sequence 2 from patent US 5821354.
AR048768
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Sequence 3 from patent US 5824793.
AR049970. GI:5971962
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Gaps

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PAT 31-AUG-2000

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Unknown.
Unknown.
Unclassified.
I (bases 1 to 15)
Pecker, I., Vlodavsky, I. and Feinstein, E.
Pecker, I., Vlodavsky, I. and Feinstein, E.
Polymuclectide encoding a polypeptide having heparanase activity and expression of same in transduced cells
and expression of same in transduced cells
Location/Qualifiers
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Matson, R.S., Coassin, P.J., Rampal, J.B. and Caskey, C.Thomas.
Oligonucleotide repeat arrays
Patent: US 5981185-A 5 09-NOV-1999;
Location/Qualifiers
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Sequence 5 from patent US 5981185.
AR084516
AR084516.1 GI:10011287
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Location/Qualifiers
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Best Local Similarity 100.0%
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Unclassified.
Unclassified.
I (bases 1 to 15)
Hirschbein, B.L., Fearon, K.L., Gryaznov, S.M., McCurdy, S.N.,
Nelson, J.S. and Schultz, R.G.
Solid phase synthesis of oilgonucleotide N3'-P5' phosphoramidates
Patent: US 5824793-A 4 20-OCT-1998;
Location/Qualifiers
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1 (bases 1 to 15)
Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
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1 (bases 1 to 15)
Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
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Patent: US 5837542-A 361 17-NOV-1998;
Location/Qualifiers
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Patent: US 5837542-A 362 17-NOV-1998;
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AR056157.1 GI:5981734
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 4 from patent US 5824793.
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Patent: US 6132967-A 361 17-OCT-2000;
Location/Qualifiers
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Draims, S., Stinchcomb, D.T., McSwiggen, J., Sullivan, S. and
Draper, K.G.
Ribozyme treatment of diseases or conditions related to levels of
intercellular adhesion molecule-1 (ICAM-1)
Patent: US 613267-A 362 17-OCT-2000;
Location/Qualifiers
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Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
Draper,K.G.
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Sequence 361 from patent US 6132967.
AR113915
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/mol_type="unassigned DNA"
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DEFINITION Sequence 1 from patent US 6291438.
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/organism="unknown"
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Location/Qualifiers
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Matson, R.S., Coassin, P.J., Rampal, J.B. and Caskey, C.Thomas.
Oligonucleotide repeat arrays
Patent: US 5981185-A 7 09-NOV-1999,
Location/Qualifiers
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Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
Oligonucleotide repeat arrays
Patent: US 5981185-A 9 09-NOV-1999;
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    /organism="unknown"
    /mol_type="unassigned DNA"

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    /organism="unknown"
    /mol_type="unassigned DNA"

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/organism="unknown"
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Sequence 4 from patent US 6103474.
AR105981.
AR105981.1 GI:12820046
Sequence 7 from patent US 5981185.
AR084518
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AR084520
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E12591.1 GI:325142
JP 1997028381-A/8.
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unclassified.
1 (Janes 1 to 15)
Tei, I., Nakada, K., Ito, T., Horiuchi, H., Ota, A., Takagi, M.,
Tsubura, H., Tanaka, H. and Ishiguro, Y.
S-RIBONUCLBASE SPECIFIC TO STYLE AND DNA SEQUENCE CODING THEREFOR
Patent: JP 1994335389-A 7 06-DEC-1994;
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PC C12N9/22,C12N15/52;
CC strandedness: Single;
CC topology: Linear;
FH Key
FT source 1.15
/organism='Artificial sequences'.
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                                                                                                  Wang, J.H.
Antiviral anticancer poly-substituted phenyl derivatized oligoribonucleotides and methods for their use Patent: US 6291438-A I 18-SEP-2001;
Location/Qualifiers
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/organism='Artificial sequences'.
Location/Qualifiers
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JP 1994335389-A/7
06-DEC-1994
27-MAY-1993 JP 1993126286
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AR170375
AR170375.1 GI:17908334
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JP 1994335389-A/7.
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1 (bases 1 to 15)
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E08522
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PAT 27-APR-1998
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Cook, P.D., Delecki, D.J. and Guinosso, C.
Acyclic nucleoside analogs and oligonucleotide sequences containing
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/organism='Artificial sequences'
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ative 0; Mismatches 0;
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/organism="unknown"
/mol_type="unassigned DNA"
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Location/Qualifiers
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Sequence 6 from patent US 5576427.
129068.1 GI:1819859

    .15
    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:3264"

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Patent: US 6357163-A 20 19-MAR-2002;
Location/Qualifiers
                                                        /mol_type="unassigned DNA"
                              1. .15
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AR371280/c
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AR266630/c
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Cook, P.D. and Sanghvi, Y.S.
Nuclease resistant, pyrimidine modified oligonucleotides that
Nuclease resistant, pyrimidine modified oligonucleotides that
detect and modulate gene expression
Patent: uS 5614617-A 1 25-MAR-1997;
Location/Qualifiers
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( Dasses 1 to 15)

Buchardt, O., Egholm, M., Nielsen, P.E. and Berg, R.H.

Use of nucleic acid analogues in diagnostics and analytical
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1 (bases I to 15)

1 (bases I to 15)

Use of nucleic acid analogues in diagnostics and analytical procedures
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Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0;
                                           DNA
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Patent: US 6357163-A 19 19-MAR-2002;
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Sequence 19 from patent US 6357163.
AR200476.1 GI:20251364
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                                     15 bp
Sequence 1 from patent US 5614617.
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AR200477
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McClelland,M., Welsh,J. and Trenkle,T.
Reduced complexity nucleic acid targets and methods of using same
Patent: US 6495319-A 68 17-DEC-2002;
Location/Qualifiers
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      Length 15;
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Query Match

0.9%; Score 15; DB 1; Lv
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0;
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1 (bases 1 to 15)

Kurz,M., Lohse,P. and Wagner,R.
Peptide acceptor ligation methods
Patent: US 6429300-A 21 06-AUG-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 68 from patent US 6495319.
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Sequence 21 from patent US 6429300.
AR222461

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PAT 24-AUG-2000
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Method for isolating anionic organic substances from aqueous systems using cationic polymer nanoparticles
Patent: WO 9910277-A 6 04-MAR-1999;
SUEDDEUTSCHE KALKSTICKSTOPF (DB); BAYER ERNST (DE)
Location/Qualifiers
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Coffea arabica mannanase
Patent: WO 0028046-A 4 18-MAY-2000;
NESTLE SA (CH); MARRACCINI PIERRE (FR); ROGERS JOHN (FR)
Location/Qualifiers
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/noTe="3' palmityl modified oligonucleotide"
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/note="OLIGONUCLEOTIDE DE SYNTHESE"
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Sequence 6 from Patent WO9910527.
AX004877.
AX004877.1 GI:9928277
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AX026066/c
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Monforte,J.A., Becker,C.H., Pollart,D.J. and Shaler,T.A.
Releasable nonvolatile mass label molecules
Patent: US 6635452-A 9 21-OCT-2003;
Location/Qualifiers
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Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
Peptide nucleic acids
Patent: US 6395474-A 18 28-WAY-2002;
Location/Qualifiers
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Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
Peptide nucleic acids
Patent: US 6395474-A 17 28-MAY-2002;
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Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0;
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Sequence 17 from patent US 6395474. AR371280
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Sequence 9 from patent US 6635452.
AR410213.1 GI:40161460
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   Schmidt, \tilde{W}_{\cdot}, Hiller, R., Huber, M. and Mueller, M. Branched compound for use in nucleic acid detection and analysis
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Branched compound for use in nucleic acid detection and analysis
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Patent: EP 1111068-A 4 27-JUN-2001;
LION Bioscience AG (DE); VBC Genomics GmbH
Location/Qualifiers
                                               Datent: EP 1111068-A 3 27-JUN-2001;
LION Bioscience AG (DE); VBC Genomics GmbH
Location/Qualifiers
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/db_xref="taxon:32630"
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/db_xref="taxon:32630"
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Best Local Similarity 100.
Matches 15; Conservative
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AX127273/c
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Detection system for separating constituents of a sample and production and use of the same
Patent: WO 007147-A 6 30-NOV-2000;
Aventis Research & Technologies GmbH & Co. KG (DE)
Location/Qualifiers
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Sequence 26 from Patent WO0125442.
AX106973.1 GI:13922522
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/note="N/A"
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Cellular kinases involved in cytomegalovirus infection and their
Inhibition
Patent: EP 1201765-A 1 02-MAY-2002;
Axxima Pharmaceuticals Aktiengesellschaft (DE)
Location/Qualifiers
Branched compound for use in nucleic acid detection and analysis
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Branched compound for use in nucleic acid detection and analysis
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/db_xref="taxon:32630"
/note="stem of branched oligonucleotide - base 1
modified-Modification is (MH2-C6-TTT)2-branch-"
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db tyref="trace:"stref" | foreigned for
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                                                 Patent: WO 0146464-A 3 28-JUN-2001;
LION Bioscience AG (DE)
Location/Qualifiers
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Patent: WO 0146464-A 4 28-JUN-2001;
LION Bioscience AG (DE)
LOCation/Qualifiers
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Sequence 4 from Patent W00146464.
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Query Match 0.9%; Score 15; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 4.1e+02; Matches 15; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0;
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PAT 31-MAR-2003

AX633197/c LOCUS

RESULT 634

ORGANISM

REFERENCE AUTHORS

JOURNAL

TITLE

FEATURES

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Polymucleotide encoding polypeptide having heparanase activity and expression of the polypeptide in induced cell.
BD074424
BD074424.1 GI:22620027
JP 201514855-A/5.
unidentified
unidentified
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Method and polynukleotides for assaying the activity of a dna modifying enzyme
Patent: WO 3008643-A 6 30-JAN-2003;
Cancer Resarch Technology Limited (GB)
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Macejak, D.G. and reagent for inhibiting HBV viral replication Patent: EP 128296-A 476 05-MAR-2003;
RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0;
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                    DNA
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              Sequence 6 from Patent W003008643. AX696087
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Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0;
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RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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Sequence 338 from Patent EP1260586.
AX633199
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Sequence 336 from Patent EP1260586.

    15. 15
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LOCUS
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Best Loca Matches

ORGANISM

REFERENCE AUTHORS

JOURNAL

TITLE

FEATURES

ACCESSION VERSION KEYWORDS SOURCE

RESULT 635

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PAT 27-AUG-2002

ORGANISM

RESULT 636

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Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.

BD206432 BD206432 BD206432 GI 33016202 BD206432 Unidentified unidentified unidentified unidentified unidentified unidentified unidentified unidentified
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100.0%; Pred. No. 4.1e+02;
tive 0; Mismatches 0;
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JP 2002360271-A/647.
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Matches 15; Conservative
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BD184668/c
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BD206432/c
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1 (bases 1 to 15)
Pecker, I., Vlodavsky, I. and Elena, F.
Polynucleotide encoding polypeptide having heparanase activity and expression of the polypeptide in induced cell
Patent: JP 2001514855-A 5 18-SEP-2001;
INSIGHT STRATEGY & MARKETING LTD, HADASIT MEDICAL RESEARCH SERVICES
                                                                                                                                                                                  PF 31-AUG-1998 JP 2000508806
PR 02-SEP-1997 US 08/922170,02-JUL-1998 US 09/109386 PI
IRIS PECKER, ISRAEL VLODAVSKY, FEINSTEIN ELENA
PC C12N15/09, A61K38/00, A61P9/10, A61P17/00, A61P29/00, A61P35/00, PC
A61P37/00
PC A61P43/00, C12N5/10, C12N9/24, C12Q1/68, G01N33/15, G01N33/50// PC
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S JP 2015284808-A/5.
synthetic construct
synthetic construct
artificial sequences.

I (bases 1 to 15)
Releasable nonvolatile mass-label molecules
Releasable nonvolatile mass-label molecules
A partificial Sequence
PN Artificial Sequence
PN Artificial Sequence
PN 19 201524808-A/5
PN 10-DEC-1997 JP 1998526924
PR 10-DEC-1997 UP 1998526924
PR 10-DEC-1996 US 60/033037, 16-MAY-1997 US 60/046719 PI
THOMAS A SHALER
PC CL2Q1/68,GOIN15/06,GOIN33/53.GOIN33/542 CIDDIART, PI
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Description of Artificial Sequence: oligo dT15 primer FH
                                                                                                                                                                                                                                                                                                                                                                                    expression of the polypeptide in induced cell FH Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.9%; Score 15; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 4.1e+02; Matches 15; Conservative 0; Mismatches 0; Indels
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PC A61K39/395,
CC Polynucleotide encoding polypeptide having CC expression and cc expression.
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Releasable nonvolatile mass-label molecules.
BD084687
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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                                                                                                                                Nucleic acid
JP 2001514855-A/5
18-SEP-2001
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BD084687/c
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TITLE
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Gaps

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KING CAR FOOD INDUSTRIAL CO LTD
OS Artificial Sequence
PN JP 2003360271-A/647
PN GAW-2001 JP 2001362595
PR 04-MAY-2001 JW 90110785
PR 04-MAY-2001 JW 90110785
PN GHMG-YEE LING, RUEY-WEN LIN, ZHOU-MENG YOO, XIN-HSUAN HUANG, BOW-PI GHNG-HSIUNG LEE, YI-JU LIN, CI-CHUNG HUANG, HAN-CHANG HSU, CHA-PI SHENG LEE, YI-JU LIN, CI-CHUNG HUANG, HAN-CHANG HSU, CHA-PI WARS SHI,
PN SHI,
PN SHI,
PN C1201/70,090,C12015/09,C12M1/34,C1201/04,C1201/42,C1201/68 PC
C1201/70,090121/64,
PC G101N33/53,G01N33/574,G01N33/59,G01N37/00/(C12M1/34,C12R1:93),
PC G101N33/53,G01N33/574,G01N33/59,G01N37/00/(C12M1/34,C12R1:93),
PC G101N33/53,G01N33/574,G01N33/59,G01N37/00/(C12M1/34,C12R1:93),
PC Added sequence for 3' end labeling of oligonucleic acid. FH
Key
Location/Qualifiers
FT SOURCE
1. 1. 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAT 17-JUN-2003
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synthetic construct
artificial sequences.

1 (bases 1 to 15)
Ling,C., Lin,R., Yoo,Z., Huang,X., Lee,B., Lee,S., Lin,Y.,
Huang,C., Hau,H., Shi,C., Yao,C., Cao,Y. and Pan,C.
Method and detector for identifying subtypes of human papiloma patent: JP 2002360271-A 647 17-DEC-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BD184668 15-JUN BELHOO and detector for identifying subtypes of human papiloma
                                                                                                   Score 15; DB 1; Length 15; Pred. No. 4.1e+02;
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/db_xref="taxon:32630"

                                                                                                   Query Match 0.9%; Score 15; DB Best Local Similarity 100.0%; Pred. No. 4.1 Matches 15; Conservative 0; Mismatches
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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PAT 26-SEP-2002
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Unclassified.
Unclassified.
I (bases 1 to 16)
Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
Covalently linked oligonucleotide minor groove binder conjugates
Patent: US 6426408-A 4 30-JUL-2002;
Location/Qualifiers
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Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
Covalently linked oligonuclectide minor groove binder conjugates
Patent: US 6426408-A 3 30-JUL-2002;
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                    /organism='Hepatitis virus (hepatitis C
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0.9%; Score 15; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0;
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Sequence 3 from patent US 6426408.
AR221693.1 GI:23328765
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Sequence 4 from patent US 6426408.
AR221694
AR221694.1 GI:23328766

    .15
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/db_xref="taxon:32644"

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/organism="unknown"
/mol_type="genomic DNA"
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AR221693/c
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1 (bases 1 to 15)
Blatt, L., Mcswiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.
Braymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection
Patent: JP 2002512791-A 22 08-MAY-2002;
RIBOZYME PHRMACEUTICALS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAT 17-JUL-2003
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1 (bases 1 to 15)
Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
Enzymatic nucleic acid treatment of diseases or conditions related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BDZ09488
Enzymatic nucleic acid treatment of diseases or conditions related
                                                                                                                                                                                                                                              DENNIS MACEJAK
C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
A61K37/66,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DENNIS MACEJAK
C1209/00, A61K31/7105, A61K38/21, A61K48/00, A61P31/12, C12N15/09,
A61K37/66,
C12N15/00
Enzymatic nucleic acid treatment of diseases or conditions C
                                                                                                                                                                                                                                                                                                                    Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.

Location/Qualifiers
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                                                                                                   OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/22
PD 08-MAY-1209
PF 26-APR-1999 JP 2000545991
PR 27-APR-1999 US 60/083217,18-SEP-1999 US 60/100842 PR 25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI LAWRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PI PAVCC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to hepatitis C virus infection
Patent: JP 2002512791-A 3078 08-MAY-2002;
RIBOZYME PHARMACEUTICALS INC
OS Hepatitis virus (hepatitis C virus)
PN 3P 2002512791-A/3078
PP 26-APR-1999 JP 2000545991
PR 27-APR-1999 US 60/003127,18-SEP-1999 US 60/100842 PR 25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
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related to
hepatitis C virus infection.
Location/Qualifiers
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'organism="unidentified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic RNA"
/db_xref="taxon:32644"
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JP 2002512791-A/3078.
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BD209488/c
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PAT 26-SEP-2002
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Kutyavin, I.V., Lukhtanov, E.A., Gamper, H.B. and Meyer, R.B. Jr.
Covalently linked oligonucleotide minor groove binder conjugates
Patent: US 6426409-A 8 30-JUL-2002;
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Kupyavin,I.V., Lukhtanov,B.A., Gamper,H.B. and Meyer,R.B. Jr.
Covalently linked oligonuclectide minor groove binder conjugates
Patent: US 6486308-A 3 26-NOV-2002;
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100.0%; Pred. No. 4.4e+02;
tive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0;
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Sequence 4 from patent US 6486308.
AR257439
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AR221698/c
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AR257438/c
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AR257439/c
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Unclassified.
1 (bases 1 to 16)
1 (bases 1 to Lukhtanov, E.A., Gamper, H.B. and Meyer, R.B. Jr.
Kutyavin, I.V., Lukhtanov, E.A., Gamper, H.B. and Meyer, R.B. Jr.
Covalently linked oilgonucleotide minor groove binder conjugates
Patent: US 6426408-A 5 30-JUL-2002;
Location/Qualifiers
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Unclassified.
I (bases I to 16)

Kutyavin'I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
Covalently linked ollgonucleotide minor groove binder conjugates
Patent: US 6426408-A 7 30-JUL-2002;
Location/Qualifiers
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Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
Covalently linked oligonucleotide minor groove binder conjugates
Patent: US 6426408-A 6 30-JUL-2002;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels
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AR221695.
AR221695.1 GI:23328767
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AR221697
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AR221695/c
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AR221696/c
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PAT 20-DEC-2002
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Unclassified.
Unclassified.
Unclass 1 to 16)
Kutyavin,I.V., Lukhtanov,B.A., Gamper,H.B. and Meyer,R.B. Jr.
Kutyavin,I.V., Lukhtanov,B.A., Gamper,H.B. and Meyer,R.B. Jr.
Covalently linked oligonucleotide minor groove binder conjugates
Patent: US 6486308-A 8 26-NOV-2002;
Location/Qualifiers
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Kutyavin, I.V., Lukhtanov, B.A., Gamper, H.B. and Meyer, R.B. Jr.
Covalently linked oligonucleotide minor groove binder conjugates
Patent: US 6486308-A 7 26-NOV-2002;
Location/Qualifiers
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Sequence 8 from patent US 6486308.
AR257443
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Best Local Similarity 100.0%;
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AR057478/c
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AR257442/c
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AR257443/c
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                                                            Unclassified.

1 (bases 1 to 16)

Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.

Covalently linked oligonuclectide minor groove binder conjugates

Patent: US 6486308-A 4 26-NOV-2002;
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1 (bases 1 to 16)

Kutyavin, I.V., Lukhtanov, E.A., Gamper, H.B. and Meyer, R.B. Jr.

Kutyavin, I.V., Lukhtanov, E.A., Gamper, H.B. and Meyer, R.B. Jr.

Covalently linked oligonuclectide minor groove binder conjugates

Patent: US 6486308-A 5 26-NOV-2002;

Location/Qualifiers
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I (bases 1 to 16)

Kutyavin, I.V., Lukhtanov, E.A., Gamper, H.B. and Meyer, R.B. Jr.

Covalently linked oligonucleotide minor groove binder conjugates
Patent: US 6486308-A 5 26-NOV-2002;

Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0;
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Sequence 5 from patent US 6486308.
AR257440
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Sequence 6 from patent US 6486308.
AR257441
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 GI:27307450
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Matches 15; Conservative
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AR257440/c
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MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KAORU OGAWA
CIZNIS/09,A61K31/00,A61K39/36,A61K45/00,CIZQ1/68,CIZNIS/00 CC
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Location/Qualifiers
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0.9%; Score 15; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0;
 Topology: Linear;
/note= 'M = A, C, G; N = A, C, G, T'
Key
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Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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                                                                            1. .17
/organism="unidentified"
/mol_type="genomic_DNA"
/db_xref="taxon:32644"
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Pollinosis-associated gene.
E34259
E34259.1 GI:18624264
JP 2000106879-A/3.
synthetic construct
synthetic construct
                                                1. .17.
Location/Qualifiers
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JP 2000106879-A/2.
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E34258/c
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unclassified.
unclassified.
1 (bases 1 to 17)
Kozian, D. and Reuner, B.
Two-color differential display as a method for detecting regulated
Patent: JP 2002524088-A 2 06-AUG-2002;
AVENTIS PHARMA DEUTSCHLAND GMBH
OS Unidentified
PN JP 2005524088-A/2
PD 06-AUG-2002
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Two-color differential display as a method for detecting regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
Patent: US 6132967-A 1682 17-OCT-2000;
Location/Qualifiers
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07-SEP-1998 DE 198 40 731.9
DETLEF KOZIAN, BIRGIT REUNER
C12Q1/68, G01N33/58//A61K45/00, C12N15/09, C12N15/09, C12N15/00, C12N15/09, Strandedness: Single;
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Grimm, S., Stinchcomb, D.T., McSwiggen, J., Sullivan, S. and Draper, K.G.
Intercellular adhesion molecule-1 (ICAM-1) ribozymes
Patent: US 5837542-A 1682 17-NOV-1998,
Location/Qualifiers
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Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
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0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels
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/organism="unknown"
/mol_type="unassigned DNA"
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/wol_type="unassigned DNA"
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BD233654.1 GI:33043424
JP 2002524088-A/2.
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BD233654/c
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AR241830
AR241830.1 GI:27287642
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AR241830/c
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MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
NING NO,
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Licial sequences.

L (bases 1 to 17)

Wageu, T., Sugite, Y., Kashiwabara, T., Oshida, T., Obayashi, M., Gunji, S., Obayashi, I., Imai, Y., No, N. and Ogawa, K.

FITLE
Pollinosia sasociated gene
JOURNAL Patent: JP 2000106879-A 3 18-APR-2000;
GENOX RESERCH INC
COMMENT
OF Artificial Sequence
PN JP 2000106879-A/3
PD 18-APR-2000
PR 06-OCT-1998 JP 1998284610
PR
PI TAKESHI NAGASU, YII''
PI MASAYA OBAYAR''
PI NING NO
PI KAOFF
                                                                                                                                                                                                                                                                                                                                                 C12N15/09, A61K31/00, A61K39/36, A61K45/00, C12Q1/68, C12N15/00 CC
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Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
Rethod and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6346398-A 2549 12-FEB-2002;
Location/Qualifiers
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Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xrefe"taxon:32630"
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Sequence 2552 from patent US 6346398.
AR187064
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/mol_type="unassigned DNA"
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AR187064/c
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AR187061/c
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McClelland,M., Welsh,J. and Trenkle,T.
Reduced complexity nucleic acid targets and methods of using same
Patent: US 6495319-A a 17-DEC-2002;
Location/Qualiflers
Integration (17)
Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6346398-A 5552 12-FEB-2002;
Location/Qualifiers
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Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
Polymorphic repeats in human genes
Patent: 16 472154-A 118 29-OCT-2002;
Location/Qualifiers
                                                                                                                                                                                                                                       Query Match 0.9%; Score 15; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 4.8e+02; Matches 15; Conservative 0; Mismatches 0; Indels
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Sequence 118 from patent US 6472154.
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AR266625.
AR266625.1 GI:29695689
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/organism="unknown"
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PAT 18-JUN-2002

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Akhtar,S., Fell,P. and McSwiggen,J.A.
Enzymatic nucleic acid treatment of diseases of conditions related to levels of epidermal growth factor receptors
Patent: US 6623962-A 32 23-SEP-2003;
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Method and reagent for the inhibition of erg
Patent: WO 0188124-A 836 22-NOV-2001;
RIBOZYME PHARMACHICALS, INC. (US); GLAXO GROUP LIMITED (GB
Location/Qualifiers
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Method and reagent for the inhibition of erg
Patent: WO 0188124-A 837 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (G
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100.0%; Pred. No. 4.8e+02;
live 0; Mismatches 0;
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Sequence 836 from Patent WO0188124.

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/db_xref="taxon:9606"

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Sequence 837 from Patent WO0188124.

    .17
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/db_xref="taxon:9606"

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/organism="unknown"
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AX422501.1 GI:21525883
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                                                                                                                                                                                                                          Unknown.
Unclassified.
1 (bases 1 to 17)
Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6566127-A 1073 20-MAY-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 17)
Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Mathod and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6566127 - A 1076 20-MAY-2003;
Location/Qualifiers
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Sequence 1073 from patent US 6566127.
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Sequence 1076 from patent US 6566127.
AR323674.1 GI:33709482
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Sequence 35 from patent US 6623962.
AR401695
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     PAT 22-NOV-2002
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                             Human posh-like protein 1
Patent: EP 1239051-A 1505 11-SEP-2002;
Acomica, Inc. (US)
Location/Qualifiers
Sequence 1505 from Patent EP1239051.
AX531996
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Sequence 5260 from Patent BP1281758.
AX692528.1 GI:29415486
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Homo sapiens
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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     Length 17;
   0.9%; Score 15; DB 1; Length 17; 100.0%; Pred. No. 4.8e+02; tive 0; Mismatches 0; Indels
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Patent: EP 123905-A 1503 11-SEP-2002;
Aeomica, Inc. (US)
Location/Qualifiers
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Patent: EP 1239051-A 1504 11-SEP-2002;
Aeomica, Inc. (US)
Location/Qualifiers
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Sequence 1503 from Patent EP1239051.
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AX531995

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    .17
    /organism="Homo sapiens"
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    /db_xref="taxon:9606"

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Homo sapiens
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 Query Match 0.9
Best Local Similarity 100.
Matches 15; Conservative
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REFERENCE AUTHORS JOURNAL

TITLE

FEATURES

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Synthetic construct
artificial sequences.

CE 1 (bases 1 to 17)
Rogasu, T., Sugita, Y., Kashiwabara, T., Oshida, T., Obayashi, M.,
RS Nagasu, T., Sugita, Y., Kashiwabara, T., Oshida, T., Obayashi, M.,
RS Nagasu, T., Sugita, Y., Kashiwabara, T., Oshida, T., Obayashi, M.,
RS Nagasu, T., Sugita, Y., Yoshida, N., Ogawa, K., Matsui, K.,
Takahashi, E. and Yokoi, A.
795, a novel gene related to pollen allergy
Patent: WO 0055050-A 3 02-NOV-2000;
GENOX RESEARCH INC, TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA,
TAKAHASHI, AKIRA YOKOI
TAKAHASHI, AKIRA YOKOI
OS Artificial Sequence
PN WO 0065050-A/3
PD 02-NOV-2000
PF 26-APR-1999 JP 99P 120494
PR 27-APR-1999 JP 99P 120494
PI TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,
PI NASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI, YUKHO INAI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description of Artificial Sequence. Artificially Synthesized CC Primer Sequence
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1 (bases 1 to 17)

Akhtar, S., Fell, P. and Mcswiggen, J.A.

Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors

Patent: JP 2001511003-A 35 07-AUG-2001;

RIBOZYME PHARMACEUTICALS INC, ASTON UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PI NEI YOSHIDA,
PI KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC CL2NIS/12,CO7K14/47,CO7K16/18,C12Q1/68,G01N33/50//A61K31/00,CC Description of artific
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PN JP 2001511003-A/35
PD 07-AUG-2001
PF 14-JAN-1998 UP 1998532913
PR 31-JAN-1997 US 60/036476,04-DEC-1997 US SAGHIR AKHTAR, PATRICIA FELL, JAMES A MCSWIGGEN PC C12N9/00, COTK14/71
CC Strandedness 1
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              17 bp DNA li
795, a novel gene related to pollen allergy.
BD011731
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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JP 2001511003-A/35.
unidentified
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synthetic construct
artificial sequences.

artificial sequences.

1 (bases 1 to 17)

8 (Bases 1 to 17)

8 (Bases 1 to 17)

9 Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,

195, a novel gene related to pollen allergy

195, a novel gene related to pollen allergy

196 TARAHASHI,AKIRA NAGASHI NAGASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,

197 ADAHIRO OSHIDA,MASASHA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,

198 NAGO 100500-0.4/2

199 W 0 005000-0.4/2

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                Shannon, M., Gu, Y. and Nguyen, C.T. Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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17 bp DNA 13
1955, a novel gene related to pollen allergy.
180011730
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    17
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                                                                                                                                                     Patent: EP 1281758-A 5260 05-FEB-2003;
Aeomica, Inc. (US)
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                  Inc. (US)
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WO 0065050-A/2.
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Bynthetic construct

Synthetic construct

artificial sequences.

I (bases 1 to 17)

Nagasu, T., Sugita, Y., Kashiwabara, T., Oshida, T., Obayashi, M.,

Rakahashi, E. and Yokol, A.

Takahashi, E. and Yokol, A.

Gunji, S., Obayashi, I., Imai, Y., Yoshida, N., Ogawa, K., Matsui, K.,

Takahashi, E. and Yokol, A.

GENOX RESEARCH INC, TAKESHI NGGASU, YUJI SUGITA, TOWOKO KASHIWABARA,

TADAHIRO OSHIDA, MASAYA OBAYASHI, SHIGEMICHI GINAI, IZUMI OBAYASHI,

TAKAHASHI, AKIRA YOKOI

OS Artificial Sequence

N WO 0073439-A/2

PD 07-DEC-2000

PF 18-MAY-2000 WO 2000JP003191

PR 27-MAY-1999 JP 99P 148784

PI TAKESHI NAGASU, YUJI SUGITA, TOWOKO KASHIWABARA, TADAHIRO OSHIDA,

PI NASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI, YUKIHO IWAI,

PI NEI YOSHIDA,
BD091743.1 GI:22637354

WO 0073435-A/3.

WO 0073435-A/3.

Synthetic construct
artificial sequences.

I (bases 1 to 17)

SNagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K. and Matsui,K.
441, a novel gene related to pollen allergy
At patent: WO 0073435-A 3 07-DEC-2000;
GENOX RESEARCH INC, TAKESHI NAGASU, YUJI SUGITA,TOWOKO KASHIWABARA,
TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
OS Artificial Sequence
PN WO 0073435-A/3

PD 07-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KAORU OGAWA, KEIKO MATSUI
C12N15/10, C12Q1/68, G01N33/15, G01N33/50
Description of Artificial Sequence: Artificially Synthesized CC
                                                                                                                                                                                                                                                                                                                                                                               18-MAY-2000 WO 2000JP003190
27-MAY-1999 DP 918-188783
TAKESHI NGASU YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,
MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI, YUKIHO IMAI,
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465, a novel gene related to pollen allergy.
BD091750
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Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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100.0%; Pred. No.
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Best Local Similarity 100.
Matches 15; Conservative
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C12N15/10,C12Q1/68,G01N33/15,G01N33/50
Description of Artificial Sequence:Artificially Synthesized CC
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TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
NEI YOSHIDA,
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Patent: WO 0073435-A 2 07-DEC-2000;
GENOX RESEARCH INC, TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA, MASAYA OBAYASHI, SHIGEMICHI GUNI, IZUMI OBAYASHI, YUKIHO IMAI, NEI YOSHIDA, KAORU OGAWA, KEIKO MATSUI

SA ARTIFICIAL SEQUENCE

NO 0073435-A/2
Topology: Linear;
Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors

Key
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Pred. No. 4.8e+02;
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                                                                                                                                                 'organism='Unidentified'.
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441, a novel gene related to pollen allergy.
BD091742
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441, a novel gene related to pollen allergy.
BD091743
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100.0%; Pred. No. 4.8e+02;
iive 0; Mismatches 0;
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    .17
    /organism="unidentified"
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/db_xref="taxon:32644"

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27-MAY-1999 JP 99P 148783
                                                                                                                                                                    Location/Qualifiers
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WO 0073435-A/2.
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1 (bases 1 to 17)
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Matches 15, Conserv
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BD091742/c
LOCUS
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BD091743/c
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AUTHORS
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PAT 27-AUG-2002

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Gaps

FEATURES

RESULT 680 BD091751/c

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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artificial sequences.

I (bases 1 to 17)

St Nagasu,T., Suglita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,
Takahashi,E. and Yokoi,A.
Takahashi,E. and Yokoi,A.

Takahashi,E. and Yokoi,A.

Takahashi,E. and Yokoi,A.

GENOX RESEARCH INC,TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
TABAHIRO OSHIDA,MASAYA OBAYASHI,SHIGENICHI GUNJI,IZUMI OBAYASHI,
YUKIHO IMAI,NEI YOKOI

OS Artificial Sequence
NO 0073440-A/2

PD 07-DEC-2000

PP 18-MAY-2000 WO 2000JP003192

PR 27-MAY-1999 JP 99P 148785

PI MASAYA OBAYASHI,SHIGENICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
PI NESAYA OBAYASHI,SHIGENICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
PI NESAYA OBAYASHI,SHIGENICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
PI NEI YOSHIDA,
PI NEI YOSHIDA,
TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
PI KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
C12N15/12,C12Q1/68,C12N5/06,C07K14/415 CC Description of
Artificial Sequence.Artificially Synthesized CC Primer Sequence
FH Key Location/Qualifiers
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Takahashi, E. and Yokoli, A.

187, a novel gene related to pollen allergy

Batent: WO 0073440-A 3 07-DEC-2000,

GENOX RESEARCH INC, TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA,

TADAHIRO OSHIDA, MASAYA OBAYASHI. SHIGEMICHI GUNJI, IZUMI OBAYASHI,

YUKIHO IMAI, NEI YOSHIDA, KAORU OGAWA, KEIKO MATSUI, EIKI

TAKAHASHI, AKIRA YOKOI

OS Artificial Sequence

PN WO 0073440-A/3

PD 07-DEC-2000

PR 27-MAY-1999 JP 99P 148785

PR 77-MAY-1999 JP 99P 148785

PR 77-MAY-
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100.0%; Pred. No. 4.8e+02;
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787, a novel gene related to pollen allergy.
BD091774
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Matches 15; Conservative
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BD091774/c
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27-MXY-1999 JP 99P 148784
TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,
MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI, YUKIHO IMAI,
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NN 0003439-A/3
PD 07-DEC-2000
PF 18-MAY-2000 WO 2000JP003191
PR 27-MAY-1999 JP 99P 148784
PR 27-MAY-1999 JP 99P 148784
PR TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA PI TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA PI NASAYA OSHIDA, PI KAORU OGAWA, KEIKO MATSUI, EIKI TAKAHASHI, AKIRA, YOKOI PC C12N15/12,C12Q1/68,A61P3/08,A61K39/36,A61K45/00 CC Description of Artificial Sequence Artificially Synthesized CC Primer
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BD091751
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1787, a novel gene related to pollen allergy.
18091773
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0.9%; Score 15; DB 1; Lv
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0;
           Location/Qualifiers.
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    .17
    /organism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"

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/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                         Location/Qualifiers
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WO 0073440-A/2.
synthetic construct
synthetic construct
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WO 0073439-A/3.
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GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, HIROMITSU NAKAUCHI,YUTAKA FULIKT,KAZUO FUKAWA,OSAMU KUDO TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI OSBAYASHI,KEIKO MATSUI, HIROHISA SAITO OSBAYASHI,KEIKO MATSUI, HIROHISA SAITO OPT-SEP-2001 PO 07-SEP-2001 WO 2001JP001372 PP 23-FEB-2001 WO 2001JP001372 PP 02-MAR-2000 JP 00P 61832 PI TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI OBAYASHI,KEIKO MATSUI, PI
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synthetic construct

artificial sequences.

artificial sequences.

CE 1 (bases 1 to 17)

S Sugita, Y., Hashida, R., Ogawa, K., Fujishima, T., Nagasu, T.,

Tsujimoto, G. and Takahashi, E.

Method of examining allergic disease

Method of examining allergic disease

L Patent: WO 0224903-A 2 28-MAR-2002;

GGNOX RESERRICH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF

NATIONAL CHILDREN'S HOSPITAL, YUJI SUGITA, RYOICHI HASHIDA, KAORU

GGAWA, TOWNKO FUJISHIMA, TAKESHI NAGASU, GOZO TSUJIMOTO, EIKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ...SPITAL, YUJI SUGITA, RYOICHI HASHIDA, KAORL

ATLIFICIAL SEQUENCE

BY ATLIFICIAL SEQUENCE

PN WO 0224903-A/2

PD 28-WAR-2002

PP 21-SEP-2001

PP 21-SEP-2000 JP 00P

PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, PI

TAKESHI NAGASU,

PI GOZO TSUJIMOTO, EIKI TAKAHASHI

PC CL2115/09, CL2N5/10, CO7K14/47, CO7K16/18, CL2P**

CL201/69, CL2N5/10, CO7K14/47, CO7K16/18, CL2P**

PC GOIN33/50'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAT 18-SEP-2002
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GOIN33/50//C12P21/08, (C12N5/10,C12R1:91), (C12P21/02,C12R1:91)
Description of Artificial Sequence:an artificially synthesized
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A61P37/08
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CI2N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
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/organism='Artificial Sequence'
Location/Qualifiers
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.organism='Artificial Sequence'
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Pred. No. 4.8e+02;
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Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Method of examining allergic disease.
BD142808
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BD142808/c
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ACCESSION
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JOURNAL
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KEYWORDS
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synthetic construct
artificial sequences.

1 (bases 1 to 17)
S Nagasu,T., Obhida,T., Obayashi,I., Matsui,K. and Sait,H.
S Nagasu,T., Oshida,T., Obayashi,I., Matsui,K. and Sait,H.
Method for examination for allergosis
Method for examination for allergosis
AL Patent: WO 0165259-A 5 07-SEP-2001;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, HIROMITSU NAKAUCHI,YUTAKA
FUJIKI,KAZUO FUKANA,OSAMU KUDO TARESHI NAGASU,TADAHIRO OSHIDA,IZUMI
OBAYASHI,KAZUO FUKANA,OSAMU KUDO TARESHI NAGASU,TADAHIRO OSHIDA,IZUMI
OBAYASHI,KELKO MATSUI, HIROMISA SAITO
OS Artificial Sequence
PN WO 0165259-A/5
PN WO 0165259-A/5
PN WO 0165259-A/5
PN WO 2001JP0001372
PR 02-MAR-2000 JP 00P 61832
PR 02-MAR-2000 JP 00P 61832
PR 02-MAR-2000 JP OOP 61832
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: GO1N33/53,C12Q1/68,C12N15/12,G01N33/15,A01K67/027,A61K39/395,
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synthetic construct
artificial sequences.
1 (bases 1 to 17)
Nagasu, T., Oshida, T., Obayashi, I., Matsui, K. and Sait, H.
Method for examination for allergosis
Patent: WO 0165259-A 6 07-SEP-2001;
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                                                                   Query Match 0.9%; Score 15; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 4.8e+02; Matches 15; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0;
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/organism="synthetic construct"
/mol_type="genomic DNA"
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WO 0165259-A/5.
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Method fo
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BD097335/c
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ORGANISM
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BD097334/c
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BD143834.1 GI:27849592
JP 2002095500-A/2.
synthetic construct
SW synthetic construct
artificial sequences.
E 1 (bases 1 to 17)
S Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
Tsujimoto,K.
Method of examining allergic disease
L Patent: JP 2002095500-A 2 02-APR-2002;
GENOX RESEARCH INC.THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL
OS Artificial Sequence
PN JP 2002095500-A/2
PP 25-SBP-2000
PP 25-SBP-2000
PP 2002095500-A/2
PP 25-SBP-2000
PP 2002095500-A/2
PP 25-SBP-2000
PP 2002095500-A/2
PP 200209500-A/2
PP 20020900-A/2
PP 200209500-A/2
PP 
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artificial sequences.

E 1 (bases 1 to 17)

S Sugite, Y., Hashida, R., Ogawa, K., Obayashi, M., Nagasu, T. and
Tsujimoto, K.
Method of examining allergic disease
Patent: JP 2002095500-A

Bathorial Sequence
No Artificial Sequence
PD 02-APR-2002
PD 02-APR-2002
PP 25-SEP-2000 JP 2002091316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C07K14/47,
PC C07KK6/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/10 PC
,C12N15/09,C12P211/02,
PC C12Q1/02,G01N33/15,G01N33/50//C12P21/08,C12N5/00,C12N5/00, PC
C12N15/00
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C12Q1/68,A01K67/027,A61K31/7088,A61K31/711,A61K45/00,A61P37/08, PC
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YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI,
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/organism='Artificial Sequence'.
Location/Qualifiers
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    17
    Aorganism="synthetic construct",
|mol_type="genomic DNA"
|db_xref="taxon:32630"

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                                                                                                                                                                                                                                                                                                                                                                                                                         TAKESHI NAGASU
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GOIN33/50//C12P21/08, (C12N5/10, C12R1:91), (C12P21/02, C12R1:91)
Description of Artificial Sequence:an artificially synthesized
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CI2N15/09, C12NS/10, C07K14/47, C07K16/18, C12P21/02, C12Q1/02, PC
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Sugita, Y., Hashida, R., Ogawa, K., Fujishima, T., Nagasu, T.,
Tsujimoto, G. and Takahashi, E.
Method of examining allergic disease
Patent: WO 0224903-A 3 28-MAR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, YUJI SUGITA, RYOICHI HASHIDA, KAORU
OGAWA, TOMOKO FUJISHIMA, TAKESHI NAGASU, GOZO TSUJIMOTO, EIKI
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00 0224903-A/3
28-MAR-2003-A/3
21-SEP-2001 WO 2001JP008246
25-SEP-2000 JP 00P 291318
YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA,
                                                                                                                                                                                          Gaps
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                                                                                                                                    Query Match
0.9%; Score 15; DB 1; L.
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0;
                          /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_kref="taxon:32630"
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Method of examining allergic disease.
BD143834
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C12Q1/68,
PC G01N3
PC G01N3
CC Descr
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BD143834/c
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Method for examination of allergosis.

Nethod for examination of allergosis.

Nethod for examination of allergosis.

S B1057836.1 G1:27873648

S WO 0233122-A/3.

T (bases 1 to 17)

RS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H.

and Takahashi,E.

Method for examination of allergosis

Method for examination of allergosis

AL PARENT: WO 0233122-A/3 25-AR-2002;

GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF

NATIONAL CHILDREN'S HOSPITAL, RINAKO NAKAGAWA YUJI SUGITA,RYOICHI

HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA

SAITO, EIKI TAKAHASHI

OS ATLIficial Sequence

PN WO 0233122-A/3

PD 25-ARR-2002

PP 11-OCT-2000 WO 2001JP008937

PR 11-OCT-2000 JP 00P 314093

PI TAKESHI NAGASHI, PI

TAKESHI NAGASHI, PI

TAKESHI NAGASHI, PI

TAKESHI NAGASHI, PI
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Description of Artificial Sequence:an artificially synthesized
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Patent: WO 0226962-A 6 04-APR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C12Q1/68, C12N15/09, G01N33/53, G01N33/50, C12Q1/02, A61K48/00,
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artificial sequences.
1 (bases 1 to 17)
Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and
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Location/Qualifiers
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100.0%; Pred. No. 4.8e+02;
iive 0; Mismatches 0; Indels
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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    1736 AAAAAAAAAAAAA 1750
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BD167836/c
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BD167907/c
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BD167835.1 GI:27873647

BD167835.1 GI:27873647

BD167835.1 GI:27873647

BD167835.1 GI:27873647

SYNThetic construct
artificial sequences.

Chases 1 to 17)

SS Sudita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H.

AL Patent: WO 0233122-A 2 25-APR-2002;

BROX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, RINAKO NAKAGAWA YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA SAITO, BIKI TAKAHASHI

SS ATTIGICIAL Sequence
PN WO 0233122-A/2

PN WO 0233122-A/2

PN 11-OCT-2001 WO 2001JP008937

PR 13-OCT-2000 JP 00P 314093

PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI
TAKESHI NAGASU, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI
TAKESHI NAGASU, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI
TAKESHI NAGASU, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI
TAKESHI NAGASU, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI
TAKESHI NAGASU, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI
TAKESHI NAGASU, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI
TAKESHI NAGASU, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI
TAKESHI NAGASU, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI
TAKESHI NAGASU, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI
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Description of Artificial Sequence:an artificially synthesized
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                                                                                       Description of Artificial Sequence: an artificially synthesized
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PC C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N3/10,L12N3/10,C12N15/09,C12P21/02,PC C12Q1/02,G01N33/15,G01N33/50//C12P21/08,C12N5/00,C12N5/00,PC
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C12Q1/68,C12N15/09,G01N33/53,G01N33/50,C12Q1/02,A61K48/00, PC
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Location/Qualifiers
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/organism='Artificial Sequence'
Location/Qualifiers
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                                                                                                                                                                        Location/Qualifiers

    .17
    .07 Organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

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/organism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"
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for examination of allergosis.
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Best Local Similarity
Matches 15; Conserv
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PC A011
CC Des
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BD167835/c
LOCUS
DEFINITION
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SOURCE
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JOURNAL
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Method for examination for allergosis
Patent: WO 0233069-A 18 25-APR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
MATIONAL CHILDREN'S HOSPITAL, TOMOYUKI FUKASAWA, CHUHEI NOJIRI, NOBUO
MATSUHASHI, KOJI NISHIZAMA, YUJI SUGITA, RYOTCHI HASHIDA, KAORU
OGAWA, MASAYA OBRYASHI, TAKESHI NAGASU, HIROHISA SAITO
OS Artificial Sequence
N WO 0233069-A/18
PD 25-APR-2002
PP 28-SEP-2001 WO 2001JP008574
PR 13-OCT-2000 JP 00P 314093
PR 13-OCT-2000 JP 00P 314093
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI
TAKESHI NAGASU,
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Description of Artificial Sequence:an artificially synthesized
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CI2N15/09, C12N15/63, C12Q1/68, C12Q1/02, G01N33/53, C12N5/10,
                                                                                                                                                                                                                                   Gaps
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synthetic construct
artificial sequences.
1 (bases 1 to 17)
Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
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                                                       /organism='Artificial Sequence'. Location/Qualifiers
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                                                                                                                                                                                               Length 17;
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100.0%; Pred. No. 4.8e+02;
tive 0; Mismatches 0;
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100.0%; Pred. No. 4.8e+02;
ive 0; Mismatches 0;
                     Location/Qualifiers
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/organism="synthetic construct"
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/db_xref="taxon:32630"
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Method for examination for allergosis.
BD168111 GI:27873923
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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PC C12N15/
A61K39/395,
PC C07K14/
CC Descrip
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BD168111/c
LOCUS
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VERSION
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BD168112/c
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JOURNAL
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SOURCE
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G01N33/50//C12P21/08, (C12N5/10, C12R1:91), (C12P21/02, C12R1:91)
Description of Artificial Sequence:an artificially synthesized
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C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
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                                                                                         04-APR-2002
21-SEP-2001 WO 2001JP008247
26-SEP-2000 JP 00P 293021
YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Method of examining allergic disease
Patent: WO 0226962-A 7 04-APR-2002;
BENDK RESPERSENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI, KAZUO MIYANAGA YUJI
SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, TAKESHI
NAGASU, HIROHISA SAITO
OS Artificial Sequence
PN WO 0226962-A/7
PD 04-APR-2002
NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI,KAZUO MIYANAGA YUJI
SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, TAKESHI
NAGASU, HIROHISA SAITO
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26-SEP-2000 JP 00P 293021
YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, PI
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WO 0226962-A/7.
synthetic construct
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1 (bases 1 to 17)
Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and
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100.0%; Pred. No. 4.8e+02;
tive 0; Mismatches 0;
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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                                                   Artificial Sequence
WO 0226962-A/6
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Best Local Similarity 100.0
Matches 15; Conservative
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PC A01K6
PC G01N3
PC G01N3
CC Descr
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PC C12N1
C12Q1/68,
PC A01K6
                                                   OS Art.
PN WO (PD 04-2)
PF 21-8
PR 26-8
PR 26-8
PR 26-8
PR YUJ
TAKESHI PL
PI HIR
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BD167908/c
LOCUS
DEFINITION
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VERSION
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JOURNAL
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SOURCE
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PAT 17-JAN-2003
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Patent: WO 0250269-A 3 27-JUN-2002;
GENOX RESEARCH INC. JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, MASAMICHI TAKAGI, AKINORI OTA YOSHIKO
MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUJI SUGITA, TAKESHI NAGASU,
                                                                                CI2NI5/11, CO7K16/18, A61K67/027, A61K31/711, A61K45/00, A61K48/00, A61P37/08,
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     21-DEC-2000 JP 00P 389476
YOSHIKO MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUJI SUGITA, PI
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C12Q1/68,G01N33/50
Description of Artificial Sequence:'GT15C', an artificially
synthesized
                                                                                                                                                                   Description of Artificial Sequence: GT15A', an artificially synthesized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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/organism='Artificial Sequence'
Location/Qualifiers
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100.0%; Pred. No. 4.88+02;
ive 0; Mismatches 0; Indels
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xrefe"taxon:32630"
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Artificial Sequence
WO 0250263-A/3
27-JUN-2002
21-DEC-2001 WO 2001JP011286
21-DEC-2000 JP 00P 389476
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BD171178.1 GI:27876990
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1 (bases 1 to 17)
                                                                                                                                                                                                                        primer sequence
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synthetic construct
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ses 15; Conservative
  PR 21-DEC-2000
PI YOSHIKO MATE
TAKESHI NAGASU,
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Best Local Si
Matches 15;
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BD171178/c
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                                                                                                                                                                                                                                  Salto, H.

Method for examination for allergosis
Method for Mo 0233069-A 19
MATSUHAGHI, WO 1 NISHIZAMA, YUJI SUGITA, RYOICHI HASHIDA, KAORU
NATSUHAGHI, KOJI NISHIZAMA, YUJI SUGITA, RYOICHI HASHIDA, KAORU
OGAWA, MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA SAITO
OS Artificial Sequence
N WO 0233069-A/19
PD 25-APR-2002
PP 25-APR-2001
PP 20-SEP-2001
PP 20-SEP-2001
PP 314093
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COTXI4/47,COTXI6/18//C12P21/02,C12P21/08
Description of Artificial Sequence:an artificially synthesized
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       PAT 17-JAN-2003
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1 (bases 1 to 17)

Matsumoto, Y., Imai, Y., Oshida, T., Sugita, Y., Nagasu, T. and

Matsumoto, G.

Method of examining allergic disease

Method of examining allergic disease

Method of examining allergic disease

Mathod of Examining alle
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Location/Qualifiers
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       linear
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100.0%; Pred. No. 4.8e+02;
tive 0; Mismatches 0;
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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                           for examination for allergosis.
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BD171177
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OS Artificial Sequence
N WO 0250269-A/2
PD 27-JUN-2002
PF 21-DEC-2001 WO 2001JP011286
                                                                         BD168112.1 GI:27873924
WO 0233069-A/19.
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WO 0250269-A/2.
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                                                                                                                                                                      artificial sequences.
1 (bases 1 to 17)
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synthetic construct
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Matches 15; Conserv
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PC C12N15/
A61K39/395,
PC C07K14/
CC Descrip
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BD171177/c
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Engyme-specific cleavable polynucleotide substrate and assay method.
BD140103.1 GI:23235048
JP 2002508935-A/3.
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C12P21/02, C12P21/08//(C12N5/10, C12R1:91), (C12P21/08, C12R1:91),
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CI2N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
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Mammal-derived tissue specific physiologically active protein.
E32461
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synthetic construct
artificial sequences.
1 (bases 1 to 18)
Jun, N., Yusuke, N. and Toshihiro, T.
Mammal-derived tissue specific physiologically active protein
Datent: JP 2000037190-A 21 08-FEB-2000;
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5.1e+02;
hes 0; Indels
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                 C12N15/00,
C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
                                                              Key Location/Qualifiers primer_bind (1). .(18).
Location/Qualifiers 1. .18
/organism="synthetic construct"/mol_type="genomic DNA"
/db_xref="taxon:32630"
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imer_bind (1). (18).
Location/Qualifiers
1. 18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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JP 2000037190-A/21
08-PEB-2000
23-JUL-1998 JP 199822528
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PN JP 20
PD OB 29
PD 23-DU
PR JUN N
PC C12N15/02,
PC C12P2
PC C12P2
PC C12P5
PC C12P5
PC C12P5
PT Key
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E32461/c
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BD140103/c
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C12N15/00,
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PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
C12N15/02,
                                                                                                                                                                                                                                                                                                                                                                                                                                     JUN NISHIU, YUSUKE NAKAMURA, TOSHIHIRO TANAKA
CI2N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
                                                                                                                                                                                                          Synthetic construct
artificial sequences.
E 1 (bases 1 to 18)
E Jun,N., Yusuke,N. and Toshihiro,T.
Mammal-derived tissue specific physiologically active protein
L Patent: JP 2000037190-A 18 08-FEB-2000;
OS Artificial Sequence
PN JP 2000037190-A/18
PD 08-FEB-2000
PF 23-JUL-1998 JP 1998255228
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synthetic construct
artificial sequences.

1 (bases 1 to 18)
Jun,N., Yusuke,N. and Toshihiro,T.
Mammal-derived tissue specific physiologically active protein
Datent: JP 2000037190-A 19 08-FEB-2000;
JAPAN TOBACCO INC
SARTIficial Sequence
PN JP 2000037190-A/19
PD 08-FEB-2000
                                                                                                                       18 bp DNA linear PAT 18-UDN
Mammal-derived tissue specific physiologically active protein.
E32458
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0.9%; Score 15; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 0;
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/organism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"
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Location/Qualifiers
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JP 2000037190-A/18.
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E32459.1 GI:13018695
JP 2000037190-A/19.
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E32459/c
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E32458/c
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                 Symmetric construct
artificial sequences.
1 (bases 1 to 19)
8 Wei,A.P. and Mach,P.A.
Enzyme-specific cleavable polynucleotide substrate and assay method
AL PECOLS 08935-A 3 26 MAR-2002;
MINNESOTA MINING MANUFACTURING CO
OS Artificial Sequence
ND 26-MAR-2002
PF 20-ANG-1998 US 2000527669
PF 20-ANG-1998 US 09/005260
PF 30-ANG-1998 US 09/005260
PF 09-JAN-1998 US 09/00
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unclassified.
NCE 1 (bases 1 to 20)
OSS OSDURN, B. BOWYER, P. and Daniels, M.J.
OSS OSDURN, B., BOWYER, P. and Daniels, M.J.
E IDENTIFICATION, PRODUCTION AND USE OF SAPONIN GLYCLOSYL HYDROLASES
E.E. RNAL
Batent: WO 9530009-A 23 09-NOV-1995;
GATSBY CHARITABLE FOUNDATION (GB)
OTHER Publication AU 1899795 951129.
LOCATION/QUalifiers

LOCATION/QUalifiers
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    .19
    forganism="synthetic construct"
|mol type="genomic DNA"
|db_xref="taxon:32630"

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0.9%; Score 15; DB 1; I
Best Local Similarity 78.9%; Pred. No. 5.4e+02;
Matches 15; Conservative 0; Mismatches 4;
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LOCUS AR067594 20 bp
DEFINITION Sequence 1 from patent US 5851769.
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Sequence 23 from Patent WO9530009.
A46856
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Wyatt, J. and Freier, S.M.
Antinsense modulation of Her-1 expression
Patent: US 6444465-A 116 03-SEP-2002;
Location/Qualifiers
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Pred. No. 5.7e+02;
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AR226053
AR226053.1 GI:27264207
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1 (bases 1 to 20)
Aizawa,A., Kawakami,A. and Kondo,T.
Testis-specific gene
Patent: US 6555670-A 4 29-APR-2003;
Location/Qualifiers
Unclassified.

1 (bases 1 to 20)
Gray,J.W. and Weier,H.-U.G.
Quanticative DNA fiber mapping
Patent: US 5851769-A 1 22-DEC-1998;
Location/Qualifiers

    .20
    /organism="unknown"
    /mol_type="unassigned DNA"

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Sequence 4 from patent US 6555670.
AR109844
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/organism="unknown"
/mol_type="genomic DNA"
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/organism="unknown"
/mol_type="genomic DNA"
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     UD143115.77-4/3.

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S Aizawa,A., Kawakami,A. and Kondo,T.

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NOVEL RESELS DESCRIFT GENE
NOVEL LESSING SEQUENCE
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PP 16-APR-2002
PP 03-OCT-2000 JP 2000303994
PI 16-APR-2002
PP 03-OCT-2000 JP 2000303994
PI AKIRA AIZAWA,AKIKO KAWAKAMI, TOSHIHIKO KONDO
PC C12N15/09,C07K4/47,C12N15/00
CC NOVEL LESTIS -SPECIFIC GENE
FH KEY
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FT SOURCE
//organism='Artificial Sequence'.
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Unclassified.
1 (bases 1 to 18)
Villeponteau, B., Feng, J., Funk, W. and Andrews, W.H. Assays for the DNA component of human telomerase Patent: US 5776679-A 36 07-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.9%; Score 15; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 5.7e+02; Matches 15; Conservative 0; Mismatches 0; Indels
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Pred. No. 5.4e+02;
0; Mismatches 2;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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    .18
    /organism="unknown"
    /mol_type="unassigned DNA"

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 BD143136.1 GI:27848894
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Best Local Similarity 88.9%;
Matches 16; Conservative
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Methods employing fluorescence quenching by metal surfaces
Patent: WO 0218951-A 2 07-MAR-2002;
THE ROCKEPELLER UNIVERSITY (US)
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iive 0; Mismatches 0;
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"

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    forganism="synthetic construct"
|mol type="unassigned DNA"
|db_xref="taxon:32630"

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Sequence 2 from Patent WO0218951
AX498346 GI:23343165
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AR075538/c
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Unclassified.
In (bases 1 to 18)
SK Hanccak.R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,
Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and
Imbach,J.Louis.
Oligonucleotides having a conserved G4 core sequence
Interest is 5952490-A 54 14 SEP-1999;
Location/Qualifiers
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Hanecak, R.C., Anderson, K.P., Bennett, C.Frank., Chiang, M.-Y.,
Brown-Driver, V.L., Ecker, D.J., Vickers, T.A., Wyatt, J.R. and
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Oligonucleotides having a conserved G4 core sequence
Patent: US 5952490-A 38 14-SEP-1999;
Location/Qualifiers
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Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels
1 (bases 1 to 18)
Villeponteau, B., Feng, J., Funk, W. and Andrews, W.H. Assays for the DNA component of human telomerase Patent: US 5776679-A 37 07-JUL-1998;
Location/Qualifiers
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Sequence 54 from patent US 5952490.
AR074246 AR074246.1 GI:10001001
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Sequence 38 from patent US 5952490.
AR074230
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Unclassified.
1 (bases 1 to 18)
Hanecak, R.C., Anderson, K.P., Bennett, C.Frank., Chiang, M.-Y., Brown-Driver, V.L., Ecker, D.J., Vickers, T.A., Wyatt, J.R. and Imbach, J.Louis.
Oligonucleotides having a conserved G4 core sequence Patent: US 595490-A 111 14-SEP-1999;
Location/Qualifiers
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Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels
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Sequence 111 from patent US 5952490.
AR074303. GI:10001058
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Unclassified.
1 (bases 1 to 18)
Egholm, M., Nielsen, P., Buchardt, O., Dueholm, K.L., Christensen, L.,
Coull, J.M., Kiely, J. and Griffith, M.
                                                                                                                                                                                              Unclassified.

1 (bases 1 to 18)

Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.

Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6346388-A 3043 12-PEB-2002;

Location/Qualifiers
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1 (bases 1 to 18)

Soberts, L. M. and Cowsert, L.M.
Antisense modulation of human Rho family gene expression
Patent: US 6410323-A 169 25-JUN-2002;
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Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2;
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88.9%; Pred. No. 5.4e+02;
attive 0; Mismatches 2;
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Sequence 169 from patent US 6410323.
AR215621
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Sequence 3043 from patent US
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Best Local Similarity 88.9
Matches 16; Conservative
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AR187555/c
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1 (bases 1 to 18)

Draper, K.G., Crooke, S.T., Mirabelli, C.K., Ecker, D.J., Hanecak, R.C., Anderson, K.P., Brown-Driver, V.L. and Wyatt, J.R.
Oligonucleotide therapies for modulating the effects of herpes viruses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 18;
                                                                                                                                                  Length 18;
1 (bases 1 to 18)
Villeponteau, B., Feng, J., Funk, W. and Andrews, W.H.
Mammalian telomerase
Patent: US 595860-A 36 28-SEP-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                             linear
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0.8%; Score 14.8; DB 1;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Unclassified.
Unclassified.
1 (bases 1 to 18)
Cowsert, L.M.
Antisense modulation of RhoG expression
Patent: US 595370-A 26 12-OCT-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent: US 5514577-A 57 07-MAY-1996;
Location/Qualifiers
1. .18
/organism="unknown"
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Sequence 57 from patent US 5514577.
120478
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/organism="unknown"
/mol_type="unassigned DNA"
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/organism="unknown"
/mol_type="unassigned DNA"
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Seguence 26 from patent US 5965370.
AR078882
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PAT 17-AUG-2003
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                                 PAT 12-JUN-2003
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Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions
related to levels of vascular andothelial growth factor receptor
Patent: US 6566127-A 1471 20-MAY-2003;
Location/Qualifiers
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Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
WightL,J.R.
WightL,J.R.
Wightlebrides having a conserved g4 core sequence
Patent: EP 1016715-A 38 05-JUL-2000;
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88.9%; Pred. No. 5.4e+02;
tive 0; Mismatches 2; Indels
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                                                                                                                                                      1 (bases 1 to 18)
Villeponteau, B., Feng, J., Funk, W. and Andrews, W.H.
Mammalian telomerae
Patent: US 6548298-A 36 15-APR-2003;
Location/Qualifiers
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                                 DNA
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                          Sequence 36 from patent US 6548298.
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Sequence 38 from Patent BP1016715.
AX032592. GI:10279530
                                                                                                                                                                                                                                                         /organism="unknown"
/wol_type="genomic DNA"
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Matches 16; Conservative
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AX032592
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RESULT 722
AR306484/c
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Unclassified.
1 (bases 1 to 18)
1 (bases 1 to 18)
2 Sebolam, N. Nielsen, P., Buchardt, O., Dueholm, K.L., Christensen, L., Coull, J.M., Kielsy, J. and Griffith, M.
Coull, J.M., Kielsy, J. and Griffith, M.
Peptide nucleic acids
Patent: US 6451968-A 33 17-SEP-2002;
Location/Qualifiers
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llarity 88.9%; Pred. No. 5.4e+02;
Conservative 0; Mismatches 2; Indels
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1 (Dases 1 to 18)

Villeponteau, B., Feng, J., Funk, W. and Andrews, W.H. Wammalian telomerses
Patent: US 6548298-A 35 15-APR-2003;
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88.9%; Pred. No. 5.4e+02;
ative 0; Mismatches 2;
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0.8%; Score 14.8; DB 1;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2;
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Peptide nucleic acids
Patent: US 6451968-A 32 17-SEP-2002;
Location/Qualifiers
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Sequence 33 from patent US 6451968.
AR231296
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Sequence 35 from patent US 6548298.
AR306483
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/organism="unknown"
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Artificial Sequence
JP 2001321190-A/507
20-NOV-2001
12-MRZ-2001
BIICHI SOEDA
CIZNIS/09,CIZNIS/09,CIZQI/68,G01N33/53,G01N33/566, PC
                                                                                                                                                            PAT 28-FEB-2001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: JP 2001321190-A 507 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
GENOTECHS
A Prificial Sequence
PN JP 2001321190-A/507
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
PP H EICHI SOEDA
PC CIINIS/09,CIINIS/09,CIINIS/53,GOIN33/53
                                                                                                                                                                                                                                                                                                                                   Bowman, B.M. and Wang, K.
Dna sequences isolated from human colonic epithelial cells
Patent: Wo 0111047-A 25 15-FBB-2001;
Bayer Corporation (US)
Location/Qualifiers
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Location/Qualifiers
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                                                                                                                                                            DNA
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   0; Mismatches

    .18
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

                                                                                                                                                          AX082574 18 bp
Sequence 25 from Patent WO0111047.
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                                      1019 TTGGGGATGGGGCTGGGG 1036
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JP 2001321190-A/507.
synthetic construct
synthetic construct
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   Matches 16; Conservative
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Bennett, C.F., Chiang, M.Y., Anderson, K.P., Hanecak, R.C. and
Wyatt, J.R.
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Patent: EP 1016715-A 54 05-JUL-2000;
ISIS PHARMACEUTICALS INC (US)
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    .18
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Sequence 111 from Patent EP1016715.
AX032665

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Sequence 54 from Patent EP1016715.
AX032608
ISIS PHARMACEUTICALS INC (US)
Location/Qualifiers
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PN JP 2002272489-A/44

PN JP 2002272489-A/44

PD 24-SEP-2002

PF 06-MAR-2002 JP 2002061125

PR 07-JUL-1994 US 08/472202,27-OCT-1994 US 08/330123 PI
07-JUL-1995 US 08/472202,07-JP 1995 US 08/482115 PI BI
VILLEPOWTEAU, UTNI PENG, WALTER FUNK, WILLIAM H ANDREWS PC
CI2NIS/09,C12N9/99,C12Q1/68,G01N33/53,G01N33/566,C12N15/00 CC
Strandedness Single,
CC TOPOLOGY: Linear;
CC Mammalian telomerase
FH Key Location/Qualifiers
FT Gource /ocation/Qualifiers
FT /ocation/Qualifiers
 PR 07-JUL-1994 US 08/272102,27-OCT-1994 US 08/330123 P
07-JUN-1995 US 08/472802,07-JUN-1995 US 08/432115 PI B
VILLEPONTEAU JUNLI FERG, WALTER FUNK, WILLIAM H ANDREWS PC
C12N15/09,C12N9/99,C12Q1/68,G01N33/53,G01N33/566,C12N15/00 CC
Strandedness: Single;
CC Topology: Linear;
CC Mammalian telomerase
FH Key Location/Qualifiers
FT Source Location/Qualifiers
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Villeponteau, B., Feng, J., Funk, W. and Andrews, W.H. Mammalian telomerase
Patent: 1P 2002272489-A 44 24-SEP-2002;
GERON CORP
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Pred. No. 5.4e+02;
0; Mismatches 2;
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JP 2002272489-A/44.
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Best Local Similarity 88.9%;
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                       A gene coding for aceto-lactate-sythetase
Patent: WO 0244385-A 2 06-JUN-2002;
KUMIAI CHEMICAL INDUSTRY CO LTD, NATIONAL INSTITUTE OF
AGROBIOLOGICAL SCIENCES, TSUTOMU SHIMIZU, ISHIZUE NAKAYAMA, KOZO
NAGAYAWA, ATSUNORI FUKUDA, YOSHIYUKI TANAKA, KOICHIRO KAKU
OS Artificial Sequence
NW 0 0244385-A/2
                                                                                                                                                                                                                                                         synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 18)
Shimizu,T., Nakayama,I., Nagayama,K., Fukuda,A., Tanaka,Y. and
                        Gaps
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Villeponteau, B., Feng, J., Funk, W. and Andrews, W.H.
TE Mammalian telomerase
RNA Patent: 19 2002272489-A 43 24-SEP-2002;
CS Unidentified
PN JP 2002272489-A/^2
PP A-SEP-200272489-A/^2
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     Pred. No. 5.4e+02;
0; Mismatches 2; Indels
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PI YOSHIYUKI TANAKA,KOICHIRO KAKU
PC C12N15/60,C12N9/88,C12N5/14,A01H5/00
CC Description of Artificial Sequence:primer
Location/Qualifiers
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BD169501

    .18
/organism="synthetic construct"

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29-NOV-2000 JP 00P 362630
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/db_xref="taxon:32630"
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   88.9%;
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BD176184
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Best Local Similarity 88.3.
Thea 16; Conservative
                     16; Conservative
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SOURCE ACCESSION VERSION KEYWORDS

REFERENCE AUTHORS

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PAT 14-JUN-2002
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1 (bases 1 to 16)
Norberg, L. Torbjorn., Andersson, M. Kristina. and
Lindstrom, P. Harry. Rutger.
Methods for assessing cardiovascular status and compositions for
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Patent: Wo 0226968-A 2 04-APR-2002;
University of Ottawa (CA); Aegera Therapeutics Inc. (CA)
Location/Qualifiers
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93.8%; Pred. No. 5.3e+02;
iive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="based on Homo sapiens"
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Location/Qualifiers
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Sequence 12 from patent US 6197505.
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                                                                                                                     AX411902 19 bp Sequence 2 from Patent WO0226968.
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/organism="unknown"
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                    2 GCTGCCTCCAGAGGATG 19
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JP 2002527079-A/12.
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Best Local Similarity, 93.8
Matches 15; Conservative
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Best Local S:
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AR137265/c
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BD231248/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="forward primer for human STS sts-stSG4981 at 1p36 sts-stSG4981 obtained from clones B277F16, B370B7, B133B1, B137C2, B182L10, B123L12, B200L1, B200L2, B215B22, Human BAC library RPCT-11"
                                                                                                                                                       Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
Tel:81-22-717-8042, Fax:81-22-717-8047)
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A BAC-based STS-content map spanning a 35-Mb region of human
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88.9%; Pred. No. 5.4e+02;
cive 0; Mismatches 2; Indels
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Pred. No. 5.7e+02;
0; Mismatches 2; Indels
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1. 18
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IMMUSOL, INC. (US)
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AX129282
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Genomics 74 (1), 55-70 (2001)
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                  AB069090
AB069090.1 GI:15129894
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synthetic construct
artificial sequences.
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Best Local Similarity 88.99
Matches 16; Conservative
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Matches 16; Conservative
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RESULT 733 AX129282 LOCUS

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VERSION

KEYWORDS SOURCE ORGANISM

AUTHORS

TITLE

REFERENCE

JOURNAL

FEATURES

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source

FEATURES

MEDLINE PUBMED REFERENCE

JOURNAL

TITLE

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BD075139 16 bp DNA 'linear PAT 27-AUG-2002 Methods for assessing cardiovascular status and compositions for
                                                                                                                                    BD075139.1 GI:22620742
JP 200151960-A/12.
Synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 16)
Norberg, LT., Andersson, M.K. and Lindstrom, P.H.R.
Methods for assessing cardiovascular status and compositions for use thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blatt, L., Mcswiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0159103-A 2363 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                Patent: JP 2001519660-A 12 23-OCT-2001;
EURONA MEDICAL AB

OS Artificial Sequence
PN JP 2001519660-A/12
PD 23-OCT-2001
PF 01-APR-1998 JP 1998542530
PR 04-APR-1997 US 60/042930
PI LEIF TORBJORN NORBERG, MARIA KRISTINA ANDERSSON, PER HARRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 16;
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Description of Artificial Sequence: PCR PRIMER
Location/Qualifiers
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93.8%; Pred. No. 5.3e+02;
tive 0; Mismatches 1;
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Sequence 2363 from Patent WO0159103.
AX216921
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Best Local Similarity 93.8°
Matches 15; Conservative
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                                                                                                   use thereof.
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                                   artificial sequences.
1 (bases 1 to 16)
Norberg, L. T., Andersson, M. K., Lindstrom, P. H. R. and Jonsson, L. Genes for assessing cardiovascular status and compositions for use
                                                                                                                                                                                                                                                                                                                                           Genes
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PN UP 2002527079-A/12
PD 27-AUG-2002
PF 13-OCT-1999 JP 2000576056
PR 14-OCT-1999 US 60/104286,14-OCT-1998 US 60/104302 PI
LEIF TORBJORN NORBERG, MARIA KRISTINA ANDERSSON, PER HARRY PI
RUTGER LINDSTROM,
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C1201/68,C12N15/09//G01N33/53,G01N33/566,C12N15/00 CC
assessing cardiovascular status
compositions for
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    .16
    /organism='Artificial Sequence'

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/organism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer"
                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers

    16 / Organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

                                                                                                                                      Patent: JP 2002527079-A 12 27-AUG-2002;
PAIROSEAKENSINGU AB
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synthetic construct
artificial sequences
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Shannon, M., Gu, Y. and Nguyen, C.T.
Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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METHOD FOR IDENTIFYING AN UNKNOWN ALLELE
PATENT: WO 972019-7-A 6 05-JUN-1997;
ANTHONY NOLAN BONE MARROW TRUS (GB)
Other publication AU 7703796 19970619.
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1 (bases 1 to 18)

Bennett, C. Frank. and Cowsert, L.M.
Antisense modulation of CD71 expression
                                                                                                                                                                                                               Patent: EP 1281758-A 5254 05-FEB-2003;
   Seguence 5254 from Patent EP1281758,
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 71 from patent US 6004814.
AR095850
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/db_xref="taxon:32644".
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Sequence 6 from Patent WO9720197.
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Location/Qualifiers
                                     AX692522.1 GI:29415480
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                                                                        Homo sapiens (human)
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Best Local Similarity 93.8<sup>†</sup>
Matches 15; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method and reagent for the inhibition of erg
Patent: WO 0188124-A 835 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
Location/Qualifiers
                                                                                                                                                                                                                                                                                   Blatt, L., Mcswiggen, J. and Chowrira, B.M. Method and reagent for the modulation and diagnosis of cd20 and
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Patent: WO 0159103-A 3501 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US)
MCSWiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon.32630"
/note="Nucleic Acid"
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Sequence 3501 from Patent WO0159103.
AX218059
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/organism="Homo sapiens"
/mol_type="unassigned RNA"
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 861 AGGAAGAGGAAGAGA 876
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                        AGGAGGAGGAAGAGGA 17
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AX422499
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AX692522/c
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PAT 08-SEP-2000

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D00269S07 18 bp DNA linear PRI 21-SEP-2002
Homo sapiens gene for tyrosine hydroxylase, exon 6, partial
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 PAT 18-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                            Query Match 0.8%; Score 14.4; DB 1; Length 18; Best Local Similarity 93.8%; Pred. No. 6e+02; Matches 15; Conservative 0; Mismatches 1; Indels
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                                                                                                      Unclassified.

1 (bases 1 to 18)
Bennett, C.F. and Cowsert, L.M.
Antisense inhibition of Her-2 expression
Patent: US 6613567-A 35 02-8EP-2003;
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/nofce="primer"
    DNA
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              Sequence 35 from patent US 6613567. AR392120
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Sequence 346 from Patent WO0129262.
AX115223
                                                                                                                                                                                                               /organism="unknown"
/mol_type="genomic DNA"
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                                              AR392120.1 GI:40116010
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Homo sapiens (human)
Homo sapiens
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D00275.1 GI:220105
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AX115223/c
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Cowmert.L.M.
Antisense inhibition of cyclin D2 expression
Patent: 15 6492173-A 49 10-DEC-2002;
Location/Qualifiers
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1 (bases 1 to 18)

1 squello, R., Avakian, H. and Madrigal, A.
Method for identifying an unknown allele
Patent: US 6500614-A 6 31-DEC-2002;
Location/Qualifiers
                                                                                         0.8%; Score 14.4; DB 1
93.8%; Pred. No. 6e+02;
tive 0; Mismatches
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 Patent: US 6004814-A 71 21-DEC-1999;
Location/Qualiflers
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AR268656
AR268656.1 GI:29699271
                                            /organism="unknown"
/mol_type="unassigned DNA"

    18
    /organism="unknown"
    /mol_type="genomic DNA"

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/mol_type="genomic DNA"
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Best Local Similarity 93.83
Matches 15; Conservative
                                                                                       Query Match 0.8 Best Local Similarity 93.8 Matches 15; Conservative
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Best Local Similarity 93.8
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="unassigned DNA"
Dxref="taxon:9606"
/nofe="cyclin D2 ribozyme binding site"
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93.8%; Pred. No. 6.4e+02;
tive 0; Mismatches 1;
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Sequence 148 from patent US 6617122.
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Sequence 4 from Patent WO02102824.
AX659402
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/organism="unknown"
/mol_type="genomic DNA"
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AR393609
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Isolation and characterization of the human tyrosine hydroxylase gene: identification of 5' alternative splice sites responsible for
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Kobayashi,K., Kaneda,N., Ichinose,H., Kishi,F., Nakazawa,A.,
Kurosawa,Y., Fujita,K. and Nagatsu,T.
Structure of the human tyrosine hydroxylase gene: alternative
splicing from a single gene accounts for generation of four mRNA
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1 (bases 1 to 19)

Port, J. David. and Bristow, M.R.

Transgenic model and treatment for heart disease
Patent: US 6218597-A 4 17-APR-2001;

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/tissue_type="Placenta"
/note="54 bp_after segment 6"
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/note="AA 244 at 1"
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                                                                      Biochemistry 26 (22), 6910-6914 (1987)
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/mol_type="unassigned DNA"
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Sequence 4 from patent US 6218597.
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1735 CAAAAAAAAAAAA 1749
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Best Local Similarity 93.37
Matches 14; Conservative
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AR029887/c
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E53842.
E53842. GI:18633612
Unidentified
Beimfohr,C. and Snaidr,J.
Method for specific fast detection of relevant bacteria in drinking
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C C12N15/09,CONK14/47,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10//A61K31/00,
PC A61K38/00,A61K48/00,C12P21/02,C12N15/00,C12N5/00,A61K37/02 CC
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0.8%; Score 14.2; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 5.7e+02;
Matches 14; Conservative 1; Mismatches 0; Indels
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0.8%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 6.46+02;
Matches 15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                      linear
                                    Patent: WO 02102824-A 4 27-DEC-2002;
Vermicon AG (DE)
Location/Qualifiers
Location/Qualifiers
L. 19
/crganism="synthetic construct"
/mol_type="unassigned DNA"
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/note="oligonucleotide"
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    .16
    /organism='Unknown'

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Ogawara,T., Suzuki,M. and Ozaki,K.
TSA7005 gene
Patent: JP 2001025389-A 3 30-JAN-2001;
OTSUKA PHARMACEUT CO LTD

    .16
    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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30-JAN-2001
15-JUL-1999 JP 1999201279
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JP 2001025389-A/3.
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E53842/c
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E52143/c
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PI MORITO KADOTA, YOSHIYUKI FUJIWARA, RYUJI WATANABE, KOICHI OZAKI
PC (12N15/09, COTK14/82, CO7K16/32, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10, C12Q1/68,
PC G01N33/15, G01N33/50, G01N33/566, G01N33/574/A61K31/713, PC
A61K35/12, A61K35/76,
PC C12N15/00,
PC C12N15/00,
PC C12N15/00,
PC C12N15/00,
PC FR Key
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Tobases 1 to 16)
Kadota,M., Fujiwara,Y., Watanabe,R. and Ozaki,K.
LUNX gene and method for detecting micrometastasis of cancer
Patent: JP 2001079772-A 3 27-MAR-2001;
OTSUXA PHARMACEUT CO LID
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Wang, C. G. and Hepburn, A. G.
Mang, C. G. and Hepburn, A. G.
Panetic sequence assay using DNA triple strand formation
Patent: US 5861244-A 75 19-JAN-1999;
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/organism='Unidentified'.
Location/Qualifiers
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0.8%; Score 14; DB 1; Lv
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0;
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Sequence 76 from patent US 5861244.
AR029887.1 GI:5943101

    .14
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    /mol_type="unassigned DNA"

    .16
    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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Synthetic construct
SM synthetic construct
attificial sequences.

Lough a synthetic construct
attificial sequences.

Dale, R.M.K., Gatton, S.L. and Arrow, A.

Nucleic acid having blocked terminals modified with an acid-stable skeleton and therapeutic method thereof

Digos ETC INC
OLIGOS ETC INC
ON Artificial Sequence
PN JP 2002534434-A 2 15-OCT-2002;

OLIGOS ETC INC
ON ARTIFICIAL Sequence
PN JP 2002534434-A/2
PD 15-OCT-2002
PR 16-DEC-1999 JP 2000592300
PR 30-DEC-1999 US 09/32498,19-JUL-1999 US 09/356069 PI
RODERIC M K DALE, STEVEN L GATTON, AMY ARROW
PC COTHIL/OO, A61K9/127, A61K9/50, A61K31/7088, A61K47/44, A61K48/00,
                                                                                                BD237464 linear PAT 17-JUL-2003 Nucleic acid having blocked terminals modified with an acid-stable skeleton and therapeutic method thereof.
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Nucleic acid having blocked terminals modified with an acid-
stable
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C12NS/10,
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Key Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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1 (bases 1 to 14)

Kurz,M., Lohse,P. and Wagner,R.

Peptide acceptor ligation methods

Patent: US 6429300-A 20 06-AUG-2002;

Location/Qualifiers
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Sequence 20 from patent US 6429300.
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/organism="unknown"
/mol_type="genomic DNA"
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Best Local Similarity 100.0%; Pi
Matches 14; Conservative 0;
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                    14 ACAAAAAAAAAAA
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AUTHORS
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Petkovich, P.Martin., White, J.A., Beckett, B.R. and Jones, G. Retinoid metabolizing protein
Patent: US 6306624-A 14 23-OCT-2001;
Location/Qualifiers
       Unknown.
Unclassified.
I (bases 1 to 14)
Wang,C.-G. and Hepburn,A.G.
Genetic sequence assay using DNA triple strand formation
Patent: US 5861244.A 76 19-JAN-1999;
Location/Qualifiers
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1 (bases 1 to 14)
D'Andrea,A.D. and Zhu,Y.
DeUBiquitinating enzymes that regulate cell growth Patent: US 6287855-A 26 11-SEP-2001;
Location/Qualifiers
                                                                                                                                                                                        Score 14; DB 1; Lengtn 11,
Pred. No. 5.2e+02;
O. Indels
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0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels
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0.8%; Score 14; DB
Best Local Similarity 100.0%; Pred. No. 5.2
Matches 14; Conservative 0; Mismatches
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Sequence 14 from patent US 6306624.
AR174024
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Sequence 26 from patent US 6287858.
AR168510
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AR174024/C
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PAT 26-SEP-2002

TITLE JOURNAL

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AX827014
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1 (bases 1 to 14)
Caruthers,M.H., Marshall,W.S., Brill,W. and Nielsen,J.
Polynucleotide phosphorodithicate
Patent: US 5453496-A 4 26-SEP-1995;
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Caruthers,M.H., Marshall,W.S., Brill,W. and Nielsen,J.
Polynucleotide phosphorodithioate
Patent: US 5453496-A 5 26-SEP-1995;
Location/Qualifiers
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Sequence 4 from patent US 5453496.
AR364948.1 GI:34428168
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Sequence 5 from patent US 5453496.
AR364949
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Sequence 5 from Patent W00071747.
AX048406
AX048406.1 GI:12225570
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100.0%; Pre
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Patent: EP 1348713-A 11 O-CT-2003;
Enzo Life Sciences, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rabbani, E., Stavrianopoulos, J.G., Donegan, J.J., Coleman, J. and
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Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
Detection system for separating constituents of a sample and production and use of the same
Patent: WO 0071/47-A 5 30-NOV-2000;
Aventis Research & Technologies GmbH & Co. KG (DE)
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0;
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/note="Region A"

    14
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Sequence 11 from Patent EP1344835.
AX827014
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AX839906
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Use Synthetic construct

Synthetic construct

synthetic construct

artificial sequences.

I (Alases I to 14)

RS Komlyama, M. and Asanuma, H.

Oligonucleotide for SNP detection

AL Patent: JP 2001346579-A 2 18-DEC-2001;

MAKCOTO KOMIYAMA, HIROYUKI ASANUMA

OS Artificial Sequence

PP 02-JUN-2000 JP 2000165441

PP 02-JUN-2000 JP 200016541

PF 02-JUN-2000 JP 200016
                                                                                                                                                                                                                                                                                                                                                         /02 CC Polymorphisms hemochromatosis gene
                                                                                                                                            PROGENTION INC.
OS Home sapiens (human)
PN JP 2001525663-A/15
PD 11-DEC-2001
PF 30-SEP-1997 JP 1998516815
PF 01-OCT-1996 US 08/724394,07-MAY-1997 US 08/852495 PI JOHN N FEDER, GRECORY S KRONYAL, PETER M LAUER, DAVID A RUDDY, PI WINSTON J THOMAS, ZENTA TSUCHIHASHI, ROGER K WOLFF PC C07H21/04,012Q1/68,C12M15/63,C12M15/85,C12P21/02 CC Polymorph and new genes in the region of the human CC hemochromatosis g PH Key
Feder, J. N., Kronmal, G.S., Lauer, P. M., Ruddy, D. A., Thomas, W. J., Tsuchihashi, Z. and Wolff, R. K.
Polymorphisms and new genes in the region of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism='Homo sapiens (human)'. Location/Qualifiers
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                                                                                    hemochromatosis gene
Patent: JP 2001528663-A 15 11-DEC-2001;
PROGENTIOR INC
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BD096963/c
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28-AUG-2001

PF 05-AUG-1998 JP 2000506375

PR 08-AUG-1997 US 08/908873

PI RAREN SUISHBEM, SUZANNE HOSIER, MANFRED KUBBIES PC C1201/68, COTK14/435, COTK16/18, C12N1/19, C12N15/09, PC C12P21/02, C2 Strandedness: Single;

CC Topology: Linear;

CC Topology: Linear;

CC Topology: Linear;

CC Topology: Linear;

FF Key

FT Source
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 14)
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  1. .14
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/note="Description of Artificial Sequence: Primer"
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Location/Qualifiers
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Suishelm, K., Hosier, S. and Kubbies, M.
Isolation of novel aging factor gene P23
Batcht: JP 2001512698-A 15 28-AUG-2001;
UNIVERSITY OF WASHINGTON
OS Unidentified
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/organism="unidentified"
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/db_xref="taxon:32644"
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BD073890.1 GI:22619493
JP 2001512698-A/15.
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Homo sapiens (human)
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Pred. No. 5.2e+02; Mismatches 0;

Mismatches

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BD176800/c
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                                                                                        S JP 2001346579-A/4.

Synthetic construct

Synthetic construct

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attificial sequences.

I (bases 1 to 14)

IS Koniyama, M. and Asanuma, H.

Oligonucleotide for SNP detection

L Patent: JP 2001346579-A 4 18-DEC-2001;

MAKATO KOMIYAMA, HIROYUKI ASANUMA

OS Artificial Sequence

PN JP 2001346579-A/4

PD 18-DEC-2001

PF 02-JUN-2000 JP 2000165441

PI MAKATO KOMIYAMA, HIROYUKI ASANUMA

PC C12N15/09,C12N15/09,C12Q1/68,G01N21/78,G01N33/566,
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artificial sequences.

1 (bases 1 to 14)
Methods of nucleic acid detection
Methods of nucleic acid detection
Patent: JP 2002509443-A 1 26-MAR-2002;
CS Artificial Sequence
PD 26-MAR-2002
PP 30-OCT-1998 JP 1999526687
PR 31-OCT-1997 US 60/063969
PP 31-OCT-1997 US 60/063969
PP WILLIAM G WEISBURG, PAUL D STULL, MICHAEL R RESHATOFF PC
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    forganism="synthetic construct"
/mol type="genomic DNA"
    /db_xref="taxon:32630"

    .14
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/mol_type="genomic DNA"</pr>
        <pr/>/db_xref="taxon:32630"</pr>

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                                                            Oligonucleotide for SNP detection.
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BD132850.1 GI:23227795
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BD176800 14 bp DNA linear PAT 18-MAR-2003 Method of constructing cDNA tag for identifying expressed gene and method of analyzing gene expression.
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I (bases 1 to 14)
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Synthetic sequence
Method of constructing cDNA tag for identifying expressed gene and method of canalyzing gene expression
In Patent: WO 02074951-A 47 26-SEP-2002;
KUNITAKA HIROSE, JUN SAKAI
OS Artificial Sequence
DN WO 02074951-A/47.
PD 26-SEP-2002;
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/organism='Artificial Sequence'
Location/Qualifiers
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100.0%; Pred. No. 5.2e+02;
tive 0; Mismatches 0;

    14
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WO 02074951-A/42.
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synthetic construct
artificial sequences.
1 (bases 1 to 14)
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1736 AAAAAAAAAAAA 1749
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Best Local Similarity 100.0
Matches 14; Conservative
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Page 196

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BD176804.1 GI:29122516

WO 02074951-A/51.

WO 02074951-A/51.

WO 02074951-A/51.

Synthetic construct
artificial sequences.

I (bases 1 to 14)

X mamocto,M., Yamamoto,N., Hirose,K. and Sakai,J.

Rethod of constructing cDNA tag for identifying expressed gene and method of fanalyzing gene expression
method of analyzing gene expression
RCNUTARA HIROSE,JUN SAKAI

SAKAI HIROSE,JUN SAKAI

OS Artificial Sequence
PN WO 02074951-A/51

PP 13-MAR-2002
PP 13-MAR-2001
PP 073959

PI MIKIO YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
C12N15/09,C1201/68

CC Synthetic DNA

FY Source

//organism=/Artificial Sequence'.
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1 (bases 1 to 15)
Grimm, S., Stinchcomb, D.T., McSwiggen, J., Sullivan, S. and
Draper, K.G.
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/organism='Artificial Sequence'.
Location/Qualifiers
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100.0%; Pred. No. 5.6e+02;
1ve 0; Mismatches 0;
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/organism="synthetic construct"
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Sequence 360 from patent US 5837542.
AR056156.
AR056156.1 GI:5981733
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AR055852
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attificial sequences.

I (bases 1 to 14)

Yamamoto, N., Hirose, K. and Sakai, J.

Nethod of constructing cDNA tag for identifying expressed gene and method of constructing cDNA tag for identifying expressed gene and method of constructing cDNA tag for identifying expressed gene and method of analyzing gene expression

NI KUREHA CHEMICAL INDUSTRY CO LTD, MIKIO YAMAMOTO, NAOKI YAMAMOTO, KUNITAKA CHEMICAL INDUSTRY CO LTD, MIKIO YAMAMOTO, NAOKI YAMAMOTO, NAOKI YAMAMOTO, NAOKI YAMAMOTO, NAOKI YAMAMOTO, NAOKI YAMAMOTO, NAOKI YAMAMOTO, KUNITAKA HIROSE, JUN SAKAI PC C12N15/09, C12Q1/68

CC Synthetic DNA

FR SOURCE

CC Synthetic DNA

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// Organism='Artificial Sequence'.
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PF 13-MAR-2002 WO 2002JP002338
PR 15-MAR-2001 JP 01P 073959
PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC C12N1s/09,C12Q1/68
CC Synthetic DNA Location/Qualifiers
FH Key L. 14
/organism='Artificial Samione'
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Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0;

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/db_xref="taxon:32630"

    .14
    /organism="synthetic construct"
|mol_type="genomic DNA"
|db_xref="taxon:32630"

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WO 02074951-A/50.
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BD176803/c
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Patent: US 6132967-A 56 17-OCT-2000;
Location/Qualifiers
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Patent: US 6132967-A 360 17-OCT-2000;
Location/Qualifiers
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Grimm, S., Stinchcomb, D.T., McSwiggen, J., Sullivan, S. and
Draper, K.G.
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1 (bases 1 to 15)
Grimm.S., Stinchcomb.D.T., McSwiggen.J., Sullivan.S. and Draper.K.G.
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Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 14; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 14; Conservative 0; Mismatches 0;
100.0%; Pred. No. 5.6e+02; tive 0; Mismatches 0;
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Seguence 360 from patent US 6132967.
AR113914
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Sequence 363 from patent US 6132967.
AR113917
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Sequence 56 from patent US 6132967.
AR113610
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Matches 14; Conservative
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AR113917/c
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                                                               1 (bases 1 to 15)
Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
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1 (bases 1 to 15)
Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
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1 (bases 1 to 15)
Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
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Intercellular adhesion molecule-1 (ICAM-1) ribozymes
Patent: US 5837542-A 363 17-NOV-1998;
Location/Qualiflers
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Patent: US 5837542-A 597 17-NOV-1998;
Location/Qualifiers
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Patent: US 5837542-A 360 17-NOV-1998;
Location/Qualifiers
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0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels
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Sequence 363 from patent US 5837542.
AR056159.1 GI:5981736
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Sequence 158 from patent US 6472154. AR241870
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AR241870/c
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Cook, P.D., Delecki, D.J. and Guinosso, C.
Acyclic nucleoside analogs and oligonucleotide sequences containing
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                                                                                                                  Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
Patent: US 6132967-A 363 17-OCT-2000;
Location/Qualifiers
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Patent: US 6132967-A 597 17-OCT-2000;
Location/Qualifiers
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Unclassified.
1 (bases 1 to 15)
Grimm, S., Stinchcomb, D.T., McSwiggen, J., Sullivan, S. and
                                                                         1 (bases 1 to 15)
Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
Draper,K.G.
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Seguence 597 from patent US 6132967.
AR114151
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Location/Qualifiers
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 AR113917.1 GI:14094239
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Cook, P.D., Delecki, D.J. and Guinosso, C.
Aryclic nucleoside analogs and oligonucleotide sequences containing
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Stinchomb, D.T., Draper, K.G. and McSwiggen, J.
Rel a targeted thosywes
Patent: US 5658780-A 16 19-AUG-1997;
Query Match
0.8%; Score 14; DB 1; I
Best Local Similarity 93.3%; Pred. No. 5.6e+02;
Matches 14; Conservative 0; Mismatches 1.
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Sequence 16 from patent US 5658780.
161462
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Location/Qualifiers
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Sequence 4 from patent US 5576427.
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Woolf,T. Method and reagent for inhibiting the expression of disease related
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Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 14; Conservative 0; Mismatches 0;
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                                                Patent: BP 1260586-A 334 27-NOV-2002; RIBOZYME PHARMACEUTICALS, INC. (US) Location/Qualifiers
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RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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Sequence 340 from Patent EP1260586.
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    /organism="unidentified"

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Garner, H.R., Wren, J.D., Minna, J.D. and Fondon, J.W. III.
Polymorphic repeats in human genes
Patent: US 6472154-A 158 29-OCT-2002;
Location/Qualifiers
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Best Local Similarity 93.3%; Pred. No. 5.6e+02;
Matches 14; Conservative 0; Mismatches 1;
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RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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Sequence 334 from Patent EP1260586.
AX633195.1 GI:28468809
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Sequence 20 from Patent EP1260586.
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 GI:27287682
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Method and reagent for inhibiting the expression of disease related
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Gryaznov, S.M. and Lloyd, D.H.
Oligonucleotide clamps having diagnostic and therapeutic
applications 3817795-A 6 06-OCT-1998;
Location/Qualifiers
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Convergent synthesis of branched and multiply connected macromolecular structuras Structuras Patent: 1831058-A 6 03-NOV-1998;

Location/Qualifiers
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AR045207
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Sequence 6 from patent US 5830658.
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      Matches 14; Conservative
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AR051238/c
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Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
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100.0%; Pred. No. 5.6e+02;
ive 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 14; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 6e+02;
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RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers
   Patent: EP 1260586-A 438 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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Sequence 3016 from Patent EP1260586.
AX635877

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Gryaznov, S.M. and Lloyd, D.H.
Oligonucleotide clamps
Patent: US 5741643-A 6 21-APR-1998,
Location/Qualifiers
                                               1. .15
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Best Local Similarity 100.0
Matches 14; Conservative
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AX635877
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PAT 16-JUN-2001

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1 (bases 1 to 16)
Mezes, P.S., Gourlie, B.B., Rixon, M.W., Schlom, J., Kaplan, D.A. and Anderson, W.H.Kerr.
Family of high affinity, modified antibodies for cancer treatment Patent: US 6207815-A 39 27-MAR-2001,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 16)
Grysznov,S.M. and Lloyd,D.H.
Oligonucleotide clamps having diagnostic applications
Patent: US 5473060-A 6 05-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.8%; Score 14; DB 1; Length 16; Best Local Similarity 100.0%; Pred. No. 6e+02; Matches 14; Conservative 0; Mismatches 0; Indels
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/organism="unknown"
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Sequence 6 from patent US 5473060.
116032
116032.1 GI:1250940
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1 (bases 1 to 16)

1 (bases 1 to 16)

Anderse, P.S., Gourlie, B.B., Rixon, M.W., Schlom, J., Kaplan, D.A. and Anderson, W.H. Kerr.

Family of high affinity, modified antibodies for cancer treatment. Patent: US 6207915-A 23 27-MAR-2001;
                           1 (bases 1 to 16)
Mezes, P.S., Gourlie, B.B., Rixon, M.W., Schlom, J., Kaplan, D.A. and Anderson, W.H. Kerr.
Family of high affinity, modified antibodies for cancer treatment Patent: US 5993813-A 23 30-NOV-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 16)
Mezes, P.S., Gourlie, B.B., Rixon, M.W., Schlom, J., Kaplan, D.A. and
Anderson, W.H. Kern
Anderson, W.H. Kern
Family of high affinity, modified antibodies for cancer treatment
Patent: US 5993813-A 39 30-NOV-1999;
Location/Qualifiers
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100.0%; Pred. No. 6e+02;
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Sequence 39 from patent US 5993813.
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AR089052.1 GI:10015809
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PAT 06-FEB-1997

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                                                                                         Sequence 64 from Patent W00200691.
AX359760
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AR187060.1 GI:20233025
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   3 GAGGAGACTGTGAG 16
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Best Local Similarity 100.
Matches 14; Conservative
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Matches 14; Conserva
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Mezes, P.S., Gourlie, B., Rixon, M.W. and Anderson, W.H.K.
Probing method for identifying antibodies specific for selected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unclassified.

1 (bases 1 to 16)
Mezes, P.S., Gourlie, B., Rixon, M.W. and Anderson, W.H.K.
Probing method for identifying antibodies specific for selected
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1 (bases 1 to 16)
Gryaznov, S.M.
Convergent synthesis of branched and multiply connected
maczomomolecular structures
Patent: US 5571677-A 6 05-NOV-1996;
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0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels
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Location/Qualifiers
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Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 23 from patent US 6641999.
AR428275.1 GI:40187730
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Sequence 39 from patent US 6641999.
AR428288.1 GI:40187743
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/organism="unknown"
/mol_type="genomic DNA"
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/organism="unknown"
/mol_type="genomic DNA"
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AR428275
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PAT 13-FEB-2002
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6346398-A 2548 12-FEB-2002;
Location/Qualifiers
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100.0%; Pred. No. 6.4e+02;
tive 0; Mismatches 0; Indels
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Sequence 2553 from patent US 6346398.
AR187065
AR187065.1 GI:20233030
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Sequence 2548 from patent US 6346398.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Randi, A.M.
Method and reagent for the inhibition of erg
Patent: WO 0188124-A 838 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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100.0%; Pred. No. 6.4e+02;
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Patent: EP 1239051-A 1502 11-SEP-2002;
Aeomica, Inc. (US)
Location/Qualifiers
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/mol_type="unassigned RNA"
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Sequence 838 from Patent WO0188124.
AX422502
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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KEYWORDS
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AX531997/c
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AX531993/c
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Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Batco, P., McSwiggent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6566127-A 1072 20-MAY-2003;
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1 (Dases 1 to 17)

Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.

Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.

Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 656127-A 1077 20-MAY-2003;

Location/Qualifiers
                                                     1 (bases 1 to 17)
Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6346398-A 2553 12-FEB-2002;
Location/Qualifiers
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0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 6.4e+02;
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100.0%; Pred. No. 6.4e+02;
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/mol_type="unassigned RNA"
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/mol_type="unassigned RNA"
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AR323675.1 GI:33709483
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                                   Unclassified.
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Best Local Similarity
Matches 14; Conserv
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Best Local Similarity
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RESULT 807 AR323670/c LOCUS DEFINITION

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RESULT 808

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Medicines
Patent: WO 03025176-A 2303 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
1. .17
/organism="Mus musculus"
/mol type="unassigned DNA"
/db_xref="taxon:10090"
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0.8%; Score 14; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 14; Conservative 0; Mismatches 0;
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Sequence 5789 from Patent WO03025176.
AX728102
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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    .17
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/mol_type="unassigned DNA"
    /db_xref="taxon:10090"

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Mus musculus
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AX728167.1 GI:30507510
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AX728102/c
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shannon,M., Gu,Y. and Nguyen,C.T.
Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels
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Aeomica, Inc. (US)
Location/Qualifiers
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Patent: EP 1239051-A 1506 11-SEP-2002;
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Seguence 2303 from Patent WO03025176.
AX724616
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Sequence 5261 from Patent EP1281758.
AX692529
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Sequence 1506 from Patent EP1239051.
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Location/Qualifiers
                                  AX531997.1 GI:25255760
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                                                                Homo sapiens (human)
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Homo sapiens
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AX692529/c
LOCUS
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DEFINITION
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
Patent: WO 03025176-A 5854 27-MAR-2003;
Molecular Engines Laboratories (FR)
1. 17
Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as
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PAT 25-JUN-2003

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BD198714 17-JUL-2003 Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response.
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PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
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DP 2002509721-A/1740
02-APR-2002
24-MAR-1999 JP 2000541291
27-MAR-1998 US 60/079678
PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 17)

1 (bases 1 to 17)

Pavco, P.A., Roberts, B., Jarvis, T., Coeshott, C. and Mcswiggen, J.A. Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response

Patent: JP 2002509721-A 1740 02-APR-2002;

RIBOZYME PHARMACEUTICALS, INC
                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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CI2N15/09, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61P17/06,
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Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
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Key Location/Qualifiers
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Patent: WO 03040369-A 5791 15-MAY-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
                                                                                                                                                      AX762470 17 bp DNA
Sequence 5791 from Patent WO03040369.
AX762470 GI:32257086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="unassigned DNA" /db_xref="taxon:9606"
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JP 2002509721-A/1740.
Homo sapiens (human)
Homo sapiens
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                    620 CAGCCTCTTACACT 633
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                                         4 CAGCCTCTTACACT 17
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
Patent: WO 03025177-A 5244 27-WAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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100.0%; Pred. No. 6.4e+02;
ative 0; Mismatches 0; Indels
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vative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 14; Conservative 0; Mismatches 0;
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Sequence 3226 from Patent W003040369.
AX759905
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Molecular Engines Laboratories (FR)
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DP 2001321190-A/375
20-W0V-2001 JP 2001068285
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CI2NIS/09,C12NIS/09,C12MI/00,C12Q1/68,G01N33/53,G01N33/566, PC
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A method of arraying genome clone

Patent: JP 2001321190-A 375 20-NOV-2001;

THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
GENOTECHS
OS Artificial Sequence
PN JP 2001321190-A/375
PP 12-NNV-2001
                                                                                                                                                                                                                                                                                                Lieber, C.M., Woolley, A.T., Hahm, J.I. and Housman, D.
Direct haplotyping using carbon nanotube probes
Patent: WO 0222899-A 5 21-MAR-2002;
PRESIDENT AND FELLOWS OF HARVARD COLLEGE (US); Massachusetts
Institute Of Technology (US)
Location/Qualifiers
1. 18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="traxon:32630"
/note="Synthetic PNA label"
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/organism='Artificial Sequence'.
Location/Qualifiers
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                                                                                                                                      Sequence 5 from Patent W00222889.
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                  1122 CGTGGAGAGGAGGG 1135
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artificial sequences.
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/note="Lys"
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                                            15 CGTGGAGAGGAGGG
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AX685128/c
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BD088131
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                  'organism='Homo sapiens (human)'.
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Patent: WO 0129265-A 1726 26-APR-2001;
Orchid BioSciences, Inc. (US)
Location/Qualifiers
                                                                                                                                          Length 17;
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| xref="taxon:32630"
|noTe="Hybridization Tag"
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Sequence 1726 from Patent W00129262.
AX116603
AX116603.1 GI:14033545
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AX661797/c
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BD241460 17 bp DNA linear PAT 17-JUL-2003 Methods and products related to genotyping and DNA analysis.
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JP 2002525127-A/407

D 13-AUG-2002

F 24-SEP-1999 JP 2000572407

F 25-SEP-1999 US 60/101757

JOHN E LANDERS, BARBARA JORDAN, DAVID E HOUSMAN, ALAIN CHAREST PC

C12N15/09,C12Q1/68,G01N33/53,G01N33/566,G01N33/58,G01N37/00, PC
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Methods and products related to genotyping and DNA analysis FH
Wethods Location/Qualifiers
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Landers, J.E., Jordan, B., Housman, D.E. and Charest, A.
Methods and products related to genotyping and DNA analysis Patent: JP 200525127-A, 407 13-AUG-2002;
MASSACHUSETTS INSTITUTE OF TECHNOLOGY
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    1. 17
/organism='Homo sapiens (human)'.

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88.2%; Pred. No. 6.8e+02;
tive 0; Mismatches 2; Indels
                                                            0.8*; Score 13.8; DB 1; Length 17;
18.2*; Pred. No. 6.8e+02;
ve 0; Mismatches 2; Indels
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/organism="unknown"
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JP 2002525127-A/407.
Homo sapiens (human)
Homo sapiens
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JP 2002525127-A/409.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity 88.2%;
Matches 15; Conservative
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Best Local Similarity 88.2%
Matches 15; Conservative
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Synthetic construct DNA, forward primer for human STS sts-D29643 at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen, Y. Z., Hayashi, Y., Wu, J. G., Takaoka, E., Maekawa, K., Watanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H., Morohashi, A., Ohira, M., Nakagawara, A., Liu, S., Hoshi, M., Horii, A. and Soeda, E.

A BAC-based STS-content map spanning a 35-Mb region of human chromosome 1p35-p36
Genomics 74 (1), 55-70 (2001)
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Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.
C-myb ribozymes having 2'-5'-linked adenylate residues
Patent: US 5817796-A 196 06-OCT-1998;
Location/Qualifiers
               Query Match 0.8%; Score 14; DB 1; Length 18; Best Local Similarity 100.0%; Pred. No. 6.8e+02; Matches 14; Conservative 0; Mismatches 0; Indels
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    18 / Organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
    18 / 18

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Sequence 196 from patent US 5817796.
AR045403
AR045403.1 GI:5966868
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synthetic construct
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                                                                                                    383 TCCAGCACACGCAG 396
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"He (bases 1 to 17)

Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.

Regulation of repressor genes using nucleic acid molecules
Regulation of repressor genes using nucleic acid molecules

Regulation of repressor genes using nucleic acid molecules

Regulation of repressor genes using nucleic acid molecules

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(C12N5/00,C12R1:91)
Regulation of repressor genes using nucleic acid molecules
Location/Qualifiers
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PN JP 2002541795-A/2540
PN JP 2002541795-A/2540
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN SCI2N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC C12P21/02,
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BD254747
UP 2002541795-A/2540.
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Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Begulation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 2540 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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Regulation of repressor genes using nucleic acid molecules.
BD255543
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88.2%; Pred. No. 6.8e+02;
iive 0; Mismatches 2; Indels
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Location/Qualifiers

    .17
    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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JP 2002541795-A/3336.
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Best Local Similarity 88.2'
Matches 15; Conservative
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PN JP 2002525127-A/409
PD 13-AUG-2002
PF 24-SEP-1999 JD 2000572407
PR 25-SEP-1999 US 60/101757
PI JOHN E LANDERS, BARBARA JORDAN, DAVID E HOUSMAN, ALAIN CHAREST PC CLINIS/09, CL2Q1/68, G01N33/53, G01N33/566, G01N33/59, PC
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CIZNIS/00
Methods and products related to genotyping and DNA analysis FH
Location/Qualifiers
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(C12NS/00,C12R1:91)
Regulation of repressor genes using nucleic acid molecules FH
Location/Qualifiers
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PN JP 2002541795-A/2196
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PF 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MCHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC C12P21/02,
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C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
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1 (bases 1 to 17)
AUTHORS Blatt, ... Zaick, M., Pavco, P. and Mcswiggen, J.
FILLE Regulation of repressor genes using nucleic acid molecules OURNAL PARAMACEUTICALS INC
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Regulation of repressor genes using nucleic acid molecules.
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Location/Qualifiers
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/organism="unidentified"
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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PC C12N1
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                                   BDS27671 17-JUL-2003 Regulation of repressor genes using nucleic acid molecules.
BD257671
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CC (CI2NS/00,CI2R1:91)

CC Regulation of repressor genes using nucleic acid molecules
                                                                                                                                                                                                                                                                                                                                                                                                                           OS Eukaryote
PN JP 2002541795-A/5464
PN JP 2002541795-A/5464
PD 10-DEC-2002
PP 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN | CLEAR COMPAND CO
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DN JP 200254195-A/6372
PN JP 200254195-A/6372
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWENCE BLATT,MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN |
CLEANES, 09, A61K38/00, A61K48/00, A61P43/00, CL2N5/10, PC
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Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Regulation of repressor genes using nucleic acid molecules
Patent: JP 2002341755-A 5464 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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1 (bases 1 to 17)

Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Regulation of repressor genes using nucleic acid molecules Patent: JP 2002541795-A 6372 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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/mol_type="genomic DNA"
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JP 2002541795-A/5464.
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JP 2002541795-A/6372.
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(C12N5/00,C12R1:91)
Regulation of repressor genes using nucleic acid molecules FH
Location/Qualifiers
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C12P21/02, C12P21/02//A61K31/711, (C12N5/10,C12R1:91), (C12P21/02, PC
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PN JP 2002541795-A/3373
PD 10-DEC-2002
PF 11-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN ICTANTS/09, A61K38/00, A61K48/00, A61P43/00, A61D8/10, PC
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Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Blatt, L., 2 2015K, M., Pavco, P. and Mcswiggen, J.
Pegulation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 3373 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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/db_xref="taxon:32644"

    .17
    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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(C12N5/00, C12R1:91)
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(C12N5/00,C12R1:91)
Regulation of repressor genes using nucleic acid molecules FH
Location/Qualifiers
                                                        Regulation of repressor genes using nucleic acid molecules FH Location/Qualifiers
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PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PP 1AMRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC CI2NS/509, AGIK38/00, AGIK48/00, AGIP43/00, CI2NS/10, PC CI2NS/10,
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            (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,A61K37/02,(C12N5/00,C12R1:91)
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Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
gequlation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 6373 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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Regulation of repressor genes using nucleic acid molecules.
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                                                                                                      'organism='Eukaryote'
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                                                                                                                    Location/Qualifiers
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JP 2002541795-A/6373.
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Artificial Sequence
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PD 10-DEC-2002
PP 14-APR-2000 JP 2000511726
PR 14-APR-2000 JP 2000611726
PR 14-APR-1999 US 09/291902,13-APR-2000 US 09/548449 PI JAMES NORIS, GARY CLAWSON, CAROLINE WESTWATER, DAVID SCHOFIELD, PI MICHAEL SCHMIDT, BRIAN HOBEL, JOSEPH DOLAN, WEI HUA PAN PC C12N15/09, A61K35/74, A61K35/76, A61K38/00, A61K48/00, A61P31/04, PC CC Dromoter
FH Key Location/Artificial Location/Artificial Location/Artificial Source
FT Source
BD272764 17-JUL-2003
Tissue-specific and pathogen-specific toxic agents and ribozymes.
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                                                                                                                                             artificial sequences.

1 (bases 1 to 17)

Norris,J. Clawson,G., Westwater,C., Schofield,D., Schmidt,M.,
Hoel,B., Dolan,J. and Pan,W.H.

Tissue-specific and pathogen-specific toxic agents and ribozymes
Patent: JP 2002541822-A 13 10-DEC-2002;

MUSC FOUNDATION FOR RESEARCH DEVELOPMENT, THE PENN STATE RESEACH
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Stinchcomb.D.T., Draper,K., McSwiggen,J. and Jarvis,T.
C-myb targeted ribozymes
Patent: 18 5646042-A 196 08-JUL-1997;
Location/Qualifiers
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88.2%; Pred. No. 6.8e+02;
ive 0; Mismatches 2; Indels
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    .17
    /organism="synthetic construct"
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|db_xref="taxon:32630"

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Sequence 196 from patent US 5646042.
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/organism="unknown"
/mol_type="unassigned DNA"
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PAT 20-APR-2002

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Unclassified.

1 (bases 1 to 17)

1 (bases 1 to 17)

2 (bases 1 to 17)

Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6146398-A 7818 12-PEB-2002;

Location/Qualifiers
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Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
Rethod and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6346398-A 7819 12-FEB-2002;
Location/Qualifiers
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18.2%; Pred. No. 6.8e+02;
ve 0; Mismatches 2; Indels
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Sequence 7818 from patent US 6346398.
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Sequence 7819 from patent US 6346398.

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AR192332/c
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                                                                                                                          Unclassified.

1 (bases 1 to 17)

1 (bases 1 to 17)

2 Agroo, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.

Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor

Patent: US 6346398-A 2130 12-FEB-2002;

Location/Qualifiers
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Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6346398-A 2554 12-PEB-2002;
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Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6346598-A 2555 12-FEB-2002;
Location/Qualifiers
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               AK186642 17 bp DNA Sequence 2130 from patent US 6346398.
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US 6346398.
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                                                                                                                                                                                                                                                                /organism="unknown"
/mol_type="unassigned DNA"
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AR187067.1 GI:20233032
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AR186642.1 GI:20232607
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Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P.Ann.Owens.,
Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
Nucleic acid encoding delta-9 desaturase
Patent: US 6350934-A 881 26-FEB-2002;
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Tyagi,S., Kramer,F.R. and Vartikian,R.

High specificity primers, amplification methods and kits

Patent: US 6365729-A 3 02-APR-2002;
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Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2;
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88.2%; Pred. No. 6.8e+02;
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Sequence 881 from patent US 6350934.
AR196416
       /organism="unknown"
/mol_type="unassigned DNA"
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AR262702/c
AR262702
DEFINITION Sequence 3 from patent US 6331140.
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AR204408/c
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                                                                                                                         Unclassified.

1 (bases 1 to 17)

Pavov. P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.

Rethod and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6346398-A 7820 12-FEB-2002;

Location/Qualifiers
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Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6346598-A 7821 12-FEB-2002;
Location/Qualifiers
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Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6346398-A 7823 12-FEB-2002;
Location/Qualifiers
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88.2%; Pred. No. 6.8e+02;
tive 0; Mismatches 2; Indels
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Sequence 7820 from patent US 6346398.
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Sequence 7823 from patent US 6346398.
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Best Local Similarity 88.2
Matches 15; Conservative
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AR323676/c
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AR323677/c
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                                                                              1 (bases 1 to 17)
Mollet, B., Germond, J.E. and Lapierre, L.
Mobile genetic elements as tools for genetic modification of
delbrueckii or L. helveticus
Patent: US 6331140-A 3 18-DEC-2001;
Location/Qualifiers
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88.2%; Pred. No. 6.8e+02;
ative 0; Mismatches 2; Indels
                                                                                                                                                                                                                  0.8%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 6.8e+02;
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Beigelman, L., Burgin, A., Beaudry, A., Karpeisky, A., Matulic-Adamic, J., Sweedler, D. and Zinnen, S. Synthetic ribonucleic acids with RNAse activity Patent: US 6528640-A 467 04-MAR-2003;
Location/Qualifiers
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Beigelman, L., Burgin, A., Beaudry, A., Karpeisky, A., Matulic-Adamic, J., Sweedler, D. and Zinnen, S. Synthetic ribonucleic acids with RNAse activity Patent: US 6528640-A 564 04-MAR-2003;
Location/Qualifiers
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AR286095
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AR286192
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/wol_type="unassigned RNA"
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/mol_type="genomic DNA"
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  AR262702
AR262702.1 GI:28074345
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Best Local Similarity 88.2
Matches 15; Conservative
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Best Local Similarity 88.2
Matches 15, Conservative
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Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
Pavco,P., McSwiggent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6566127-A 675 20-MAY-2003;
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Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Pavco, P., McSwiggent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6566127-A 1078 20-MAY-2003;
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88.2%; Pred. No. 6.8e+02;
tive 0; Mismatches 2; Indels
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Query Match 0.8%; Score 13.8; DB 1; Best Local Similarity 88.2%; Pred. No. 6.8e+02; Matches 15; Conservative 0; Mismatches 2;
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Sequence 1079 from patent US 6566127.
AR323677
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Sequence 675 from patent US 6566127.
AR323273.1 GI:33709081
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Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 656127-A 8604 20-MAY-2003;
Location/Qualifiers
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Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 3605 20-MAY-2003;
Location/Qualifiers
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88.2%; Pred. No. 6.8e+02;
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38.2%; Pred. No. 6.8e+02;
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Sequence 3607 from patent US 6566127.
AR326205
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/mol_type="unassigned RNA"
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/organism="unknown"
/mol_type="unassigned RNA"
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                                                                                   1 (bases 1 to 17)
Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 656127-A 1079 20-MAY-2003;
Location/Qualifiers
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1 (bases 1 to 17)

Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.

Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6566127-A 3602 20-MAY-2003;
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Unclassified.

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1 (bases 1 to 17)

2 Acco.p., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.

Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6566127-A 3603 20-MAY-2003;

Location/Qualifiers
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88.2%; Pred. No. 6.8e+02;
tive 0; Mismatches 2; Indels
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Sequence 3602 from patent US 6566127.
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/mol_type="unassigned RNA"
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/organism="unknown"
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 GI:33709485
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AR326200.1 GI:33712008
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1 (bases 1 to 17)

Bicgelman, L., Burgin, A.B., Beaudry, A., Karpeisky, A., Matulic-Adamic, J., Sweedler, D. and Zinnen, S. Oligoribonucleotides with enzymatic activity Patent: 18, 6617418-A 563 09-55P-2003;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                           0.8%; Score 13.8; DB 1; Length 17;
88.2%; Pred. No. 6.8e+02;
tive 0; Mismatches 2; Indels
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88.2%; Pred. No. 6.8e+02;
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1 (bases 1 to 17)

Gu,Y. and Shannon,M.E.

1soforms of human pregnancy-associated protein-E

Patent: US 6656700-A 484 02-DEC-2003;

Location/Qualifiers
Pred. No. 6.8e+02;
0; Mismatches 2
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Sequence 563 from patent US 6617438.
AR398182
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Sequence 484 from patent US 6656700.
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/mol_type="unassigned RNA"
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Sequence 68 from Patent WO0063441.
AX039679
AX039679.1 GI:1122970R
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/wol_type="genomic DNA"
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                                                          1 (bases 1 to 17)
Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J. Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6566127-A 3607 20-MAY-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases I to 17)
Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 5015 20-MAY-2003;
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88.2%; Pred. No. 6.8e+02;
ative 0; Mismatches 2; Indels
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1 (bases 1 to 17)

Beigelman, L., Burgin, A.B., Beaudry, A., Karpeisky, A., Matulic-Adamic, J., Sweedler, D. and Zinnen, S.
Oligoribonucleotides with enzymatic activity
Patent: US 6617438-A 466 09-SEP-2003;
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88.2%; Pred. No. 6.8e+02;
ative 0; Mismatches 2;
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Sequence 5015 from patent US 6566127.
AR327613
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Seguence 466 from patent US 6617438.
AR398085
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/organism="unknown"
/mol_type="unassigned RNA"
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/organism="unknown"
/mol_type="unassigned RNA"
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Best Local Similarity 88.2
Matches 15; Conservative
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Best Local Similarity 88.2
Matches 15; Conservative
                                             Unclassified.
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AR398085
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McSwiggen, James (US); Chowrira, Bharat M. Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="teaxon:32630"
/note="Nucleic Acid"
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Best Local Similarity 88.2
Matches 15; Conservative
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Matches 15; Conservative
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AX216916
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                                           Herrnstadt, C. and Davis, R.E. Single nucleotide polymorphisms in mitochondrial genes that segreg stee with alzheimer's disease Patent: WO 0063441-A 68 26-OCT-2000; MITOKOR (US)
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 153103-A 1375 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
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Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0159103-A 2357 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
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38.2%; Pred. No. 6.8e+02;
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88.2%; Pred. No. 6.8e+02;
tive 0; Mismatches 2;
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/organism="synthetic construct"
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/db_xref="teaxon:32630"
/note="Nucleic Acid"
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/note="PCR primer"
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Sequence 1375 from Patent WO0159103.
AX215933.1 GI:15525976
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Sequence 2357 from Patent WO0159103.
AX216915.
AX216915.1 GI:15526976
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Matches 15; Conservative
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AX215933/c
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0159103-A 2358 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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88.2%; Pred. No. 6.8e+02;
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88.2%; Pred. No. 6.8e+02;
tive 0; Mismatches 2; Indels
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/note="Nucleic Acid"
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PAT 29-0CT-2001
                                                                                                                                                                           Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                  Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Hamblin, P.A. and Ellis, J.H.
Method and reagent for the inhibition of grid
Patent: WO 0162911-A 275 30-AUG-2001;
RIBOZYWE PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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Method and reagent for the inhibition of grid
Patent: WO 0162911-A 276 30-AUG-2001;
RIBOZYME PHRAMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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88.2%; Pred. No. 6.8e+02;
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88.2%; Pred. No. 6.8e+02;
tive 0; Mismatches 2; Indels
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Sequence 276 from Patent WO0162911.
AX272707
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Sequence 373 from Patent WO0162911.
AX272804
AX272804.1 GI:16545541
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Seguence 275 from Patent WO0162911.
AX272706
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Matches 15; Conservative
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Best Local Similarity 88.2
Matches 15; Conservative
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0159103-A 3744 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
                                          Gaps
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Query Match 0.8%; Score 13.8; DB 1; Length 17; Best Local Similarity 88.2%; Pred. No. 6.8e+02; Matches 15; Conservative 0; Mismatches 2; Indels
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88.2%; Pred. No. 6.8e+02;
trive 0; Mismatches 2; Indels
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/organism="synthetic construct"
/mol type="unassigned RNA"
/db_xref="taxon:32630"
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Sequence 3744 from Patent WO0159103.
AX218302

    .17
    /organism="Homo sapiens"
    /mol_type="unassigned RNA"
    /db_xref="taxon:9606"

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Sequence 92 from Patent WO0162911.
AX272523
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                                  1. .17
/organism="Rattus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:10118"
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/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"
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/mol_type="unassigned RNA"
/db_xref="taxon:9606"
 Roche Vitamins AG (CH)
Location/Qualifiers
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AX422503
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AX422924
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Hamblin, P.A. and Ellis, J.H.
Method and reagent for the inhibition of grid
Patent: WO 0162911-A 373 30-AUG-2001;
RIBOZYME PHARMACHITCALS, INC. (US); GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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Method and reagent for the inhibition of grid
Patent: WO 0162911-A 521 30-AUG-2001;
PROZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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Use of phytanic acid for the treatment of diabetes
Patent: EP 1177789-A 31 06-FEB-2002;
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/mol_type="unassigned RNA"
/db_xref="taxon:9606"
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Seguence 521 from Patent WO0162911.
AX272952
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/mol_type="unassigned RNA"
/db_xref="taxon:9606"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method and reagent for the inhibition of erg
Patent: WO 0188124-A 1260 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
Location/Qualifiers
                                                                       Gaps
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Query Match 0.8%; Score 13.8; DB 1; Length 17; Best Local Similarity 88.2%; Pred. No. 6.8e+02; Matches 15; Conservative 0; Mismatches 2; Indels
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Human udp-galnac:polypeptide n-acetylgalatosaminyltransferase 10
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88.2%; Pred. No. 6.8e+02;
tive 0; Mismatches 2; Indels
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Patent: EP 1239051-A 1507 11-SEP-2002;
Aeomica, Inc. (US)
Location/Qualifiers
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Sequence 228 from Patent EP1243660.
AX544715

    17 .17
/organism="Homo sapiens"
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Sequence 647 from Patent EP1229046.
AX499340
                                    AX499340.1 GI:23381633
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Rendi, A.M.
Method and reagent for the inhibition of erg
Patent: WO 0188124-A 1517 22-NOV-2001;
RIBOZYME PHARMACHITCALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
      2; Indels
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Patent: EP 1229046-A 384 07-AUG-2002;
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Sequence 1517 from Patent WO0188124.
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Sequence 384 from Patent EP1229046.
AX499077
      Mismatches

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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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AX423181.1 GI:21526563
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AX499340/c
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AX423181
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Human udp-galnac:polypeptide n-acetylgalatosaminyltransferase 10
Patent: EP 1243660-A 257 25-SEP-2002;
Aeomica, Inc. (US)
Location/Qualifiers
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88.2%; Pred. No. 6.8e+02;
tive 0; Mismatches 2; Indels
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Sequence 1079 from Patent EP1281758.
AX688347
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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DEFINITION Sequence 62 from Patent WO03010335.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human udp-galnac:polypeptide n-acetylgalatosaminyltransferase 10
Patent: EP 1243660-A 229 25-SEP-2002;
Aeomica, Inc. (US)
Location/Qualifiers
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Human udp-galnac:polypeptide n-acetylgalatosaminyltransferase 10
Patent: EP 1243660-A 230 25-SEP-2002;
Aeomica, Inc. (US)
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88.2%; Pred. No. 6.8e+02;
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Patent: EP 1243660-A 228 25-SEP-2002;
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Sequence 229 from Patent EP1243660.
AXS44716.1 GI:25809927

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    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Sequence 230 from Patent EP1243660.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                   Aeomica, Inc. (US)
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Thrhes 15, Conservative
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                             Mirel, D.B., Erlich, H.A., Bugawan, T.L., Noble, J.A. and Valdez, A.M. 11-4 receptor sequence variation associated with type 1 diabetes Patent: Wo 03010318-A 62 06-FEB-2003; Roche Diagnostics GmbH (DE); F. HOFFMANN-LA ROCHE AG (CH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Telerman, A., Amson, R. and Tuijnder, M. Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as
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                                                                                                                                                                                                             /organism="synthetic construct"
/mol type="unassigned DNA"
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Sequence 5387 from Patent WO03025176.
AX727700
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 AX698573.1 GI:29499401
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
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Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
Patent: WO 03023177-A 2966 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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Patent: WO 03050284-A 2412 19-UNN-2003;
Amersham Biosciences (SV) Corp. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                       0.8%; Score 13.8; DB 1;
88.2%; Pred. No. 6.8e+02;
rative 0; Mismatches 2;
                                                                                   Patent: WO 03025175-A 2478 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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AX784081
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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El (bases 1 to 17)

Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response

L Patent: JP 2002509721-A 2033 02-APR-2002;

RIBOZYME PHARMACEUTCALS INC
OS Homo sapiens (human)
PN 2002509721-A/2033
PD 02-APR-2002
PP 24-MAR-1999 UP 2000541291
PR 24-MAR-1999 UP 2000541291
PR 27-MAR-1999 US 60/079678
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PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
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PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
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BD200582.1 G1:33010352
UP 2002509721-A/3608.
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Location/Qualifiers
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88.2%; Pred. No. 6.8e+02;
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88.2%; Pred. No. 6.8e+02;
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    .17
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                       organism="Rattus sp."
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JP 2002509721-A/2033.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity 85.6.
The 15; Conservative
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Best Local Similarity 88.2
Matches 15; Conservative
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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PN JP 2002104964-A/31
PD 10-APR-2002
PF 01-AUG-2001 JP 2001233070
PR 04-AUG-2000 EP 00116848.3
PI BEAT FLUEHWANN, MANUEL HELM, WILLI HUNZIKER, PETER WEBER PC
AG1X31/20, A23L1/30, A61X31/16, A61X31/201, A61X31/215, A61P3/00, PC
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88.2%; Pred. No. 6.8e+02;
ative 0; Mismatches 2; Indels
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88.2%; Pred. No. 6.8e+02;
tive 0; Mismatches 2; Indels
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Use of phytanic acid for the treatment of diabetes
Patent: JP 2002104964-A 31 10-APR-2002;
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                                                                          2; Indels
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Patent: WO 03040024-A 2 15-MAY-2003;
Bayer Aktiengesellschaft (DE)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/noTe="primer"
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Key Location/Qualifiers
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Sequence 2 from Patent WO03040024.
AX787049
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JP 2002104964-A/31
10-APR-2002
01-AUG-2001 JP 2001233070
04-AUG-2000 EP 00116848.3
/db_xref="taxon:9606"
                                                                                                                 1185 CTCCCAGCCCATCCTGG 1201
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Rattus sp.
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Best Local Similarity 88.2
Matches 15; Conservative
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PAT 16-MAY-1994
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Method for the production of stable cell lines from transgenic
animals for the production of specific proteins; tumour cell lines
and proteins obtained
Patent: EP 0298807-A 12 11-JAN-1989;
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/organism='Homo sapiens (human)'.
Location/Qualifiers
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ve 0; Mismatches 2; Indels
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Method and reagent for treating diseases concerning molecule participating in vasculogenic response
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88.2%; Pred. No. 7.2e+02;
Artive 0; Mismatches 2;
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Patent: WO 9728186-A 29 07-AUG-1997; SANOFI SA (FR)
Other publication AU 1727597 19970822 Other publication FR 2744455 19970808.
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Sequence 29 from Patent WO9728186.
A64610

    .17
    /organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"

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15; Conservative
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A14818.1 GI:513808
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                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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S Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J.A.

Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response

L Patent: JP 2002509721-A 3608 02-APR-2002;

RIBOXYME PHARMACEUTCALS INC
OS Homo sapiens (human)

PN JP 2002509721-A/3608

PD 02-APR-2002

PP 24-MAR-1999 JP 2000541291

PR 27-MAR-1999 UP 2000541291

PR 27-MAR-1999 UP 2000541291

PR 37-MAR-1998 US 60/079678

PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT, PI JAMES A MCSWIGGEN
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PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
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27-WAR-1998 US 60/079678
PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
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27-MAR-1998 US 60/079679
PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
JAMES A MCSWIGGEN
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C12N15/09, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61P17/06, PC
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Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J.A. Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response Pattent: JP 2002509721-A 3609 02-APR-2002; RIBOZYME PHARMACEUTICALS INC
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Location/Qualifiers
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88.2%; Pred. No. 6.8e+02;
tive 0; Mismatches 2; Indels
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    .17
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JP 2002509721-A/3609
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JP 2002509721-A/3609.
Homo sapiens (human)
Homo sapiens
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Homo sapiens (human)
Homo sapiens
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PC C12N9/50,C12P21/02,C12Q1/68,G01N33/15,G01N33/50//A61K31/00, PC
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A61K37/64
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JP 2001046065-A/21.
Synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 18)
Traurucka,N., Yamashiro,K., Mitsui,S. and Yamaguchi,N.
Patent: JP 2001046065-A 21 20-FEB-2001;
                                                                                                                                                                                                                             Query Match 0.8%; Score 13.8; DB 1; Length 18; Best Local Similarity 88.2%; Pred. No. 7.2e+02; Matches 15; Conservative 0; Mismatches 2; Indels
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                                                                                                 and O'Malley, B.W.
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    .18
    ^organism="synthetic construct"
|mol_type="genomic DNA"
|db_xref="taxon:32630"

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Cowsert,L.M., Bennett,C.Frank. and O'M
Antisense modulation of SRA expression
Patent: US 6107092-A 92 22-AUG-2000,
                                                                                                                                                                 1. .18
/organism="unknown"
/mol_type="unassigned DNA"
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JP 2001046065-A/21
20-FEB-2001
03-AUG-1999 JP 1999220522
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 AR106931.1 GI:12821461
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88.2%; Pred. No. 7.2e+02;
tive 0; Mismatches 2; Indels
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Chatterjee,M., Poon,K.A. and Chatterjee,S.K.
Monoclonal antibody 1A7 and related polypeptides
Patent: US 5977316-A 52 02-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 18)
Cowsert,L.M., Bennett,C.Frank. and O'Malley,B.W.
Antisense modulation of SRA expression
Patent: US 6107092-A 13 22-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.8%; Score 13.8; DB 1;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
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AR106852
AR106852.1 GI:12821382
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Sequence 52 from patent US 5977316.
AR083836
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/mol_type="unassigned DNA"

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    /organism="unknown"
    /mol_type="unassigned DNA"

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Sequence 92 from patent US 6107092.
AR106931
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AR106852
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AR083836/c
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AR106931
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PAT 25-SEP-2002

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(bases 1 to 18)
Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6346389-A 8372 12-FEB-2002;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.8%; Score 13.8; DB 1; Length 18; Best Local Similarity 88.2%; Pred. No. 7.2e+02; Matches 15; Conservative 0; Mismatches 2; Indels
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1 (bases 1 to 18)
Pilarski,L.M., Belch,A.R. and Szczepek,A.J.
Methode for detection of rearranged DNA
Patent: US 6416948-A 48 09-JUL-2002;
Location/Qualifiers
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88.2%; Pred. No. 7.2e+02;
tive 0; Mismatches 2;
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     Sequence 8372 from patent US 6346398.
AR192884
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Sequence 40 from patent US 6416948.
AR217329.1 GI:23317010
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/mol_type="unassigned DNA"
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Patent: US 6350580-A 2 26-FEB-2002;
Location/Qualifiers
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/mol_type="unassigned DNA"
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Sequence 2 from patent US 6350580.
AR195017

    .18
    /organism="unknown"
    /mol_type="genomic DNA"

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                                                               AR192884.1 GI:20238849
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AR217329
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                                                                                                 Synthetic construct
Synthetic construct
artificial sequences.
E 1 (bases 1 to 18)
S Tatsuo, H., Kazuyuki, O. and Yutaka, S.
Improved production of isoprenoid
I Patent: J 2000050884-A 25 22-FEB-2000;
F HOFFMANN LA ROCHE AG
OS Artificial Sequence
PN JP 2000050884-A/25
PD 22-FEB-2000
PF 06-MAY-1999 JP 1999126015
PR 1 FATSUO HOSHINO, KAZUYUKI OJIMA, YUTAKA SETOGUCHI PC C12NA15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N5/00
CC C12N5/00
CC LOSNS/00
PC 012N5/00
PC 01
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88.2%; Pred. No. 7.2e+02;
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    18
    <sup>1</sup>/<sub>2</sub> organism="synthetic construct"
| mol_type="genomic DNA"
| db_xref="taxon:32630"

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Sequence 9 from patent US 5712098.
182163.1 GI:3210460
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Improved production of isoprenoid.
E51022
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/organism="unknown"
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                                                             ES1022.1 GI:13023244 JP 2000050884-A/25.
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AR349888
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1 (bases 1 to 18)
Chatterjee, M., Foon, K.A. and Chatterjee, S.K.
Chatterjee, M., Foon, K.A. and chatterjee, S.K.
Smonoclonal antibody 1A7 and use for the treatment of melanoma and small cell carcinoma
Patent: US 6509016-A 52 21-UAN-2003;
Location/Qualifiers
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          0.8%; Score 13.8; DB 1; Length 18; 88.2%; Pred. No. 7.2e+02; ive 0; Mismatches 2; Indels
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Steele,C.L., Bohlmann,J. and Croteau,R.B.
Monoterpene synthases from grand fir (Abies grandis)
Patent: US 6429014-A 60 06-AUG-2002;
Location/Qualifiers
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Sequence 60 from patent US 6429014.
AR222132. GI:23329506
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AR275355
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/mol_type="genomic DNA"
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/organism="unknown"
/mol_type="genomic DNA"
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1 (bases I to 18)
Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Mathod and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 656127-A 4028 20-MAY-2003;
Location/Qualifiers
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88.2%; Pred. No. 7.2e+02;
tive 0; Mismatches 2; Indels
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88.2%; Pred. No. 7.2e+02;
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1 (bases 1 to 18)
Hoshino,T., Ojima,K. and Setoguchi,Y.
Isoprenoid production
Patent: US 6586202-A 30 01-JUL-2003;
Location/Qualifiers
                                                                                                                                                                         /mol_type="unassigned RNA"
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Sequence 30 from patent US 6586202.
AR349888
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Patent: US 6589743-A 2 08-JUL-2003;
Location/Qualifiers
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AR352433
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/organism="unknown"
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PAT 23-MAR-2002
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Metastasis genes and uses thereof
Patent: WO 0141815-A 2 14-JUN-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); MASSACHUSETTS
INSTITUTE OF TECHNOLOGY (US); Dana-Farber Cancer Institute Inc. (US)
                                                                                                Sorge, J.A.
Methods for detection of a target nucleic acid sequence
Patent: WO 013922-A 2 10-MAY-2001;
STRATAGENE (US)
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/note="FEN nuclease cleavage product"
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/note="Primer"
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Sequence 22 from Patent EP1184468.
AX391641
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Sequence 2 from Patent WO0141815.
AX172296
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Dna sequences encoding enzymes involved in production of
isoprenoids
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0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
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/note="primer"
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HOFFMANN LA ROCHE (CH)
Location/Qualifiers
 0; Mismatches
                                                                                                                                                                                                                                                                                                                                           Patent: US 5182262-A 6 26-JAN-1993;
Location/Qualifiers
                                                                                                                                         Sequence 6 from patent US 5182262. AR362789
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20guence 30 from Patent EP0955363.
AX012429 AX012429.1 GI:9998468
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Sequence 2 from Patent WO0132922.
AX135661
                                                                                                                                                                                                                                                                                                                                                                                              /organism="unknown"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1156 GTGGCCACCCTGGAGAA 1172
                                 1736 AAAAAAAAAAAAAA 1752
                                                                                                                                                                                             AR362789.1 GI:34423191
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                                                              1 AAAATAAATAAAAA 17
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synthetic construct
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AX135661
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AR362789
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AX012429
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Beimfohr,C. and Snaidr,J.
Method for the specific fast detection of bacteria which is harmful
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
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1. 18
//organism="synthetic construct"
//nol_type="unassigned DNA"
/db_xref="taxon.32630"
/noTe="Oligonukleotid"
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Susceptibility locus for schizophrenia
Patent: WO 03050301-A 26 19-UNY-2003;
Gurling, Hugh Malcolm Douglas (GB)
Location/Qualifiers
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Vermicon AG (DE)
                                                                                                                                Sequence 331 from Patent WO02103043. AX718767
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Sequence 26 from Patent WO03050301.
AX785415. GI:32953035
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/organism="Homo sapiens"
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AX839747
LOCUS
DEFINITION Sequence 15 from Patent EP1323823.
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                   482 ATGGGGGTCGGGGTCAT 498
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                                              2 ATGGGGCTCGGGTTCAT 18
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artificial sequences.
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AX718767/c
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AX785415/c
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Terminal labeled probe array and method of making it
Patent: EP 1213361-A 22 12-UUN-2002;
CANON KAUSHIKI KAISHA (JP)
Location/Qualifiers
                                                                                                                                       Length 18;
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0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels
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                              1.18
/organism="synthetic construct"
/mol_type="unassigned DNA"
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/note="Sample oligonucleotide"
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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/nofe="Synthesized"
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Patent: EP 118446-7 22 06-MAR-2002;
CANON KABUSHIKI KAISHA (JP)
Location/Qualifiers
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Sequence 22 from Patent EP1213361.
AX453798
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Sequence 22 from Patent EP1184467.
AX391790
CANON KABUSHIKI KAISHA (JP)
Location/Qualifiers
                                                                                                                                                                                                       482 ATGGGGTCGGGGTCAT 498
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31-00-000 JP 2000263396
NOBUNC YAMAMOTO, TADASHI OKAMOTO, TOMOHIRO SUZUKI, SHINYA TANAKA
GOIN33/53,C12M1/00,C12N15/09,C12Q1/68,G01N31/22,G01N33/566, PC
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Strandedness: Single;
Topology: Linear;
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                                                             "...tassified."

1 (bases 1 to 18)

VUTHORS Sheppard, P.O., Jelinek, L.J., Jaspers, S.R. and Whitmore, T.E.

ITLE Mammalian secretory peptide-9

VURNAL Patent: JP 2002503112-A 9 29-JAN-2002;

ZYMOGENETICS INC

NT OS zc 14,489

PN JP 2002503112-A/9

PD 29-JAN-2002

PF 02-JUL-10^^
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PN JP 2002503112-A/9
PD 29-JAN-2002;
PD 29-JAN-1998 UP 1999507420
PR 03-JUL-1997 US 60/051704,03-JUL-1997 US 08/888088
19-MAY-1998 US 60/085983,19-MAY-1998 US 09/08138 PR 17-JUN-1998 US 60/0899917-JUN-1998 US 09/08138 PR CC CINNELAURA J JELNEK,STEPHEN R JASPERS,THEODORE B PI WHITWORE
PC CILLALS,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,CILLAR,C
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1. .18
/organism='Artificial Sequence'
Location/Qualifiers
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BD135441
BD1354411 GI:21228589
JP 2002071687-A/22
Mythetic construct
artificial sequences.
I (bases 1 to 18)
Method for screening mutated gene
Patent: JP 2002071687-A 22 12-MAR-2002;
CANON INC
CS JP 12-MAR-2002
PP 12-MAR-2002
PP 31-AUG-2000 JP 2000263396
PI NOBUKO YAMAMOTO, TADASHI OKAMOTO, TOMOHIRO SUZUK
PC GOIN33/53,CI2M1/00,CI2N15/09,CI2Q1/68,GOIN31/2
                                                     linear
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88.2%; Pred. No. 7.2e+02;
iive 0; Mismatches 2;

    .18
/organism="synthetic construct"

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Method for screening mutated gene.
BD133644
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Matches 15; Conserv
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  RESULT 922
BD106774
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Synthetic construct

artificial sequences.

I (bases 1 to 18)

Synthetic construct

artificial sequences.

I (bases 1 to 18)

Synthetic construct

Probe-coupling substrate, process for producing the same, probe-array, method for detecting target substance, method for and method for quantitating the target substance in the sample, and method for quantitating the target substance in the sample, canon INC ANTEN PHARMACEUT CO LTD

OS Artificial Sequence

PN JP 2000270896-A/23

PD 03-OCT-2000
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                                                                                                                                                                     Sheppard, P.O., Jaspers, S.R., Jelinek, L.J. and Whitmore, T.E. Mammalian secretory peptide 9, antibodes against it and their use Patent: EP 1323823-A 15 02-JUL-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe coupling substrate, process for producing the same, probe-array, method for detecting target substance, method for specifying base sequence of single-stranded nucleic acid in sample, and method for quantitating the target substance in the
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PI HISASHI OKAMOTO,NOBUKO YAMAMOTO,TOMOHIRO SUZUKI PC
C12Q1/68,C12M1/00,C12N15/09,G01N33/566,C12N15/00 CC
FH Key Location/Qualifiers
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88.2%; Pred. No. 7.2e+02;
tive 0; Mismatches 2; Indels
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88.2%; Pred. No. 7.2e+02;
ative 0; Mismatches 2;

    .18
/organism="synthetic construct"

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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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/db_xref="taxon:32630"
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Location/Qualifiers
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BD000033.1 GI:18623112
JP 2000270896-A/23.
  AX839747
AX839747.1 GI:39922912
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                                                                       synthetic construct
synthetic construct
artificial sequences.
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Best Local Similarity 88.2*
Matches 15; Conservative
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method for evaluating target mass using the same Patent: JP 2002153284-A 22 28-MAY-2002; CANON INC.
OS Artificial Sequence
PN JP 2002153284-A/22
PD 28-MAY-2000
PF 24-NOV-2000 JP 2000357446
PI TADASHI OKAMOTO, NOBUKO YAMAMOTO, TOMOHIRO SUZUKI PC
CIZUNIS/00, CIZQ1/68, GOIN31/22, GOIN33/53, GOIN33/566, GOIN37/00, PC
CIZUNIS/00
CC Description of Artificial Remineration
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Synthetic construct
artificial sequences.

E 1 (bases 1 to 18)
S Yamamoto, N., Okamoto, T. and Suzuki, T.
A method of analyzing a base sequence of a nucleic acid
A method of analyzing a base sequence
CANON KK, NOBUKO YAMAMOTO, TADASHI OKAMOTO, TOMOHIRO SUZUKI
OS Artificial Sequence
PN WO 0233068-A/22
PD 25-APR-2002
PP 18-CCT-2000 WO 2000JP007244
PI NOBUKO YAWAMOTO, TADASHI OKAMOTO, TOMOHIRO SUZUKI PC
C12N15/09,C1202/68.0G1N33/56,G01N33/53
CC Sample origonucleotide
FH Key 1. 1. 18
FT Source /organism='Artificial Sequence'.
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Location/Qualifiers
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BD176966 BD176966 BD176960 BDD DNA lines
LOCUS BD17696 ADB172ing nucleic acid base sequence.
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88.2%; Pred. No. 7.2e+02;
iive 0; Mismatches 2;

    .18
        forganism="synthetic construct"
/mol_type="genomic DNA"
        /db_xref="taxon:32630"

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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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WO 0233068-A/22.
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Best Local Similarity 88.2%;
Matches 15; Conservative
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BD167483
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JP 2002065274-A/26
05-MAR-2002
13-AUG-2000 JP 200263395
NOBUKO YAMAMOTO, TADASHI OKAMOTO, TOMOHIRO SUZUKI, AKIRA SHIMIZU
C12N15/09, C12M1/00, C12M1/40, C12Q1/68, G01N31/22, G01N33/53, PC
                                                                                                                                                                                                                                                                                                                                                                                                                        synthetic construct
synthetic construct
synthetic construct
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lobaes 1 to 18)
Yamamoto, N., Okamoto, T., Suzuki, T. and Shimizu, A.
Method for detecting subjective component in specimen sample, and
substrate for detection used therefor
Patent: JP 2002065274-A 26 05-MAR-2002;
CANON INC
                                                                                                                                                                                                                                                                                                        BD135722 18 bp DNA linear PAT 18-SEP-200 Method for detecting subjective component in specimen sample, and substrate for detection used therefor.
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JP 2002153284-A/22.
synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 18)
Okamoto, T., Yamamoto, N. and Suzuki, T.
Terminal-labeled probe-array and method for preparing it, and
                                                                                                                                    Gaps
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Location/Qualifiers
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                                                                                           Length 18;
                                                                                                                                  2; Indels
                                                                                         Query Match 0.8%; Score 13.8; DB 1; Best Local Similarity 88.2%; Pred. No. 7.2e+02; Matches 15; Conservative 0; Mismatches 2;

    .18
        /organism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"

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                                /mol_type="genomic DNA"
/db_xref="taxon:32630"
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PAT 27-AUG-2002
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PN JP 20015260...

PN JP 20015260...

PD 18-DEC-1998 JP 2000525451

PR 19-DEC-1997 US 60/068179,11-SEr-1...

PC C12N15/09,A61K31/711,A61K38/00,A61P17/02,...

PC A61P39/06,

PC A61P43/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC A61P87/00,C07M13/68,C12N15/00,A61K37/02,C12N5/00 CC G01N33/50,G10318,C12N15/00,A61K37/02,C12N5/00 CC Strandedness Single,

PC G01N33/50,G1N33/68,C12N15/00,A61K37/02,C12N5/00 CC Strandedness Single,

PC G01N33/50,G1N33/68,C12N15/00,A61K37/02,C12N5/00 CC Strandedness Single,

PC G01N31/68,C12N15/00,A61K37/02,C12N5/00 CC Strandedness Single,

PC G01N31/68,C12N15/00,A61K37/02,C12N5/00 CC Strandedness Single,

PC Topology: Linear;

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: JP 2001526063-A 3 18-DEC-2001;
WARNER LAMBERT CO
OS Unidentified
PN JP 2001526063-A/3
PD 18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kazemi, A., Messer, C. and Tanguay, D.A. Haplotypes of the origi gene Patent: WO 0212561-A 16 14-FEB-2002; Genaissance Pharmaceuticals, Inc. (US) Location/Qualifiers

    .15
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

       0; Mismatches
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Sequence 16 from Patent W00212561.
AX377095. GI:19573386
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                                                                              CCGTGAAGAGGCGGCA 18
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1 (bases 1 to 18)
       Matches 15; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (basea 1 to 18)
Sugo, T. and Mori, M.
Novel polypeptide and its use
Patent: WO 02103108-A 6 27-DEC-2002;
TAKEDA CHEMICAL INDUSTRIES LTD, TSUKASA SUGO, MASAAKI MORI
OS Homo sapiens (human)
PR WO 0210318-A/6
PP 14-JUN-2002 WO 2002JP005941
PR 15-JUN-2001 JP 01P 182275,01-AUG-2001 JP 01P 233532 PI
TSUKASA SUGO, MASAAKI MORI
PC C123/15/12/C1211/21,C07K14/47,C07K16/18,C12P21/02,G01N33/15, PC
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                                                                                                                                                           OS Artificial Sequence
PN JP 202306166-A/22
PD 22-CCT-2002
PF 31-AUG-2000 JP 200263506
PI NOBUKO YAMAMOTO, HISASHI OKAMOTO, TOMOHIRO SUZUKI PC CL2NIS/09, C122NIS/09, C122NIS/09, C122NIS/09, C1201/68//C12NI/00, C12NIS/00
CC Sample origonucleotide
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Location/Qualifiers
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88.2%; Pred. No. 7.2e+02;
tive 0; Mismatches 2; Indels
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                                                                     synthetic construct
synthetic construct
synthetic construct
1 (bases 1 to 18)
Yamamoto,N., Okamoto,H. and Suzuki,T.
Yamamoto,N., Okamoto,H. and Suzuki,T.
Patent: JP 20023306166-A 22 22-OCT-2002;

    .18
        /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

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    .18
    /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

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                           BD176966.1 GI:30014225
JP 2002306166-A/22.
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WO 02103018-A/6.
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                   0.8%; Score 13.4; DB 1; Length 15; 93.3%; Pred. No. 6.7e+02; ive 0; Mismatches 1; Indels
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I (bases 1 to 15)

Watanabe, K.A., Ran, W.-Y. and Weil, R.
Complementary DNA and toxins

AL Patent: US 5571937-A 19 05-NOV-1996;

Location/Qualifiers
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Sequence 164 from patent US 6472154.
AR241876.1 GI:27287688
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1 (bases 1 to 15)
Watanabe, K. A., Ren, W.-Y. and Weil, R.
Complementary DNA and toxins
Patent: US 555250-A 19 29-JUL-1997;
Location/Qualifiers
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Sequence 19 from patent US 5571937.
128566.1 GI:1819342
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Sequence 19 from patent US 5652350.
158728 151:2477966
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/organism="unknown"
/mol_type="unassigned DNA"
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/organism="unknown"
/wol_type="unassigned DNA"
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                        Query Match
Best Local Similarity 93.33
Matches 14; Conservative
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JP 2002532063-A/1.

synthetic construct
artificial sequences.

El (bases 1 to 15)

Selletier,J. and Das,M.

Oligonucleotide primer capable of making the non-specific double strand formation unstable strand formation unstable by Delletier, JP 2002532063-A 1 02-OCT-2002;

MCGILL UNIVERSITY
OS Artificial Sequence
PN 07-0CT-1999 JP 2000574722
PR 06-OCT-1999 JP 2000574722
PR 07-OCT-1999 JP 2000574722
PR 07-OCT-1998 CA 2246623
PI JERRY PELLETIER,MANJULA DAS
PI JERRY PELLETI
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JP 202532063-A/1
02-0CT-2002
02-0CT-1999
JP 2000574722
07-0CT-1998 CA 2246623
JERRY PELLETIER, MANULLA DAS
CINNTS/09, C12021/68, C12N1S/00
Description of Artificial Sequence: synthetic oligonucleotide
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Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas. Oligonuclectide repeat arrays
Patent: US 5981185-A 8 09-NOV-1999;
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                                                                  Query Match 0.8%; Score 13.6; DB 1; Length 18; Best Local Similarity 92.9%; Pred. No. 7.6e+02; Matches 13; Conservative 1; Mismatches 0; Indels
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Best Local Similarity 93.3%; Pred. No. 6.7e+02;
Matches 14; Conservative 0; Mismatches 1;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                   DNA
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/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                     Sequence 8 from patent US 5981185.
AR084519
AR084519.1 GI:10011290
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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AR084519
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PAT 17-JUL-2003

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OS Artificial Sequence
PN JP 2002539849-A/224
PN JP 2002539849-A/224
PP 27-MAR-2000 JP 2000608794
PR 26-MAR-1999 US 60/126473,23-JUN-1999 US 60/140359 PI JIAN BING FAN,JOEL N HIRSCHHORN, XIAOHUA HUANG, PAUL KAPLAN, ERIC
PI SLANDER,
PI DAVID J LOCKHART, THOMAS RYDER, PAMELA SKLAR
PC C1201/68, C12M1/00, C12N15/09, C12N15/09, G01N33/53, PC G01N37/566,
PC G01N37/60, C12N15/00, C12N15/00, C12N15/00
PC G01N37/66,
PC Frimer Location/Qualifiers
FT SOURCE 1.6
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                                                                                                                                                                                                                                                                   Synthetic construct
artificial sequences.

E 1 (bases 1 to 16)
S Fan,J.B., Hirschhorn,J.N., Huang,X., Kaplan,P., Lander,B.S.,
Lockhart,D.J., Ryder,T. and Sklar,P.
Lockhart,D.J., Ryder,T. and Sklar,P.
Universal arrays
L Patent: JP 2002539849-A 224 26-NOV-2002;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH,AFFYMETRIX INC
OS Artificial Sequence
PN JP 2002539849-A/224
PP 27-WAR-2000 JP 2000608794
PP 27-WAR-1999 US 60/126473,23-UN-1999 US 60/140359 PI
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/organism='Artificial Sequence'
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93.3%; Pred. No. 7.1e+02;
tive 0; Mismatches 1;
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Sequence 658 from Patent WO0244994.
AX598384
0; Mismatches
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Patent: US 6146855-A 2 14-NOV-2000;
Location/Qualifiers
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Williams, K. Leslie., Vesey, G., Veal, D., Ashbolt, N. John. and
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                                                   1 (bases I to 15)
Garner, H.R., Wren, J.D., Minna, J.D. and Fondon, J.W. III.
Polymorphic repeats in human genes
Patent: US 6472154-A 164 29-0CT-2002;
Location/Qualifiers
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Patent: WO 0136673-A 43 25-MAY-2001;
Creatogen Aktiengesellschaft (DE)
Location/Qualifiers
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    15. 15
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/db_xref="taxon:306"

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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 2 from patent US 6146855.
AR141562
AR141562.1 GI:15101078
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Sequence 43 from Patent WO0136673.
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/organism="unknown"
/mol_type="genomic DNA"
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Bacteria; Proteobacteria.
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PAT 14-FEB-2003

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PAT 28-AUG-2000

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1 (bases I to 17)
Beck,J.Joseph.
Detection of fungal pathogens using the polymerase chain reaction
Patent: US 581453-A 12 29-SEP-1998;
Location/Qualifiers
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Ligon, J.M. and Beck, J.J.
Detection of fungal pathogens using the polymerase chain reaction
Patent: US 595574-A 12 21-SEP-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unknown.
Unclassified.
1 (bases 1 to 17)
Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.
C-myb ribozymes having 2'-5'-linked adenylate residues
Patent: US 5817796-A 194 06-0CT-1998;
                                                                                                                                                                                                                                                                              Query Match 0.8%; Score 13.4; DB 1; Length 17; Best Local Similarity 93.3%; Pred. No. 7.6e+02; Matches 14; Conservative 0; Mismatches 1; Indels
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AR074628
AR074628.1 GI:10001381
            Sequence 12 from patent US 5814453.
AR043128
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17 bp
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                                                 AR043128.1 GI:5964136
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AR074628/c
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AR045401/c
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Paoletti.B., de Taisne,C., Chang,S., Hui,G. and Siddiqui,W. Malaria recombinant poxvirus
Patent: US 5756101-A 16 26-MAY-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unknown.
Unclassified.
I (bases 1 to 17)
Lobman K.L., Ostrercova, N.V., Van Cleve, M. and Reid, R. Alan.
Lobman K.L., Ostrercova, N.V., Van Cleve, M. and Reid, R. Alan.
Detection of nucleic acids in cells by thermophilic strand
displacement amplification
Patent: US 5756702-A 4 26-MAY-1998;
Location/Qualifiers
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Sequence 16 from patent US 5756101.
AR009007
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Sequence 4 from patent US 5756702.
AR010206 1GI:3969011
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AR043128/c
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RESULT 945
AR098727/c
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REFERENCE AUTHORS TITLE JOURNAL FEATURES

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basout 19 DNA linear PAT 18-JUN-2001 Detection assay with the use of fluorescence and kit therefor. B35686
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1 (bases 1 to 17)

Ligon,J.M. and Back,J.J.

Detection of fungal pathogens using the polymerase chain reaction

Patent: US 558528-A 12 17-DEC-1996;

Location/Qualifiers
                                                                                                                                                                                                                                E35866.1 GI:13019158
E35666.1 GI:13019158
JP 1999225799-A/2.
SWITCHELIC CONSTRUCT
SM SYNCHETIC CONSTRUCT
SM STATELICIAL SEQUENCES.

I (Dassel 1 to 17)
SM STATELICIAL SEQUENCES.
L Patent: JP 1999225799-A 2 24-AUG-1999;
BECTON DICKINSON & CO
OS Artificial Sequence
PF O4-NOV-1999 JP 1998312790
PF 04-NOV-1999 US 08/964020
PI MICHAEL C LITTLE/GREN P VONG
PC C12Q1/68,G01N21/78,G01N33/50/C12N15/09,C12N15/00 CC
FT SOURCE

/ Organism='Artificial Sequence'.
                    Gaps
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Location/Qualifiers
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   93.3%; Pred. No. 7.6e+02;
tive 0; Mismatches 1
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                                                     828 CAAAGAGGAAGCTGC 842
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Matches 14; Conservative
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DEFINITION
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E35686/c
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C12N15/09.12Q1/68//G01N33/50,G01N33/53,G01N33/566,C12N15/00
Description of Artificial Sequence: PCR primer FH Key
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PN JP 2002534099-4/8
PD 15-0CT-2002
PP 17-12AN-12000 UP 2000592449
PR 08-JAN-1299 US 09/417386 PI JONATHAN M ROTHBERG, MICHAEL MCKENNA, PAUL PREDKI, ANDREAS PI WINDEMUTH,
PI RICHARD A SHIMKETS
PC C12N15/09.01201/68//G01N33/50,G01N33/566,C12N15/0
CC Description of Artificial Sequence: PCR primer FH Key
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artificial sequences.
1 (bases 1 to 17)
Shinketes, R.A.
Shinketes, R.A.
CURAGEN CORP.
CURAGEN CORP.
CONSTRUCT
SHIPPED AS 15-OCT-2002,
Artificial Sequence
PN JP 2002534099-A/8
PD 15-OCT-2002
                                                                                                                                                                                                                                                                                                     SM Unknown.
Unclassified.
In (bases 1 to 17)
RS Little,M.C. and Vonk,G.P.
Kit and method for fluorescence based detection assay
Incation/Qualifiers
Location/Qualifiers
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Query Match 0.8%; Score 13.4; DB 1; Length 17; Best Local Similarity 93.3%; Pred. No. 7.6e+02; Matches 14; Conservative 0; Mismatches 1; Indels
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    17
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Method for identifying nucleic acid.
BD238354
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Sequence 2 from patent US 6077669.
AR098727 1 GI:12808493
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JP 2002534099-A/8.
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BD238354 LOCUS DEFINITION ACCESSION VERSION VERSYORDS SOURCE ORGANISM

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PAT 20-APR-2002
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Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6346398-A 2776 12-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unclassified.

1 (bases 1 to 17)

Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.

Pavco, and reagent for the treatment of diseases or conditions

related to levels of vascular endothelial growth factor receptor

Patent: US 6346198-A 2777 12-FEB-2002,
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Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bp DNA
6346398.
displacement amplification
Patent: US 5733752-A 4 31-MAR-1998;
Location/Qualifiers
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Sequence 2777 from patent US
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Best Local Similarity 93.3°
Matches 14; Conservative
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Unclassified.
1 (base1 to 17)
Lohman,K.L., Ostrerova,N.V., Cleve,M.Van. and Reid,R.Alan.
Detection of nucleic acids in cells by thermophilic strand
                                                                                                                                                                                                               1 (bases 1 to 17)
Lohman,K.L., Ostrerova,N.V., Cleve,M.V. and Reid,R.A.
Lohman,K.L., Ostrerova,N.V., Cleve,M.V. and Reid,R.A.
displacement amplification
Patent: US 5631147-A 4 20-MAY-1997;
Location/Qualifiers
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Unclassified.
1 (Dases I to 17)
Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
C-myb targeted ribozymes
Patent: US 5646042-A 194 08-JUL-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.8%; Score 13.4; DB 1; Length 17; Best Local Similarity 93.3%; Pred. No. 7.6e+02; Matches 14; Conservative 0; Mismatches 1; Indels
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Sequence 194 from patent US 5646042.
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/organism="unknown"
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Sequence 4 from patent US 5631147.
143322.1 GI:2468566
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Patent: US 6566127-A 1301 20-MAY-2003;
Location/Qualifiers
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1 (bases 1 to 17)

1 (bases 2 to 17)

1 (bases 3 to 17)

1 (bases 3 to 17)

1 (bases 4 to 1.5)

1 (bases 5 to conditions between and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6346398-A 2778 12-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 17)
Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 1300 20-MAY-2003;
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Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
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llarity 93.3%; Pred. No. 7.6e+02;
Conservative 0; Mismatches 1; Indels
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0.8%; Score 13.4; DB 1;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1;
                                                            Sequence 2778 from patent US 6346398.
AR187290
AR187290.1 GI:20233255
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Sequence 1300 from patent US 6566127.
AR323898
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1 (bases 1 to 17)
Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6566127-A 1302 20-MAY-2003;
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1 (bases 1 to 17)
Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6566127-A 5090 20-MAY-2003;
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0.8%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 7.6e+02; tive 0; Mismatches 1; Indels
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Sequence 1302 from patent US 6566127.
AR323900
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Sequence 5090 from patent US 6566127.
AR327688
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artificial sequences.
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Best Local Similarity 93.3
Matches 14; Conservative
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0153103-A 2365 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
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Pred. No. 7.6e+02;
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AX218294
                      17 bp
Sequence 27 from Patent W00134834.
AX146685
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Blatt, L., Mcswiggen, J. and Chowrira, B.M.
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0159103-A 3736 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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Targeted chromosomal genomic alterations with modified single stranded oligonucleotides
Patent: WO 0173002-A 3406 04-OCT-2001;
UNIVERSITY OF DELAMARE (US)
Location/Qualifiers
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Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
Patent: WO 0173002-A 3407 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
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/mol type="unassigned RNA"
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Sequence 3406 from Patent WO0173002.
AX266015

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                                                                                                                                                                                                                                                                                       /note="Nucleic Acid"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Randi, A.M.
Method and reagent for the inhibition of erg
Patent: WO 0188124-A 881 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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Method and reagent for the inhibition of erg
Patent: WO 0188124-A 834 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GE
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Sequence 881 from Patent WO0188124.
AX422545
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Sequence 834 from Patent WO0188124.
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/mol_type="unassigned RNA"
/db_xref="taxon:9606"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Randi, A. M.
Randi, A. M.
Method and reagent for the inhibition of erg
Patent: WO O188124-A 64 62 22-NOV-2001;
RIBOZYWE PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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Rethod and reagent for the inhibition of erg
Patent: WO 0188124-A 183 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
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Sequence 183 from Patent WO0188124.
AX421847
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Sequence 646 from Patent WO0188124.
AX422310

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    /db_xref="taxon:9606"

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/mol_type="unassigned RNA"
/db_xref="taxon:9606"
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/mol_type="unassigned RNA"
/db_xref="taxon:9606"
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Method and reagent for the inhibition of erg
Patent: WO 188124-A 2035 22-NOV-2001;
RIBOZYME PARAMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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Method and reagent for the inhibition of erg
Patent: WO 0188124-A 2036 22-NOV-2001;
RIBOZYME PHRAMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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  Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Mclaughlin, F.G. Randi, A.M.
Method and reagent for the inhibition of erg
Patent: WO 0188124-A 1852 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GE
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Sequence 2036 from Patent WO0188124.
AX423700
AX423700.1 GI:21527082
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/mol_type="unassigned RNA"
/db_xref="taxon:9606"
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/mol_type="unassigned RNA"
/db_xref="taxon:9606"
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AX423699
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Randi, A.M.
Machod and reagent for the inhibition of erg
Patent: WO 0188124-A 882 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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Method and reagent for the inhibition of erg
Patent: WO 0188124-A 1851 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
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93.3%; Pred. No. 7.6e+02;
ative 0; Mismatches 1;
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Sequence 1851 from Patent WO0188124.
AX423515
AX423515.1 GI:21526897
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Seguence 1852 from Patent WO0188124.
AX423516
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/mol_type="unassigned RNA"
/db_xref="taxon:9606"

  Sequence 882 from Patent WO0188124.
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Best Local Similarity 93.39
Matches 14; Conservative
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Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)
Patent: WO 021674-A 403 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US); Syntex (U.S.A.) LLC (US);
Thompson, James (US)
Location/Qualifiers
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 2137 from Patent WO0211674.
AX580299
                              17 bp 1
Sequence 403 from Patent WO0211674.
AX578565
AX578565.1 GI:27647767
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/mol_type="unassigned RNA"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"
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Matches 14; Conservative
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AX580298/c
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AX578565/c
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                     Length 17;
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Human testis expressed patched like protein
Patent: EP 1229046-A 649 07-AUG-2002;
Aeomica, Inc. (US)
Location/Qualifiers
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Patent: EP 1229046-A 648 07-AUG-2002;
Aeomica, Inc. (US)
Location/Qualifiers
                                     Query Match

0.8%; Score 13.4; DB 1;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1;
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Sequence 648 from Patent EP1229046.
AX499341

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Sequence 649 from Patent EP1229046.
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AX493341/c
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Telerman, A., Amson, R. and Tuijnder, M.
Telerman, A., Amson, R. and Tuijnder, M.
Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and their use as medicines
Patent: WO 03004526-A 1815 16-JAN-2003;
Molecular Engines Laboratories (FR)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shannon, M., Gu, Y. and Nguyen, C.T. Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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AX688345 GI:29411045
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Aeomica, Inc. (US)
Location/Qualifiers
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Patent: EP 1281758-A 1078 05-FEB-2003;
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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AX688345
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                                                                                                                                                 and Grupe, A.
Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)
Batent: WO 0211674-A 2137 14-FEB-2002;
BATENT WO 0211674-A 2137 INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
Location/Qualifiers
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: WO 03004526-A 1078 16-JAN-2003;
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AX673370
                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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Location/Qualifiers
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/organism="Homo sapiens"
AX580299.1 GI:27649501
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                                      Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Aeomica, Inc. (US)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 17 from Patent WO03025176.
AX722330
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Location/Qualifiers
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AX692521/c
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AX690456
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Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
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Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                          Ouery Match 0.8%; Score 13.4; DB 1; Length 17; Best Local Similarity 93.3%; Pred. No. 7.6e+02; Matches 14; Conservative 0; Mismatches 1; Indels
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Aeomica, Inc. (US)
Location/Qualifiers
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Aeomica, Inc. (US)
Location/Qualifiers
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Sequence 3187 from Patent EP1281758.
AX690455
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Telerman, A., Amson, R. and Tuijnder, M.
Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
Patent: WO 03025177-A 1518 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
Patent: WO 03025177-A 2760 27-WAR-2003;
Molecular Engines Laboratories (FR)
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Sequences involved in phenomena of tumour suppression, tumour reversion, apoptocsis and/or resistance to viruses and the use thereof as medicaments
Patent: WO 03025177-A 3635 27-WAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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93.3%; Pred. No. 7.6e+02;
tive 0; Mismatches 1;
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                                                                                                                                                                                                /mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
                                                                                                                             Location/Qualifiers
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Homo sapiens
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Best Local Similarity 93.33
Matches 14; Conservative
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                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                             Telerman, A., Amson, R. and Tuijnder, M. Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
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93.3%; Pred. No. 7.6e+02;
iive 0; Mismatches 1;
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Sequence 2499 from Patent W003025176.
AX724812
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
                                       Mus musculus (house mouse)
Mus musculus
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AX722330.1 GI:30422831
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Homo sapiens
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These 14; Conservative
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RESULT 988 AX735928/c LOCUS

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Oreochromis niloticus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Labroidei; Cichlidae; Oreochromis.
                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
   Gaps
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Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
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/db_xref="texon:8128"
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Patent: WO 03060160-A 507 24-JUL-2003;
Genomar ASA (NO)
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   Mismatches
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AX759206.1 GI:32253822
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AX759206/c
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: WO 03025177A 4083 27-MAR-2003;

Molecular Engines Laboratories (FR)

Location/Qualifiers
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93.3%; Pred. No. 7.6e+02;
tive 0; Mismatches 1;
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Molecular Engines Laboratories (FR)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                         AX738493 17 bp DNA Sequence 4083 from Patent W003025177.
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/mol_type="unassigned DNA"
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                                                                                                                Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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Best Local Similarity
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                                                                                               Query Match
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AX757892/c
LOCUS
DEFINITION
ACCESSION
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KEYWORDS
SOURCE
ORGANISM
     source
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AX738493/c
LOCUS
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AUTHORS
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TITLE
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BD203288 17-JUL-2003 Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response.
BD203288.1 GI:33013058
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PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-MAR-1999 JP 2000541291
27-MAR-1998 US 60/079678
PAMELA A PAVC, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
JAMES A MCSWIGGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C12N15/09, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61P17/06, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

I (bases 1 to 1).

Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J.A. Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response.

Patent: JP 2002609721-A 6314 02-APR-2002;

RIBOZYME PHARMACEUTICALS INC
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    .17
    /organism='Artificial Sequence'

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                                                                                                                                                                                                                                 0.8%; Score 13.4; DB 1; Length 17;
llarity 93.3%; Pred. No. 7.6e+02;
Conservative 0; Mismatches 1; Indels
Location/Qualifiers
                                                                                                       1. .17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                           1692 TCTTCTCTTCCA 1706
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Homo sapiens (human)
Homo sapiens
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VERSION
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AUTHORS
TITLE
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                                                                              FEATURES
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                                                                            PAT 31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Artificial Sequence
JP 2000300281-A/4
31-000-2000
33-OCT-2000
21-SEP-1995 US 08/531749 PI
N L ROMAINS, NATARI V OSUTOREROBA, MARK VAN CLIVE, PI ROBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       synthetic construct
artificial sequences.

1 (bases 1 to 17)
Fukushima, M., Kakinuma, K. and Kawaguchi, R.
Nucleic acid for assaying genus Shigella or genus Salmonella and detection method.

Patent: JP 2001245677-A 38 11-SEP-2001;

SEL INC, MARINE BIOTECHNOLOGY INSTITUTE CO LTD, NIPPON GENE CO LTD PN JP 2001245677-A/38
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DNA probe for detecting Salmonella typhi, Salmonella CC
typhimurium and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF 27-DEC-2000 JP 2000398087
PI MASAO FUKUSHIMA, KENICHI KAKINUMA, RYUJI KAWAGUCHI PC
C12N15/09,C12N15/09,C12N1/00,C12Q1/68,G01N33/583,G01N33/566, PC
PC (C12O1/68 C1201/68 C1
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                                                                                                                                                                                                                            synthetic construct
synthetic construct
synthetic construct
artificial sequences.

1 (bases 1 to 17)
Romains, K.L., Osutoreroba, N.V., Clive, M.V. and Lead, R.A.
Detection of nucleic acid in cell by thermophilic strand
substitutive amplification
Patent: JP 2000300281-A 4 31-OCT-2000;
                                              Detection of nucleic acid in cell by thermophilic strand substitutive amplification.
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    17
    forganism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"

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JP 2000300281-A/4.
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Best Local Similarity
Matches 14; Conserv
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PN JP
PP 31
PP 31
PR 21
KENTON LE
PC CL
CC CC
FT 60
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KEYWORDS
SOURCE
ORGANISM
                   RESULT 995
BD000130/c
LOCUS
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                                                                                               DEFINITION
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AUTHORS
TITLE
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KEYWORDS
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PAT 27-APR-1998
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Location/Qualifiers
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JP 1997224671-A/4
02-SEP-1997
19-FEB-1996 JP 1996031075
SHIBATA DAISUKE, KATO TOMOHIKO, OTA HIROYUKI
C12N15/09,C12N9/02,(C12N9/02,C12R1:91);
strandedness: Single;
topology: Linear;
hypothetical: No;
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JP 1997224672-A/4
02-SEP-1996 JP 1996033973
SHIBATA DAISUKE, KATO TOMOHIKO, OTA HIROYUKI
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                                  0; Indels
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1 (bases 1 to 14)
Shibata,D., Kato,T. and Ota,H.
DNA CODING NEW DNA-CONNECTED PROTEIN
PAECH: JP 1997224672-A 4 02-SEP-1997;
MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO:KK
OS None
OC Artificial sequences.
PN JP 1997224672-A/4
PD 02-SEP-1997
PF 21-SEP-1999
PF 21-SEP-1999
PI SHIBATA DAISUKE, KATO TOMOHIKO, OTA HIRC
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 14)
Shibata, D., Kato, T. and Ota, H.
DNA CODING NEW CYTOCHROME P450
Patent: JP 1997224671-A 4 02-SEP-1997;
MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO: KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.8%; Score 13.2; DB 1;
92.9%; Pred. No. 6.6e+02;
tive 1; Mismatches 0;
       92.9%; Pred. No. 6.6e+02; ive 1; Mismatches 0
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    .14
    /organism="unidentifled"
    /mol_type="genomic DNA"
    /db_xref="taxon:32644"

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JP 1997224671-A/4.
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                                                                                 1734 ACAAAAAAAAAAAA 1747
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JP 1997224672-A/4.
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         Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                             Similarity
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PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
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                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases) Le 17)
Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J.A. Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response
Patent: JP 2002509721-A 6315 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Regulated genes by stimulation of chondrocytes with IL-lbeta Patent: EP 0705842-A 56 10-APR-1996,
HOECHST AG (DE)
Other publication ZA 9509381 960424
Other publication CA 2159957 960407
Other publication AJ 3308695 960418.
Location/Qualifiers
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molecule participating in vasculogenic response.
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    .14
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Sequence 56 from Patent EP0705842.
A52266

    .17
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/mol_type="genomic RNA"
/db_xref="taxon:9606"

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                                                      BD203289.1 GI:33013059
                                                                        JP 2002509721-A/6315.
Homo sapiens (human)
Homo sapiens
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Pesonen, U., Koulu, M., Linnoila, M., Goldman, D. and Virkkunen, M. Allelic variation of the serotonin 5HT7 receptor
Patent: US 753183-A 4 09-JUN-1998;
Location/Qualifiers
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Horie,R. and Ishiguro,T.
Optically active DNA probe having phosphonic diester linkage
Patent: W 5211354-A 1 03-APR-2001;
Location/Qualifiers
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/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                         /organism="unknown"
/mol_type="unassigned DNA"
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ARA45368
AR145368.1 GI:15107235.
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Sequence 6 from patent US 6326175.
AR179431.1 GI:20220986
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Sequence 4 from patent US 5763183.
AR012010
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                1736 AAAAAAAAAAAA 1748
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AR179431/c
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AR012010/c
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C12N15/09, A01H5/00, C07H21/04, C07K14/415//C12N5/10, C12Q1/68; CC
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McClelland,M., Welsh,J. and Trenkle,T.
Reduced complexity nucleic acid targets and methods of using same
Patent: US 6495119-A 65 17-DEC-2002;
Location/Qualifiers
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Pesonen, U., Koulu, M., Linnoila, M., Goldman, D. and Virkkunen, M. Allelic variation of the serotonin 5HT7 receptor
Patent: US 5763183. A 30-JUN-1998;
Location/Qualifiers
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/organism='Artificial sequences'
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AR266627
AR266627.1 GI:29695691
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/mol_type="unassigned DNA"
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Sequence 3 from patent US 5763183.
AR012009
AR012009.1 GI:3969999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .14
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               strandedness: Single;
    topology: Linear;
    hypothetical: No;
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Matches 13; Conservative
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PC C07H21/04,C12N15/09,C12Q1/68,C12Q1/68,G01N21/78,G01N33/50, PC
G01N33/533,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unclassified.

1 (bases 1 to 13)
Guegler,K., Tan,R. and Rose,M.J.
Fusion protein comprising an eIF-4E domain and an eIF-4G domain joined by a linker domain
Patent: US 6369199-A 6 09-APR-2002,
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Location/Qualifiers
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0.7%; Score 13; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0;
Patent: JP 1999322783-A 2 24-NOV-1999;
TOSOH CORP
OS Artificial Sequence
PN JP 1999322783-A/2
PD 24-NOV-1999
PP 06-MAY-1998 JP 1998123298
                                                                                                                                                                                                                                                                                                                                                        0.7%; Score 13; DB 1; L
100.0%; Pred. No. 6.4e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                           1. .13
/organism="synthetic construct"
/mol_type="genomic DNA"
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                                                                                                                                                                                                        Location/Qualifiers
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1 (bases 1 to 13)

Rurz, M., Lohse, P. and Wagner, R.

Peptide acceptor ligation methods

Patent: US 6429300-A 19 06-AUG-2002;
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Sequence 19 from patent US 6429300.
AR222459
AR222459.1 GI:23329990
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/wol_type="unassigned DNA"
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Sequence 6 from patent US 6369199.
AR205695
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CO7H21/04,C12N15/09,C12Q1/68,C12Q1/68,G01N21/78,G01N33/50, PC
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        Guegler,K., Tan,R. and Rose,M.J.
Methods and compositions for producing full length cDNA libraries
Patent: US 6326175-A 6 04-DEC-2001;
Location/Qualifiers
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DNA probe having optically active diphosphonate bond.
E66853
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1 (bases 1 to 13)
Ryuichi,H. and Takahiko,I.
BNA probe having optically active diphosphonate bond
Patent: JP 1999322783-A 1 24-NOV-1999;
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DNA probe having optically active diphosphonate bond.
E66854
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Ryuichi, H. and Takahiko, I.
DNA probe having optically active diphosphonate bond
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0.7%; Score 13; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0;
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|db_xref="taxon:32630"

    .13
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JP 1999322783-A/1
24-NOV-1999
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PAT 12-JAN-2001
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Patent: WO 0122972-A 867 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
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Detection system for separating constituents of a sample and production and use of the same
Patent: WO 0071/47-A 4 30-NOV-2000;
Aventis Research & Technologies GmbH & Co. KG (DE)
Location/Qualifiers
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/note="FITC moiety attached at 3' end of sequence.
Has phosphodiester backbone."
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/db_xref="taxon:32630"
/noTe="Region A"
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Sequence 867 from Patent WO0122972.
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Sequence 868 from Patent WO0122972.
AX104676
                                                            Sequence 4 from Patent WO0071747.
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Matches 13; Conservative
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Method for identifying nucleic acids by means of matrix-assisted
laser desorption/ionisation mass spectrometry
Patent: WO 9929808-A 12 T7-JUN-1999;
MAX PLANCK GESELLSCHAFT (DE); BERLIN KURT (DE); GUT IVO GLYNNE
(DE); LEHRACH HANS (DE)
LOCATION/Qualifiers
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Unclassified.
Unclassified.
1 (bases 1 to 13)
Garner, H. R., Wren, J. D., Minna, J. D. and Fondon, J. W. III.
Polymorphic repeats in human genes
Patent: US 6472154-A 29 29-OCT-2002;
Location/Qualifiers
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/organism="synthetic construct"
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/noTe="artificial sequence"
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Sequence 29 from patent US 6472154.
AR241741
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Sequence 12 from Patent W09929898.
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//organisme="synthetic construct"
//mol type="unassigned DNA"
//db_xref="taxon:32630"
//note="Synthetic oligonucleotide-phosphodiester backbone"
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Methods for enhancing antibody-induced cell lysis and treating
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                                                                                                              1. .13
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="oligomer used in this study"
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UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
Location/Qualifiers
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Patent: WO 0197843-A 836 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
Location/Qualifiers

    .13
/organism="synthetic construct"
/mol_type="unassigned DNA"

Cyclohexene nucleic acids
Patent: WO 0145887-A 25 12-JUL-2001;
K.U. LEUVEN RESEARCH & DEVELOPMENT (BE)
Location/Qualifiers
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artificial sequences.
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AX355808/c
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                                                                                                                                                                                          Immunostimulatory nucleic acids
Patent: WO 0122972-A 868 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
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/mol_type="unassigned DNA"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
11..13
/note="Blotin moiety attached at 3' end of sequence.
Has phosphorothicate and phosphodiester chimeric backbone with phosphodiester on 3' end."
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="taxon:32630"
/noTe="DNA complement"
                                                                                                                                                                      Krieg, A.M., Schetter, C. and Vollmer, J.C.
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Cyclohexene nucleic acids
Patent: WO 0149687-A 25 12-JUL-2001;
K.U. LEUVEN RESEARCH & DEVELOPMENT (BE)
Location/Qualifiers
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Sequence 25 from Patent W00149687.
AX235509
AX235509.1 GI:15593971
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     AX104676.1 GI:13920873
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Matches 13; Conservative
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AX235509/c
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ORGANISM ACCESSION VERSION KEYWORDS SOURCE

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PAT 22-JAN-2000
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               0.7%; Score 13; DB 1; Length 13;
100.0%; Pred. No. 6.4e+02;
tive 0; Mismatches 0; Indels
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00.0%; Pred. No. 7e+02;
ve 0; Mismatches 0; Indels
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Brysch, W. and Schlingensiepen, K.
AN ANTISENSE OLICGONUCLEOTIDE PREPARATION METHOD
PALENT: WO 9833904-A 298 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unidentified
unclassified.
1 (Dases 1 to 14)
Brysch, W.D. and Schlingensiepen, K.D.
An antisense oligonucleotide preparation method
Patent: EP 08565/9-A 298 05-AUG-1998;
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7e+02;
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Sequence 298 from Patent BP0856579.
A90117
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A88150
A88150.1 GI:6736720

    .14
    forganism="unidentified"
    mol_type="unassigned bNA"
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    .14
    /organism="unidentified"

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Best Local Similarity 100.09
Matches 13; Conservative
                              Best Local Similarity 100.0
Matches 13; Conservative
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A97593/c
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="teaxon:32630"
/db xref="teaxon:32630"
/nofe="Has phosphorothioate and phosphodiester chimeric backbone with phosphodiester on 3' end."
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               /note="Synthetic oligonucleotide~chimeric
phosphorothioate/phosphodiester backbone with
phosphodiester on 3' end"
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                                                                                                            0.7%; Score 13; DB 1; Length 13; 100.0%; Pred. No. 6.4e+02; tive 0; Mismatches 0; Indels
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/organism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
/note="Has phosphodiester backbone."
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/note="Conjugated to biotin moiety."
                                                                                                                                                                                                                                                                                                                                                                                                                                  Bratzler, R.L.
Inhibition of angiogenesis by nucleic acids
Patent: WO 02053141-A 867 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
Location/Qualifiers
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/note="Conjugated to FITC moiety."
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Sequence 867 from Patent WO02053141.
db xref="taxon:32630"
                                                                           /note="FITC labeled"
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synthetic construct
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Sequence 8 from patent US 6180777.
ARI27787
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AR127787
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Vary, C.P.H.
Nucleic acid sequence detection by triple helix formation at primer site in amplification reactions
Patent: US 5800994-A 33 01-SEP-1998;
Location/Qualifiers
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unclassified.
I (bases 1 to 14)
Roberts, J.A. and Paul, W.
CONTROL POP DEHISCENCE OR SHATTER
Patent: WO 9915681-A 3 01-APR-1399;
BIOGEWMA UK LIMITED (GB); ROBERTS JEREMY ALAN (GB)
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0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels
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Sequence 33 from patent US 5800984.
AR036791. GI:5954647
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/db_xref="taxon:32644"
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 2 from patent US 5747299.
AR004935.1 GI:3965814
Sequence 3 from Patent WO9915681.
A97593
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1 (bases 1 to 14)

2 (Agyaznov, S.M.

Convergent synthesis of branched and multiply connected macromolecular structures

Patent: US 5830658-A 8 03-NOV-1998;
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Unclassified.
1 (bases 1 to 14)
1 (bases 1 to 14)
Fisher, P.B. and Shen, R.
Human prostate tunduring gene-1 and uses thereof
Patent: Use 5851764-A 8 22-DEC-1998;
Location/Qualifiers
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Query, Match 0.7%; Score 13; DB 1; Length 14; Best Local Similarity 100.0%; Pred. No. 7e+02; Matches 13; Conservative 0; Mismatches 0; Indele
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/mol_type="unassigned DNA"
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Sequence 8 from patent US 5851764.
AR067459
AR067459.1 GI:5998681
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Sequence 8 from patent US 5830658.
AR051240
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PAT 20-DEC-2002
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Petkovich, P.Martin., White, J.A., Beckett, B.R. and Jones, G. Retinoid metabolizing protein
Patent: US 6306624-A 15 23-OCT-2001;
Location/Qualifiers
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Patent: US 5571677-A 8 05-NOV-1996;
Location/Qualifiers
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100.0%; Pred. No. 7e+02;
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                                                                                                              Sequence 15 from patent US 6306624.
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Gryaznov, S.M.
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1 (bases 1 to 14)

1 (bases 1 to 14)

Petkovich, P.Martin., White, J.A., Beckett, B.R. and Jones, G. Retinoid metabolizing protein

Patent: US 6306624-A:12 23-OCT-2001,

Location/Qualifiers
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1 (bases 1 to 14)
Petkovich, P.Martin., White, J.A., Beckett, B.R. and Jones, G. Retinoid metabolizing protein
Patent: US 6306624-A 13 23-OCT-2001,
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Sequence 13 from patent US 6306624.
AR174023
AR174023.1 GI:17914343
                                                                                                  Synthesis of branched nucleic acids
Patent: US 6180777-A 8 30-JAN-2001;
Location/Qualifiers
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Sequence 12 from patent US 6306624.
AR174022
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 GI:14114382
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PAT 21-FEB-2003
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Zis-sr nucleic acid and amino acid sequences involved in the regulated secretory pathway and/or the regulation of the neuroendocrine phenotype (nep)
Patent: WO 02061082-A 26 08-AUG-2002;
Universite de Sherbrooke (CA)
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Sequence 24 from Patent WO02103014.
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Sequence 26 from Patent WO02061082.
AX642208 AX642208.1 GI:28474656
                                                14 bp
Sequence 1 from Patent WO9949046.
AX016298
AX016298.1 GI:10041861
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AX016298/c
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1 (bases 1 to 14)
Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
Polymorphic repeats in human genes
Patent: US 6472154-A 94 29-OCT-2002;
Location/Qualifiers
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Lehar, S.M. and Guild, B.C.
Apoptosis gene EIZ4, compositions, and methods of use
Patent: US 6586204-A 18 01-JUL-2003;
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Lebar,S.M. and Guild,B.C.
Apoptosis gene El24, compositions, and methods of use
Patent: US 6586204-A 20 01-JUL-2003;
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AR349924
AR349924.1 GI:33750834
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AR349926.1 GI:33750836
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PAT 27-AUG-2002
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E | (bases 1 to 14)
Suishblink, Hosier,S. and Kubbies,M.
Suishblink, Hosier,S. and Kubbies,M.
Isolation of novel aging factor gene P23
L Patent: JP 2001512698-A 6 28-AUG-2001;
UNIVERSITY OF WASHINGTON
OS Unidentified
PN JP 2001512698-A/6
PD 28-AUG-2001
PF 05-AUG-1998 JP 2000506375
PR 08-AUG-1997 US 08/908873
PR 08-AUG-1997 US 08/908873
PR 08-AUG-1997 US 08/908873
PR C1201/68, CO7K14/435, CO7K16/18, C12N1/19, C12N1/19, C12N1/19, C12N1/02,
CC C1201/68, Lineari,
CC Topology: L
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i. (bases 1 to 14)

Suishelm, K., Hosier, S. and Kubbies, M.

Isolation of novel aging factor gene P23

Lo Patent: JP 2001512688-A 9 28-AUG-2001;

UNIVERSITY OF WASHINGTON
OS Unidentified

PN JP 2001512698-A/9

PD 28-AUG-2001

PF 05-AUG-1998 JP 2000506375

PR 08-AUG-1997 US 08/908873

PR 08-AUG-1998 US 08/90888 US 08/90888

PR 08-AUG-1998 US 08/90888

PR 08-AUG-1998 US 08/9088

PR 08-AUG-1998 US 08/90888

PR 08-AUG-1998 US 
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Location/Qualifiers
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AUTHORS
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                                                                                                                             Al-Mahmood, S.
Antisense oligonucleotides which can inhibit the formation of capillary tubes by endothelial cells
Patent: WO 02103014-A 24 27-DEC-2002;
Al-Mahmood, Salnan (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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3 (Chases 1 to 14)

3 Schlingensiepen,K.H. and Brysch,W.

3 Schlingensiepen,K.H. and Brysch,W.

3 Schlingensiepen,K.H. and Brysch,W.

4 An antisense oligonuclectide preparation method

4 Pacent: JP 2001511000-A 298 07-AUG-2001;

BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH

5 ON TAUGO 2001

7 PN JP 2001511000-A/298

7 PN JP 2001511000-A/298

7 PN JP 2001511000-A/298

8 PN JP 30-AN-1997 FP 97101531.8

8 PN 31-JAN-1997 FP 97101531.8

8 PN ARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH

8 PC CL2N15/11,CO7H21/04,A61K11/70

CC An antisense oligonucleotide preparation method FH Ke
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07-AUG-2001
10-2001
31-ANA-1997 BP 1998532533
31-JAN-1997 BP 97101531.8
KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
C12N15/11, C77421/04, AG1K31/70
An artisense oligonucleotide preparation method FH
Location/Qualifiers
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An antisense oligonucleotide preparation method.
BD065663
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cive 0; Mismatches 0; Indels
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/organism="synthetic construct"
/or_l_rype="unassigned DNA"
/db_xref="taxon:32630"
/noTe="Oligonucleotide anti-sens"
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/organism='Unknown'
Location/Qualifiers
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/organism="unidentified"
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                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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JP 2001511000-A/298.
unidentified
unidentified
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JP 2001512698-A/6.
                                synthetic construct artificial sequences.
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synthetic construct
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Matches 13; Conservative
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BD06563/c
LOCUS
DEFINITION ACCESSION EXCESSION EXEYMORDS
SOURCE
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BD073881/c
LOCUS
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ORGANISM

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AUTHORS TITLE JOURNAL

COMMENT

FEATURES

KEYWORDS

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REFERENCE

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PAT 18-MAR-2003
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1 (bases 1 to 14)
Yamamoto, M., Yamamoto, N., Hirose, K. and Sakai, J.
Yamamoto, M., Yamamoto, N., Hirose, K. and Sakai, J.
Yamamoto, M., Yamamoto, N., Hirose, K. and Sakai, J.
Wethod of constructing cDNA tag for identifying expressed gene and method of analyzing gene expression
Patent: WO 2020/4951-A 43 26-SEP-2002;
KUNITAKA HIROSE, JUN SAKAI
OS Artificial Sequence
DN WO 02074951-A/43
PD 26-SEP-2002
                DESTRUCTION OF THE PROPERTY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 bp DNA linear PAT 18-MAR-200:
Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression.
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OS ARTIFICIAL Sequence

PN 002074951-A/43

PD 26-ESPE-2002

PP 13-MAR-2002 WO 2002JP002338

PR 15-MAR-2001 JP 01P 073959

PN MIKTO YAMAMOTO, NAOKI YAMAMOTO, KUNITAKA HIROSE, JUN SAKAI PC

C12N15/09, C12C1/68

CC Synthetic DNA

Location/Qualifiers

FT 80urce 1...14

/ organism='Artificial Sequence'.
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/organism='Homo sapiens (human)'
Location/Qualifiers
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/organism='Artificial Sequence'
Location/Qualifiers
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100.0%; Pred. No. 7e+02;
iive 0; Mismatches 0; Indels
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100.0%; Pred. No. 7e+02;
1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                 Location/Qualifiers

    1. .14
/organism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"

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/organism="Homo sapiens"
/mol_type="genomic DNA"
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WO 02074951-A/43.
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synthetic construct
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PROGENTIOR INC
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Matches 13; Conserva
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Matches 13; Conserv
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VERSION
KEYWORDS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Feder,J.N., Kronmal,G.S., Lauer,P.M., Ruddy,D.A., Thomas,W.J., Tsuchihashi,Z. and Wolff,R.K.
Polymorphisms and new genes in the region of the human hemochromatosis gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-ANG-1993
08-ANG-1999 US 08/908873
08-ANG-1997 US 08/908873
KAREN SUISHELM, SUZANNE HOSIER, MANFRED KUBBIES PC
1/68, CO7K14/435, C07K16/18, C12N1/15, C12N1/19, C12N15/09, PC
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100.0%; Pred. No. 7e+02;
tive 0; Mismatches 0; Indels
                        Length 14;
                   0.7%; Score 13; DB 1; Length 14;
100.0%; Pred. No. 7e+02;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                   linear
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Topology: Linear,
Isolation of novel aging factor gene P23
Key
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/organism='Unidentified'
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 14)
Suishelm,K., Hosier,S. and Kubbies,M.
Isolation of novel aging factor gene P23
Patent: JP 2001512698-A 12 28-AUG-2001;
UNIVERSITY OF WASHINGTON
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Patent: JP 2001525663-A 14 11-DEC-2001;

    .14
    /organism="unidentified"

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C12P21/08,C12N15/00
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JP 2001512698-A/12
28-AUG-2001
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JP 2001525663-A/14.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                              BD073887.1 GI:22619490
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                      Query Match
Best Local Similarity 100.
Matches 13; Conservative
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Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                 CAAAAAAAAAAA 1
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C1201/
C12P21
PC C
CC C
CC T
CC I
FH K
FT 8
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BD073887/C
LOCUS
ACCESSION
VERSION
VERSION
SOURCE
ORGANISM

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BD084126/c
LOCUS
DEFINITION
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Gaps

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synthetic construct
synthetic construct
artificial sequences.

I (bases 1 to 14)

Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.

Method of constructing cDNA tag for identifying expressed gene and method of constructing cDNA tag for identifying expressed gene and method of analyzing gene expression

METHOD of CONSTRUCTING CDNA tag 26-SEP-2002;

KUNTAKA HIROSE,JUN SAKAI
OS Artificial Sequence
NO 02074951-A/48

PP 13-MAR-2001 JP 01P 073959

PF 11-MAR-2001 JP 01P 073959
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Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
Method of constructing CDNA tag for identifying expressed gene and
method of analyzing gene expression
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100.0%; Pred. No. 7e+02;
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100.0%; Pred. No. 7e+02;
ive 0; Mismatches 0; Indel8
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

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        /organism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"

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BD176801.1 GI:29122513
WO 02074951-A/48.
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WO 02074951-A/49.
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WO 02074951_A/44.

WO 02074951_A/44.

WO 02074951_A/44.

Synthetic construct
artificial sequences.

I (bases 1 to 14)

Xamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.

Rethod of constructing cDNA tag for identifying expressed gene and method of fanalyzing gene expression

Rethod of fanalyzing gene expression

Rethod of fanalyzing gene expression

RATIFICIAL SEQUENCE.

KUNEHA HIROSE,JUN SAKAI

OS Artificial Sequence

PN NO 02074951_A/4

PD 26-SEP-2002

PF 13-MAR-2002

PF 13-MAR-2001

PF 15-MAR-2001

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synthetic construct

artificial sequences.

I (bases 1 to 14)

S Yamamoto, M., Yamamoto, N., Hirose, K. and Sakai, J.

Method of constructing cDNA tag for identifying expressed gene and method of analyzing sene expression.

L Actor NO 02074951-A 45 26-SEP-2002;

KUNITAKA HIROSE, JUN SAKAI

OS ARtificial Sequence

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               BDI76797 14 bp DNA linear PAT 18-MAR-2003 Method of constructing cDNA tag for identifying expressed gene and method of analyzing gene expression.
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HIS-MAR-2001 JP 01P 073959
MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
15/09,C12Q1/68
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Location/Qualifiers
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    forganism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"

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BD176798.1 GI:29122510
WO 02074951-A/45.
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Grimm, S., Stinchcomb, D.T., McSwiggen, J., Sullivan, S. and Draper, K.G.
Intercellular adhesion molecule-1 (ICAM-1) ribozymes
Patent: US 5817542-A 364 17-NOV-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 15)
Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
Draper,K.G.
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Patent: US 5837542-A 359 17-NOV-1998;
Location/Qualifiers
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100.0%; Pred. No. 7.5e+02;
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Sequence 364 from patent US 5837542.
AR056160.1 GI:5981737
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Sequence 359 from patent US 6132967.
AR113913
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Sequence 359 from patent US 5837542.
AR056155.1 GI:5981732
                                0; Mismatches

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    /organism="unknown"
    /mol_type="unassigned DNA"

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/organism="unknown"
/mol_type="unassigned DNA"
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AR113913/c
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AR056155/c
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AL PATENT: WO 02074951-A 49 26-SEP-2002;
KUNEHA CHEMICAL INDUSTRY CO LTD, MIKIO YAMAMOTO, NAOKI YAWAMOTO,
KUNITAKA HIROSE, JUN SAKAI
OS Artificial Sequence
PN WO 02074951-A/49
PD 26-SEP-2002
PP 13-MAR-2002 WO 2002JP002338
PR 15-MAR-2001 JP 01P 073959
PI MIKIO YAMAMOTO, NAOKI YAMAMOTO, KUNITAKA HIROSE, JUN SAKAI PC
C12N15/09, C12Q1/68
CC Synthetic DNA
PK Key
Location/Qualifiers
FT SOURCE
/organism='Artificial commune'
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14 bp RNA linear PAT 17-JUL-2003
Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection.
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unclassified.
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C12N9/00, AG1K31/7105, AG1K38/21, AG1K48/00, AG1P31/12, C12N15/09,
AG1K37/66,
C12N15/00
Enzymatic nucleic acid treatment of diseases or conditions C
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PR 27-APR-1999 US 60/100317,18-SEP-1999 US 60/100842 PR 25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI LAWRENCE BLAIT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PI
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    14
    Organism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"

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/organism="unidentified"
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/db_xref="taxon:32644"
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JP 2002512791-A/2919.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 13; Conservative 0; Mismatches 0;
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Fresco, J.R. and Johnson, M.D.
Triplex in-situ hybridization
Patent: US 6461810-A 54 08-OCT-2002;
Location/Qualifiers
   Mismatches
                                                                                                                                                           Sequence 54 from patent US 6461810.
AR235555
AR235555.1 GI:27278776

    .15
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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Sequence 332 from Patent BP1260586.
AX633193. GI:28468807
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    .15
    /organism="unknown"
    /mol_type="genomic DNA"

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                                 1025 ATGGGGCTGGGGT 1037
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                                                        Dargner, K.G.
Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
Patent: US 6132967-A 359 17-OCT-2000;
Location/Qualifiers
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Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
Patent: US 6132967-A 364 17-OCT-2000;
Location/Qualifiers
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Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
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Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S.
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1 (bases 1 to 15)

1 (bases 1 to Kinzler, K.W., Zhang, L. and Zhou, W. Vogelstein, B., Kinzler, K.W., Zhang, L. and Zhou, W. Gene expression profiles in normal and cancer cells Patent: US 6333152-A 842 25-DEC-2001;

Location/Qualifiers
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Sequence 842 from patent US 6333152.
AR180774
AR180774.1 GI:20222807
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/mol_type="unassigned DNA"
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/mol_type="unassigned DNA"
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E 1 (bases 1 to 16)
(S Barsecut.).L. and Imbach, J.-L.
Oligothionucleotides
(AL Patent: US 5639873.A 4 17-UUN-1997;
Location/Qualifiers
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Georgopoulos,K.
Ikaros: A T cell pathway regulatory ge
Patent: US 6228611-A 119 08-MAY-2001;
Location/Qualifiers
1 (bases 1 to 16)
Georgopoulos.K.
Ikaros polypeptides
Patent: US 5824770-A 119 20-OCT-1998;
Location/Qualifiers
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Sequence 119 from patent US 6228611.
ARA49710.
ARA49710.1 GI:15114301
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Sequence 4 from patent US 5639873.
147692.
147692.1 GI:2471657
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                                                                                                                                                                      Method and reagent for inhibiting the expression of disease related
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                                                                         Stinchcomb, D.T., Dudycz, L.W., Chowrira, B., Grimm, S., Direnzo, A., Karpeisky, A., Draper, K.G., Kisich, K., Matulic-Adamic, J., Mcswiggen, J.A., Modak, A., Pavco, P., Beigelman, L., Sullivan, S.M., Sweedler, D., Thompson, J.D., Tracz, D., Usman, N., Wincott, F.B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stinchcomb, D.T., Dudycz, L.W., Chowrira, B., Grimm, S., Direnzo, A., Karppisky, A., Draper, K.G., Kishch, K., Watulic-Adamic, J., Moshiggen, J.A., Modk, A., Pavco, P., Beigelman, L., Sullivan, S.M., Sweedler, D., Thompson, J.D., Tracz, D., Usman, N., Wincott, F.E. and
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Patent: EP 1260586-A 332 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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    /db_xref="taxon:32644"

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Matches 13; Conservative
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RESULT 1059 AX633203/c

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1 (bases 1 to 17)
Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
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Intercellular adhesion molecule-1 (ICAM-1) ribozymes
Patent: US 5837542-A 1790 17-NOV-1998;
Location/Qualifiers
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Sequence 1790 from patent US 5837542.
AR057586.1 GI:5983163
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Sequence 1639 from patent US 5837542.
AR057435
AR057435.1 GI:5983012
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Location/Qualifiers
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AR057586/c
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Unknown.
Unclassified.
I (bases I to 16)
Egholm M., Nielsen, P., Buchardt, O., Dueholm, K.L., Christensen, L.,
Coull, J.M., Kiely, J. and Griffith, M.
Peptide nucleic acids
Patent: US 6451968-A 217-SEP-2002;
Location/Qualifiers
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Georgopoulos, K.
Isolated antibody that binds to an Ikaros polypeptide Patent: Location/Qualifiers
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100.0%; Pred. No. 8e+02;
tive 0; Mismatches 0; Indels
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Complex element micro-array and methods of use
Patent: WO 02072886-A 3 19-SEP-2002;
Expresson Biosystems Limited (GB)
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Sequence 42 from patent US 6451968.
AR231305
AR231305.1 GI:27272236
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Sequence 119 from patent US 6630141.
AR404837
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Sequence 3 from Patent WO02072886.
AX708160
AX708160.1 GI:29564093
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AR231305/c
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AX708160
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Location/Qualifiers
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AR115193/c
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Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
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Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
Draper,K.G.
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Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
Draper,K.G.
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Patent: US 5837542-A 1801 17-NOV-1998;
Location/Qualifiers
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Patent: US 5837542-A 1823 17-NOV-1998;
Location/Qualifiers
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Patent: US 5837542-A 1868 17-NOV-1998;
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100.0%; Pred. No. 8.5e+02;
cive 0; Mismatches 0; Indels
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100.0%; Pred. No. 8.5e+02;
iive 0; Mismatches 0;
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Sequence 1823 from patent US 5837542.
AR057619
                      17 bp DN Sequence 1801 from patent US 5837542. AR057597 GI:5983174
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RESULT 1068
AR057597/C
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1 (bases 1 to 17)

1 (bases 1 to 17)

Strimm, S., Stinchcomb, D.T., McSwiggen, J., Sullivan, S. and
Draper, K.G.
Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
Patent: US 613267-A 1790 17-0CT-2000;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Draper, K.G.
Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
Patent: US 6132967-A 1639 17-OCT-2000;
Location/Qualifiers
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Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
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Sequence 1639 from patent US 6132967.
AR115193
AR115193.1 GI:14095515
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/wol_type="unassigned DNA"
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BD253932 17 bp DNA linear PAT 17-JUL-2003
Regulation of repressor genes using nucleic acid molecules.
BD253932
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Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
Patent: US 6132967-A 1868 17-0CT-2000;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                          unclassified.
unclassified.
Blatt.L., Zwick,M., Pavco,P. and Mcswiggen,J.
Regulation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 1725 10-DEC-2002;
RIBOZYME PHARNACEUTICALS INC
OS Eukaryote PARNACEUTICALS INC
PP 10-DEC-2002
PP 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK, PAMELA PAVCO,JAMES MCSWIGGEN
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Draims, S., Stinchcomb, D.T., McSwiggen, J., Sullivan, S. and Draper, K.G.

Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule.1 (ICAM-1)

Patent: US 6132667-A 1801 17-OCT-2000;

Location/Qualifiers
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Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
Draper,K.G.
Ribozyme treatment of diseases or conditions related to levels of
intercellular adhesion molecule-1 (ICAM-1)
Patent: US 6132967-A 1823 17-OCT-2000;
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Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
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100.0%; Pred. No. 8.5e+02;
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                       Sequence 1801 from patent US 6132967.
ARI15355.1 GI:14095677
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Sequence 1823 from patent US 6132967.
AR115377.1 GI:14095699
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/mol_type="taxon:32630"
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AR327690 17 cm patent US 6566127.
AR327690.1 GI:33713498
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Sequence 152 from Patent WO0162911.
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                     Unclassified.
Unclassified.
1 (bases 1 to 17)
Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
Pavco, P., McSwiggen, For the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6346398-A 2547 12-FEB-2002;
Location/Qualifiers
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Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 1071 20-MAY-2003;
Location/Qualifiers
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Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 5091 20-MAY-2003;
Location/Qualifiers
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/wol_type="unassigned RNA"
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/mol_type="unassigned RNA"
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Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 5092 20-MAY-2003;
Location/Qualifiers
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0159103-A 2366 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Ellis, J.H. Method and reagent for the inhibition of grid Method and reagent for the inhibition of grid Patent: WO 0162911-A 720 30-AUG-2001; RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
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Method and reagent for the inhibition of erg
Patent: WO 0188124-A 1432 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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Method and reagent for the inhibition of erg
Patent: WO 0188124-A 1223 22-NOV-2001;
RIBOZYME PHRANACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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/mol_type="unassigned RNA"
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/organism="Homo sapiens"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                    Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Hamblin, P.A. and Ellis, J.H.
Method and reagent for the inhibition of grid
Patent: WO 0162911-A 152 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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Method and reagent for the inhibition of grid
Patent: WO 0165911-A 539 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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13; Conservative 0; Mismatches 0; Indels
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/mol_type="unassigned RNA"
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Sequence 720 from Patent WO0162911.
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Woolf, T. Method and reagent for inhibiting the expression of disease related
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100.0%; Pred. No. 8.5e+02;
:ive 0; Mismatches 0;
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RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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Seguence 1784 from Patent EP1260586.
AX634645
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Sequence 1762 from Patent EP1260586.
AX634623
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                   Length 17;
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                   Query Match 0.7%; Score 13; DB 1; Le Best Local Similarity 100.0%; Pred. No. 8.5e+02; Matches 13; Conservative 0; Mismatches 0;
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Patent: EP 1239051-A 1501 11-SEP-2002;
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RIBOZYME PHARMACEUTICALS, INC. (US)
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Sequence 1501 from Patent EP1239051.
AXS31992.
AXS31992.1 GI:25255750
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AX634500/c
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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cive 0; Mismatches 0; Indels
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Sequence 3257 from Patent W003004526.
AX674812.
AX674812.1 GI:29333160
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Location/Qualifiers
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/organism="Homo sapiens"
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  Sequence 87 from Patent WO03004526.
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                                      AX671642.1 GI:29329990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stinchcomb, D.T., Dudycz, L.W., Chowrira, B., Grimm, S., Direnzo, A., Karpeisky, A., Draper, K.G., Kisich, K., Matulic-Adamic, J., Modwiggen, J.A., Modwik, A., Pavco, P., Beigelman, L., Sullivan, S.W., Sweedler, D., Thompson, J.D., Tracz, D., Usman, N., Wincott, F.E. and
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Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels
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                                        RNA
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RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1827 from Patent EP1260586. AX634688
                                      AX634681
Sequence 1820 from Patent EP1260586.
                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="unidentified"
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/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
Patent: WO 3025177-A 1890 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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                  /mol_type="unassigned DNA" /db_xref="taxon:9606"
    organism="Homo sapiens"
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                                       Shannon, M., Gu, Y. and Nguyen, C.T. Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Aeomica, Inc. (US)
Location/Qualifiers
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Aeomica, Inc. (US)
Location/Qualifiers
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Sequence 3190 from Patent EP1281758.
AX690458.1 GI:29413339
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AX692530
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/db_xref="taxon:9606"

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Be.B.H., Portaelly, F., Machtelinckx, L., Jannes, G. and Rossau, R.
MYGHACTER THE DETECTION OF THE ANTIBIOTIC RESISTANCE SPECTRUM OF
MYCOBACTERIUM SPECIES
PATENT: WO 9531851-A 38 14-DEC-1995,
INNOGENETICS NV (BE)
Other publication AU 2789695 960104.
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1 (bases 1 to 16)
Stuyver,L., Rossau,R. and Maertens,G.
METHOD FOR TYPING AND DETECTING HBV
Patent: WO 9740193-A 27 30-OCT-1997;
INNOGENETICS NV (BE)
Location/Qualifiers
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    .16
    /organism="unidentified"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"

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    .16
    /organism="unidentified"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"

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Sequence 27 from Patent WO9740193.
A66860.
A66860.1 GI:4538231
           16 bp
Sequence 38 from Patent WO9533851.
A47824
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Unclassified.
1 (bases 1 to 16)
Gryaznov,S.M.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                        Telerman, A., Amson, R. and Tuijnder, M.
Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments and the use batent: WO 3022177-A 5106 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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100.0%; Pred. No. 8.5e+02;
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1 Similarity 100.0%; Pred. No. 8.5e+02;
13; Conservative 0; Mismatches 0;
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Sequence 5106 from Patent W003025177.
AX739516
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Homo sapiens
               209 CCCTCAGGGAG 221
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Hanecak, R.C., Anderson, K.P., Bennett, C.Frank., Chiang, M.-Y.,
Brown-Driver, V.L., Ecker, D.J., Vickers, T.A., Wyatt, J.R. and
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Hanecak, R.C., Anderson, K.P., Bennett, C.Frank., Chiang, M.-Y.,
Brown-Driver, V.L., Ecker, D.J., Vickers, T.A., Wyatt, J.R. and
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Oligonucleotides having a conserved G4 core sequence
Patent: US 5952490-A 112 14-SEP-1999;
Location/Qualifiers
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Sequence 55 from patent US 5952490.
AR074247
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/mol_type="unassigned DNA"
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/organism="unknown"
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Hancack,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,
Hancack,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,
Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and
Imbach,J.Louis.
Oligonuclectides having a conserved G4 core sequence
Patent: US 5952490.A 39 14-SEP-1999;
Location/Qualifiers
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Convergent synthesis of branched and multiply connected macromolecular structures
Patent: 18 830658-A 16 03 NOV-1998;
Location/Qualifiers
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Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
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                                                                                                           1. .16
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AR066240
AR066240.1 GI:5996456
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Moelling, K.
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**Page 272** 

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Unclassified.

Loases 1 to 16)

Draper, K.G., Crooke, S.T., Mirabelli, C.K., Ecker, D.J., Hanecak, R.C.,
Anderson, K.P., Brown-Driver, V.L. and Myatt, J.R.
Oligonucleotide therapies for modulating the effects of herpes viruses
Patent: US 5514577-A 56 07-MAY-1996;
                                                            PAT 26-JUL-1995
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                                                                                                                                                                                                                                restriction endonuclease
Patent: US 5436150-A 46 25-JUL-1995;
Location/Qualifiers
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Sequence 16 from patent US 5571677.
128377.
128377.1 GI:1819153
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Sequence 46 from patent US 5436150.
113390

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Gryaznov, S.M.
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1 (bases 1 to 16)
Ramberg, E.R.
Methods and compositions for detection of specific nucleotide
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Ferkol,T.W. Jr., Davis,P.B. and Ziady,A.-G.
Serpin enzyme complex receptor--mediated gene transfer
Patent: US 5972901-A 2 26-OCT-1999;
Location/Qualifiers
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Ferkol, T.W. Jr., Davis, P.B. and Ziady, A.-G.
Serpin enzyme complex receptor-mediated gene transfer
Patent: Us 6200801-A 2 13-WAR-2001;
Location/Qualifiers
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                                                         Patent: US 5962225-A 1 05-OCT-1999;
Location/Qualifiers
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Sequence 2 from patent US 5972901.
AR082443
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I (bases 1 to 16)

1 (bases 1 to 16)

Beenhouwer,H., Portaels,F., nckx,L.M., Jannes,G. and Rossau,R.

Method for detection of the antibiotic resistance spectrum of mycobacterium species
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0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
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Beigelman, L., Burgin, A., Beaudry, A., Karpeisky, A., Matulic-Adamic, J., Sweedler, D. and Zinnen, S. Synthetic ribonucleic acids with RNAse activity Patent: US 6528640-A 1 04-WAR-2003;

Location/Qualifiers
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Unclassified.
In (bases 1 to 16)
Beigelman, L., Burgin, A., Beaudry, A., Karpeisky, A., Matulic-Adamic, J., Sweedler, D. and Zinnen, S. Synthetic ribonucleic acids with RNAse activity Patent; US 6528640-A 21 04-MAR-2003;
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Sequence 38 from patent US 6329138.
AR366072
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Sequence 21 from patent US 6528640.
AR285649
                                            Sequence 1 from patent US 6528640.
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Murray, J.C. and Semina, E.
RGS compositions and therefor Patent: US 6518411-A 37 11-FEB-2003;
Location/Qualifiers
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Ramberg, E.R.
Methods and compositions for detection of specific nucleotide
Convergent synthesis of branched and multiply connected macromomolecular structures Patent: 18,571677-A 16 05-NOV-1996; Location/Qualifiers
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1 Similarity 87.5%; Pred. No. 8.5e+02;
14; Conservative 0; Mismatches 2;
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0.7%; Score 12.8; DB 1;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2;
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AR281424
AR281424 GI:29717111
                                                                                            /mol_type="unassigned DNA"
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/organism="unknown"
/mol_type="genomic DNA"
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/organism="unknown"
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/organism="unknown"
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Ashby, M.
Methods for the survey and genetic analysis of populations
Patent: US 6613520-A 40 02-SEP-2003;
Location/Qualifiers
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Methods for the survey and genetic analysis of populations
Patent: US 6613520-A 115 02-SEP-2003;
Location/Qualifiers
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Sequence 115 from patent US 6613520.
AR391503.1 GI:40115001
Patent: US 6329138-A 38 11-DEC-2001;
Location/Qualifiers
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Sequence 40 from patent US 6613520.
AR391428 AR391428.1 GI:40114919
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/organism="unknown"
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/organism="unknown"
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                                                                                                                             242 cgGGGCCACCACCGGC 257
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1 (bases 1 to 16)
De Beenhouwer,H., Portaels,F., Machtelinckx,L., Jannes,G. and
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Beigelman, L., Burgin, A. B., Beaudry, A., Karpeisky, A., Matulic-Adamic, J., Swedler, D. and Zinnen, S.
Oligoribonucleotides with enzymatic activity
Patent: Location/Qualifiers
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Beigelman, L., Burgin, A.B., Beaudry, A., Karpeisky, A., Matulic-Adamio, J., Swedler, D. and Zinnen, S.
Oligoribonucleotides with enzymatic activity
Patent: US 6617438-A 21 09-SEP-2003;
Location/Qualifiers
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Sequence 21 from patent US 6617438.
AR397640
Sequence 1 from patent US 6617438.
AR397620
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Oligodeoxynucleotide and its use to induce an immune response
Patent: WO 0151500-A 85 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
Location/Qualifiers
                                                                                                                                                                                                                                           Imbach, J.L., Brown-Driver, V.L., Vickers, T.A., Ecker, D.J.,
Bennett, C.F., Chiang, M.Y., Anderson, K.P., Hanecak, R.C. and
Wyatt, J.R.
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Patent: EP 1016715-A 112 05-JUL-2000;
ISIS PHARMACEUTICALS INC (US)
Location/Qualifiers
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Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2;
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    .16
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Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
Wyatt,J.R.
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Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
Wyatt,J.R.
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Patent: EP 1016715-A 39 05-JUL-2000;
ISIS PHARMACEUTICALS INC (US)
Location/Qualifiers
1. 16
/organism="unidentified"
/db_xref="taxon:32644"
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Patent: EP 1016715-A 55 05-JUL-2000;
ISIS PHARMACEUTICLS INC (US)
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Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
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Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
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Sequence 39 from Patent EP1016715.
AX032593
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Sequence 55 from Patent EP1016715.
AX032609
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/organism="unidentified"
/organism="unknown"
/mol_type="genomic DNA"
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                      Gaps
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Method and diagnostic kit for the molecular diagnosis of
pharmacologically relevant genes
Patent: WO 0318837-A 133 06-MAR-2003;
Adnagen AG (DE)
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/organism="synthetic construct"
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MOLECULAR ENGINES LAB (FR)
Location/Qualifiers
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Sequence 223 from Patent WO02059256.
AX494458

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Patent: WO 0211761-A 103 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
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Methods for the survey and genetic analysis of populations
Patent: WO 0177392-A 115 18-OCT-2001;
Ashby, Matthew (US)
Location/Qualifiers
                                                                 Ashby, M. Methods for the survey and genetic analysis of populations Patent: WO 0177392-A 40 18-OCT-2001; Ashby, Matthew (US)
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Best Local Similarity 87.5%; Pred. No. 8.5e+02;
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AX465435
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Randi,A.M.
Method and reagent for the inhibition of erg
Patent: WO 0188124-A 837 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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Grifantini, R., Frascotti, G., Galli, G. and Grandi, G.
Process for the production of D-alpha-amino acids
Patent: EP 0677585-A 6 18-0CT-1995;
ENIRICERCHE SPA (IT)
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Query Match
0.7%; Score 12.8; DB 1; Length
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
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Sequence 837 from Patent WO0188124.
AX422501
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Location/Qualifiers
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Sequence 6 from Patent EP0677585.
A46769.1 GI:2300864
                                                                         1021 GGGGATGGGGCTGGGG 1036
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PN JP 2001522588-A/1
PD 20-NOV-2001
PF 12-NOV-1999 JP 2000519613
PR 12-NOV-1997 US 60/076872
PI ELLIOT R RAMBERG
PC C12Q1/68,C12N15/09
CC Methods and compositions for detection of specific nucleotide equences
FH Key Location/Qualifiers
FT source 1...16
                                                                                                                            BD091347 16 bp DNA linear PAT 27-AUG-2002 Methods and compositions for detection of specific nucleotide
                                                                                                                                                                                               BD091347.1 GI:22636958
JP 2001522588-A/1.
Human adenovirus type 1
Human adenovirus type 1
Human adenovirus type 1
I (bases 1 to 16)
Ramberg, B.R.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Method and reagent for the inhibition of erg
Patent: WO 0188124-A 836 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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/db_xref="taxon:10533"
/note="Human adenovirus type 1"
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Sequence 836 from Patent WO0188124.
AX422500
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/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"
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 169 CCCACCTGGCTGCCCC 184
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1 CCCACCAGCCTGCCCC 16
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Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.
C-myb ribozymes having 2'-5'-linked adenylate residues
Patent: US 5817796-A 2149 06-OCT-1998;
Location/Qualifiers
                                                             Query Match 0.7%; Score 12.8; DB 1; Length 17; Best Local Similarity 87.5%; Pred. No. 9e+02; Matches 14; Conservative 0; Mismatches 2; Indels
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Stinchcomb, D. T. and McSwiggen, J.A.
Interleukin-2 receptor gamma-chain ribozymes
Patent: US 5807743-A 1067 15-SEP-1998;
Location/Qualifiers
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AR040219
AR040219.1 GI:5959582
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/mol_type="unassigned DNA"
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/mol_type="unassigned DNA"
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AR047356/c
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AR057566/c
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AR040219/c
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Wang,C.-G. and Hepburn,A.G.
Genetic sequence assay using DNA triple strand formation
Patent: US 5861244-A 96 19-JAN-1999;
Location/Qualifiers
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Stinchcomb, D.T. and McSwiggen, J.A.
Interleukin-2 receptor gamma-chain ribozymes
Patent: US 52 7867743-A 83 15-SEP-1998;
Location/Qualifiers
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Stuyver, L., Rossau, R. and Maertens, G.
METHOD FOR TYPING AND DETECTING HBV
Patent: WO 9740193.A 74 30-OCT-1997;
INNOGENETICS NV (BE)
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/organism="unknown"
/wol_type="unassigned DNA"
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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AR029907
AR029907.1 GI:5943121
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AR039235
AR039235.1 GI:5958598
                          17 bp
Sequence 74 from Patent WO9740193.
A66907
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AR115324.1 GI:14095646
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AR115448/c
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Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
Draper,K.G.
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Grimm, S., Stinchcomb, D.T., McSwiggen, J., Sullivan, S. and Draper, K.G.
Intercellular adhesion molecule-1 (ICAM-1) ribozymes Patent: US 5837542-A 1984 17-NOV-1998;
Location/Qualifiers
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Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
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                                                                                                              Draper, K.G.
Intercellular adhesion molecule-1 (ICAM-1) ribozymes
Patent: US 5837542-A 1770 17-NOV-1998;
Location/Qualifiers
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AR057690
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/mol_type="unassigned DNA"
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/mol_type="unassigned DNA"
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 AR057566
AR057566.1 GI:5983143
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AR057690/c
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AR057780/c
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Unclassified.
1 (bases 1 to 17)
Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
Braper,KG.
Ribozyme treatment of diseases or conditions related to levels of
intercellular adhesion molecule-1 (ICAM-1)
Patent: US 6132967-A 1770 17-OCT-2000;
Location/Qualifiers
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Mezes, P.S., Richard, R.A., Affholter, J.A. and Kotite, N.J.
Dimer and multimer forms of single chain polypeptides
Patent: US 6071515-A 89 06-JUN-2000;
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Query Match 0.7%; Score 12.8; DB 1; Length 17; Best Local Similarity 87.5%; Pred. No. 9e+02; Matches 14; Conservative 0; Mismatches 2; Indels
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Sequence 1894 from patent US 6132967.
AR115448
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AR115324
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Sequence 89 from patent US 6071515.
AR097026

    17
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LOCUS BD241455 17-JUL-2003 DNA linear PAT 17-JUL-2003 DEFINITION Methods and products related to genotyping and DNA analysis.
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Murray, J.C. and Semina, E.
Methods and compositions for the diagnosis and treatment of
                                                                                                                                                                                                                                                                                                                                        Unclassified.
1 (bases 1 to 17)
Shannon, K.W., Wolber, P.K., Delenstarr, G.C., Webb, P.G. and
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Method for evaluating oligonucleotide probe sequences
Patent: US 6251588-A 75 26-JUN-2001;
                               y Match 0.7%; Score 12.8; DB 1; Length 17; Local Similarity 87.5%; Pred. No. 9e+02; hes 14; Conservative 0; Mismatches 2; Indels
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Patent: US 630586-A 28 23-OCT-2001;
Location/Qualifiers
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Sequence 28 from patent US 6306586.
AR173612
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Sequence 75 from patent US 6251588.
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ARI58453.1 GI:16220493
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                                                                                                                                Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
Patent: US 6132967-A 1894 17-OCT-2000;
Location/Qualifiers
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Patent: US 6132967-A 1984 17-OCT-2000;
Location/Qualifiers
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Shannon, K.W., Wolber, P.K., Delenstarr, G.C., Webb, P.G. and
Kincaid, R.H.
Method for evaluating oligonucleotide probe sequences
Patent: US 6251588-A 74 26-UUN-2001;
Location/Qualifiers
                                                                             1 (bases 1 to 17)
Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
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Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
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Sequence 1984 from patent US 6132967.
AR115538
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Sequence 74 from patent US 6251588.
AR158452
AR158452.1 GI:16220492
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 AR115448.1 GI:14095770
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Regulation of repressor genes using nucleic acid molecules.
BD254586
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CI2P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02,
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PN JP 200254195-A/2004
PN JP 20025402
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAMRENCE BLATT,MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN I C12P15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12U5/10, PC C12P21/02,
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Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Regulation of represent genes using nucleic acid molecules Patent: JP 2002541795-A 2004 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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1 (bases 1 to 17)

1 shatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Regulation of repressor genes using nucleic acid molecules Patent: JP 2002541795-A 2379 10-DEC-2002;
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4; Conservative 0; Mismatches 2; Indels
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0.7%; Score 12.8; DB 1;
Best'Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2;
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A61K37/02,
(Ci2NS/00,Ci2R1:91)
Regulation of repressor genes using
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JP 2002541795-A/2004.
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JP 2002541795-A/2379.
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I (bases 1 to 17)
Landers,J.E., Jordan,B., Housman,D.E. and Charest,A.
Methods and products related to genotyping and DNA analysis
Patent: JP 2002525127-A 402 13-AUG-2002;
MASSACHUSETTS INSTITUTE OF TECHNOLOGY
OS Homo sapiens (human)
PD 13-AUG-2002
PP 24-SEP-1999 JP 2000572407
PP 24-SEP-1999 US 60/101757
PI JOHN E LANDERS, BARBARA JORDAN, DAVID E HOUSMAN, ALAIN CHAREST PC
C12N15/09,C12Q1/68,G01N33/53,G01N33/566,G01N33/50,
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E Landers, J. E., Jordan, B., Housman, D.E. and Charest, A.

Methods and products related to genotyping and DNA analysis

Methods and products related to genotyping and DNA analysis

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PR 25-SEP-1999 US 60/101757
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Location/Qualifiers
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BD241455.1 GI:33051225
JP 2002525127-A/402.
Homo BapienB (human)
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JP 2002525127-A/428.
Homo sapiens (human)
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PD 10-DEC-2002
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-ARR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN 1
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
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Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Regulation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 2804 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
OS EUKARYOTE
PN JP 2002541795-A/2804
PD 10-DEC-2002
PP 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAMRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO. JAMES MCSWICK
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Regulation of repressor genes using nucleic acid molecules.
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Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Regulation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 2805 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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(C12N5/00, C12R1:91)
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JP 2002541795-A/2804.
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Regulation of repressor genes using nucleic acid molecules.
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PN JP 2002441795-A/2670
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC C12N15/09, A61K38/00, A61F48/00, A61P43/00, A61P43/00, C12N5/10, PC C12P21/02, C12P21/02, A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
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Regulation of repressor genes using nucleic acid molecules FH
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OS EUKATYOCE
PN JP 2002541795-A/2379
PD 10-DEC-2002
PF 11-APR-2099 US 60/129300
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN GI2D21/02,
PC 12P21/02,
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Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Begulation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 2670 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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PC (C12N5
CC Regula
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PC (C12P;
PC A61K3
PC (C12N
CC Regul
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(C12N5/00,C12R1:91)
Regulation of repressor genes using nucleic acid molecules
Location/Qualifiers
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PN JP 2002241795-A/2824
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAMRENCE BLATT MICHARL ZMICK, PAMELA PAVCO, JAMES MCSWIGGEN ICIZNIS/09, AG1K38/00, AG1K48/00, AG1P43/00, AG1K48/10, PC
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ORS Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.

Regulation of represent genes using nucleic acid molecules

TAL Patent: JP 2002541795-A 3212 10-DEC-2002;

RIBOZYME PHARMACEUTICALS INC

OS BUKARYOLE

PN JP 2002541795-A 1000
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Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Bratt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Psegulation of represent genes using nucleic acid molecules
Patent: JP 2002541795-A 2824 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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87.5%; Pred. No. 9e+02;
tive 0; Mismatches 2; Indels
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JP 2002541795-A/3212.
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Matches 14; Conservative
        14; Conservative
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PN JP 2002541795-A/2805
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI IAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC C12N15/09, A61K38/00, A61F49/00, A61P43/00, A61P43/00, C12N5/10, PC C12P21/02, C12P21/02, A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC C12P21/02, A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
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Regulation of repressor genes using nucleic acid molecules FH
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A61K37/02,
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PF 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAWELA PAVCO, JAMES MCSWIGGEN PC CI2N15/09, AGIK438/00, AGIK48/00, AGIK48/00, AGIR48/00, AGIR48/00, AGIR48/00, PC
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Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Bregulation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 2806 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

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10-DEC-2002
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(C12N5/00,C12R1:91)
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Best Local Similarity
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PC (C12N5
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BD255013/C
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AUTHORS
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Regulation of repressor genes using nucleic acid molecules.
BD255542
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PN JP 2002541795-A/3335
PD 10-DEC-2002
PF 11-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAWELA PAVCO, JAMES MCSWIGGEN CI2NIS/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, CI2NIS/10, PC
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1 (bases 1 to 17)
Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Regulation of repressor genes using nucleic acid molecules Patent: JP 2002541795-A 3374 10-DEC-2002;
RIBOZYME PARAMACEUTICALS INC
OS Bukaryote
PN JP 2002541795-A/3374
PP 11-ARR-2000 JP 2006611654
PR 12-APR-1999 US 60/129390
                                                                                                                                                                                                                                                                                                                                                 unidentified unclassified.

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(bases 1 to 17)

Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.

Regulation of repressor genes using nucleic acid molecules Patent: JP 2002541795-A 3335 10-DEC-2002;
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Local Similarity 87.5%; Pred. No. 9e+0
nes 14; Conservative 0; Mismatches

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(C12N5/00,C12R1:91)
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JP 2002541795-A/3335.
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     1735 CAAAAAAAAAAAAA 1750
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JP 2002541795-A/3374.
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PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12P21/02, PC C12P21/02, C12P21/02, C12P21/02, C12P21/02, C12P21/02, C12P21/02, C12P21/02, C12P21/02, C12P21/02, PC C12P21/02, C1
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(C12NS/00,C12R1:91)
Regulation of repressor genes using nucleic acid molecules FH
Location/Qualifiers
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PN JP 2002541795-A/3213
PD 10-DEC-2000
PP 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI IAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/10, PC C12P21/02,
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Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Pegulation of represery genes using nucleic acid molecules Patent: JP 2002541795-A 3213 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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/organism="unidentified"
/mol_type="genomic DNA"
/do_xref="taxon:32644"
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JP 2002541795-A/3213.
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Regulation of repressor genes using nucleic acid molecules.
BD257670
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(C12P21/02,C12R1:91), (C12P21/02,C12R1:91),C12N15/00,C12N5/00,
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Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Regulation of repressor genes using nucleic acid molecules
Pactor of repressor Sylvant Construction of Sylvant Sylva
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PN JP 2002541795-A/4774
PD 10-DEC-2000
PP 11-ARR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN IC12N15/09, A61K38/00, A61K48/00, A61F43/00, A61K38/10, PC
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Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Regulation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 4774 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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    .17
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

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JP 2002541795-A/5463.
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JP 2002541795-A/4774.
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(C12N5/00,C12R1:91)
Regulation of repressor genes using nucleic acid molecules FH
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Regulation of repressor genes using nucleic acid molecules FH
Location/Qualifiers
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PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N15/10, PC C12P21/02,
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  I LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN 12N15/09, A61K38/00, A61K48/00, A61P43/00, A61L43/00, PC
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Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Batt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Pegulation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 4126 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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Location/Qualifiers
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0; Mismatches
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/db_xref="taxon:32644"

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10-DEC-2002
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BD256533.1 GI:33066303
JP 2002541795-A/4326.
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unclassified.
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PI LAWREN
C12N15/09, A
C12P21/02,
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PC (C12P2
PC A61K3
PC (C12N6
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(C12N5/00,C12R1:91)
Regulation of repressor genes using nucleic acid molecules FH Location/Qualifiers
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PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN CIZN15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, CIZNS/10, PC PC
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PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN C12N15/09, A61K38/00, A61E43/00, A61E43/00, C12N5/10, PC C12P21/02,
                                       שביטשטטט 17 bp DNA linear PAT ו Regulation of repressor genes using nucleic acid molecules.
BD258512
                                                                                                                                                                                                     MICROSITION (17)
Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Regulation of repressor genes using nucleic acid molecules
Patent: JP 200241795-A 6305 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Pageulation of repressor genes using nucleic acid molecules
Patent: JP 2012541795-A 6371 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches
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/organism="unidentified"
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10-DEC-2002
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JP 2002541795-A/6371
10-DEC-2002
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JP 2002541795-A/6305.
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(C12N5/00,C12R1:91)
Regulation of repressor genes using nucleic acid molecules FH
Regulation of repressor genes using nucleic acid molecules FH
Location/Qualifiers
                                   C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC C12R1:91),
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                                                                       (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
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PN JP 2002541795-A/5465
PD 10-DEC-2002
PF 11-APR-1999 US 60/129390
PI LAWRENCE BLATT, M.CHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN CI2NIS/09, A61K38/00, A61K48/00, A61P43/00, A61P43/10, PC
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Regulation of repressor genes using nucleic acid molecules
BD257672
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Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Bregulation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 5465 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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Location/Qualifiers
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(C12N5/00,C12R1:91)
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JP 2002541795-A/5465.
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                                              DNA
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Sequence 67 from patent US 5561041.
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                                              17 bp
                                                                      Swine serum lectin gene.
E37369
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JP 2000166569-A/6.
synthetic construct
artificial sequences.
1 (bases 1 to 17)
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C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC C12R1:91), (C12P21/02, PC C12P21/02, C12R1:91), (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), (C12N5/00, C12N5/00, C12N5/0
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(C12N5/00,C12R1:91)
Regulation of repressor genes using nucleic acid molecules FH
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PN JP 2002541795-A/6374
PD 10-DEC-2002
PF 11-APR-1200 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC C12N15/09, A61K38/00, A61K48/00, A61P43/00, C12N5/10, PC
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Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Segulation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 6374 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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/db_xref="taxon:32644"

    .17
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REFERENCE AUTHORS TITLE JOURNAL

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PAT 07-0CT-1996 PAT 31-JAN-2002 HARUYOSHI KAWASAKI C12N15/09, C07K14/47, C12P21/02//(C12N15/09, C12R1:91), C12N15/00, (C12N15/00, C12R1:91) ö ö PAT 07-0CT-1997 Gaps Gape ö ö Unclassified.

1 (bases 1 to 17)
Sidransky,D.
Nucleic acid mutation detection by analysis of.sputum
Patent: US 5561041-A 67 01-OCT-1996;
Location/Qualifiers Query Match 0.7%; Score 12.8; DB 1; Length 17; Best Local Similarity 87.5%; Pred. No. 9e+02; Matches 14; Conservative 0; Mismatches 2; Indels ce 1. .17 /organism='Artificial Sequence' Location/Qualifiers Query Match 0.7%; Score 12.8; DB 1; Length 17; Best Local Similarity 87.5%; Pred. No. 9e+02; Matches 14; Conservative 0; Mismatches 2; Indels linear linear Kawasaki, H.
Swine serum lectin gene
Patent: JP 2000166569-A 6 20-JUN-2000;
SCIENCE & TECH AGENCY
OS Artificial Sequence
PN JP 2000165569-A/6
PP 09-DEC-1998 JP 1998350283
PR HARUYOSHI KAWASAKI
PC (C12N15/00,C12R1:91)
CC (C12N15/00,C12R1:91)
CC FH Key Location/Qualifiers
FT source //organism='Artificia' RESULT 1175 154408/c LOCUS 154408 17 bp DNI DEFINITION Sequence 2149 from patent US 5646042.

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PAT 20-APR-2002

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Tables 1 to 17)

Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.

Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6346398-A 2556 12-FEB-2002;

Location/Qualifiers
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1 (bases 1 to 17)

Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.

Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6346398-A 2740 12-FEB-2002;
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0.7%; Score 12.8; DB 1; Length 17;
87.5%; Pred. No. 9e+02;
tive 0; Mismatches 2; Indels
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Sequence 2556 from patent US 6346398.
AR187068.1 GI:20233033
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Sequence 7822 from patent US 6346398.
AR192334
AR192334.1 GI:20238299
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Sequence 2740 from patent US 6346398.
AR187252
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AR187068/c
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1 (bases 1 to 17)

Sidransky, D.

Analysis of sputum by amplification and detection of mutant nucleic acid sequences
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1 (bases 1 to 17)

1 (bases 1 to 17)

2 (bases 1 to 17)

Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6346398-A 2519 12-FEB-2002;
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Unclassified.
1 (Dases 1 to 17)
Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
C-myb targeted ribozymes
Patent: US 5646042-A 2149 08-JUL-1997;
Location/Qualifiers
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87.5%; Pred. No. 9e+02;
tive 0; Mismatches 2; Indels
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Sequence 2519 from patent US 6346398.
AR187031
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Patent: US 5726019-A 67 10-MAR-1998;
Location/Qualifiers
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Sequence 67 from patent US 5726019.
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191585.1 GI:3936055
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Unclassified.
1 (bases 1 to 17)
Haugland, R. and Vesper, S.
Method of identifying and quantifying specific fungi and bacteria
Methot of S387625-A 23 14-MAY-2002;
Patent: US 6387625-A 23 14-MAY-2002;
                                                                                                                                                                                                                                                                                           Unclassified.

1 (bases 1 to 17)
Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P.Ann.Owens., Gwo.L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
Nucleic acid encoding delta-9 desaturase
Patent: US 6350934-A 882 26-FEB-2002;
Location/Qualifiers
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87.5%; Pred. No. 9e+02;
ive 0; Mismatches 2; Indels
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 Pred. No. 9e+02;
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Sequence 526 from patent US 6528640.
AR286154
                  0; Mismatches
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Seguence 23 from patent US 6387652.
AR210111
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/mol_type="unassigned DNA"
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   Best Local Similarity 87.5
Matches 14; Conservative
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                                               Unclassified.

1 (bases 1 to 17)

1 (bases 1 to 17)

Proco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.

Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6346398-A 7822 12-FEB-2002;

Location/Qualifiers
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Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6346398-A 7824 12-FEB-2002;
Location/Qualifiers
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Zwick, M.G., Edington, B.E., McSwiggen, J.A., Merlo, P. Ann. Owens., Guo, L., Skokut, T.A., Young, S.A., Polkerts, O. and Merlo, D.J. Nucleic acid encoding delta.9 desaturase
Patent: US 6350934-A 880 26-FEB-2002;
Location/Qualifiers
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Sequence 7824 from patent US 6346398.
AR192336
AR192336.1 GI:20238301
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Sequence 880 from patent US 6350934.
AR196415
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/wol_type="unassigned DNA"
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/mol_type="unassigned DNA"
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/mol_type="unassigned DNA"
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Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A., Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
Synthetic ribonucleic acids with RNAse activity
Patent: US 6528640-A 568 04 MAR-2003;
Location/Qualifiers
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Beigelman, L., Burgin, A., Beaudry, A., Karpeisky, A., Marulic-Adamic, J., Sweedler, D. and Zinnen, S.
Marulic-Intonucleic acids with RNAse activity
Patent: US 6528640-A 825 04-MAR-2003,
Location/Qualifiers
                                                                                                                         linear
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AR286196
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/mol_type="unassigned RNA"
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                  1736 AAAAAAAAAAAAA 1751
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Pred. No. 9e+02;
0; Mismatches 2; Indels
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Pred. No. 9e+02;
0; Mismatches 2; Indels
                          Dates 1 to 17)

Beigelman, L., Burgin, A., Beaudry, A., Karpeisky, A., Matulic-Adamic, J., Sweedler, D. and Zinnen, S.
Synthetic ribonucleic acids with RNAse activity
Patent: US 6528640-A 526 04-MAR-2003;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 17)
Beigolman, L., Burgin, A., Beaudry, A., Karpeisky, A., Matulio-Adamic, J., Sweedler, D. and Zinnen, S.
Synthetic ribonucleic acids with RNAse activity
Patent: US 6528640-A 558 04 MAR-2003;
Location/Qualifiers
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Beigelman, L., Burgin, A., Beaudry, A., Karpeisky, A.,
Matulio-Adamic, J., Sweedler, D. and Zinnen, S.
Synthetic Tibonuclaic acids with RNAse activity
Patent: US 6528640-A 559 04-MAR-2003;
Location/Qualifiers
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Matches 14; Conservative
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Matches 14; Conserv
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Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 656127-A 1264 20-MAY-2003;
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Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6566127-A 3566 20-MAY-2003;
Location/Qualifiers
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Sequence 3606 from patent US 6566127.
AR326204
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               16 TTTGGAAAAAAAAA
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AR326204/c
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Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 1043 20-MAY-2003;
Location/Qualifiers
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Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 1080 20-MAY-2003;
Location/Qualifiers
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87.5%; Pred. No. 9e+02;
trive 0; Mismatches 2; Indel8
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             (bases 1 to 17)
Grifantini,R., Frascotti,G., Galli,G. and Grandi,G.
Process for the production of D-.alpha.-amino acids
Patent: US 6566105-A 6 20-MAY-2003;
Location/Qualifiers
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Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches
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/mol_type="unassigned RNA"
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/organism="unknown"
/mol_type="genomic DNA"
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/organism="unknown"
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Best Local Similarity 87.5%;
Matches 14; Conservative
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Best Local Similarity 87.5
Matches 14; Conservative
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Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
Method and reagent for the treatment of diseases or conditions related to levella of vascular endothelial growth factor receptor Patent: US 6566127-A 5562 20-MAY-2003;
Location/Qualifiers
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Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 656127-A 6785 20-MAY-2003;
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Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
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Sequence 5562 from patent US 6566127.
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/organism="unknown"
/mol_type="unassigned RNA"
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/organism="unknown"
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Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 3608 20-MAY-2003;
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Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
McNod and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 5343 20-MAY-2003;
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Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
Rathod and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A $476 20-MAY-2003;
Location/Qualifiers
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87.5%; Pred. No. 9e+02;
ative 0; Mismatches 2; Indels
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87.5%; Pred. No. 9e+02;
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Pred. No. 9e+02;
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Sequence 5343 from patent US 6566127.
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/organism="unknown"
/mol_type="unassigned RNA"
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Best Local Similarity 87.5%;
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Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6566127-A 6956 20-MAY-2003;
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Mezes, P.S., Richard, R.A., Affholter, J.A. and Kotite, N.J.
Dimer and multimer forms of single chain polypeptides
Patent: US 6329507-A 89 11-DEC-2001;
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Beigelman, L., Burgin, A.B., Beaudry, A., Karpeisky, A., Matulic-Adamic, J., Swedler, D. and Zinnen, S.
Oligoribonucleotides with enzymatic activity
Patent: US 6617438-A 525 09-SEP-2003;
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87.5%; Pred. No. 9e+02;
ative 0; Mismatches 2; Indels
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Sequence 525 from patent US 6617438.
AR398144
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1 (bases 1 to 17)

Beigelman, L., Burgin, A.B., Beaudry, A., Karpeisky, A., Matulic-Adamic, J., Sweedler, D. and Zinnen, S.
Oligoribonucleotides with enzymatic activity
Patent: US 6617438-A 557 09-SEP-2003;
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Beigelman, L., Burgin, A. B., Beaudry, A., Karpeisky, A., Matulio-Adamic, J., Sweedler, D. and Zinnen, S.
Olgoribonucleotides with enzymatic activity
Patent: US 6617438-A 558 09-SEP-2003;
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1 (bases 1 to 17)

Beigelman, L., Burgin, A.B., Beaudry, A., Karpeisky, A., Matulic-Adamic, J., Sweedler, D. and Zinnen, S. Oligoribonucleotides with enzymatic activity
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Pred. No. 9e+02;
0; Mismatches
AR398176 17 bp RA
Sequence 557 from patent US 6617438.
AR398176
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Sequence 567 from patent US 6617438.
AR398186
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Sequence 558 from patent US 6617438.
AR398177.1 GI:40135776
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/mol_type="unassigned RNA"
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PAT 18-DEC-2003

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Query Match 0.7%; Score 12.8; DB 1; Length 17; Best Local Similarity 87.5%; Pred. No. 9e+02; Matches 14; Conservative 0; Mismatches 2; Indels
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                                                                                                                   Unclassified.

1 (bases 1 to 17)

Gu.Y. and Shannon, M.E.

Isoforms of human pregnancy-associated protein-E
Patent: US 6656700-A 377 02-DEC-2003;
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Gu, Y. and Shannon, M.B.
Isoforms of human pregnancy-associated protein-E
Patent: US 6656700-A 483 02-DEC-2003;
Location/Qualifiers
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Gu,Y. and Shannon,M.E.
Isoforms of human pregnancy-associated protein-E
Patent: US 6656700-A 485 02-DEC-2003;
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Sequence 485 from patent US 6656700.
AR434062
AR334062.1 GI:40196905
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Sequence 377 from patent US 6656700.
AR433954
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Beigelman, L., Burgin, A. B., Beaudry, A., Karpeisky, A., Matulic-Adamic, J., Sweedler, D. and Zinnen, S.
Oligoribomucleotides with enzymatic activity
Patent: US 6617438-A 824 09-SEP-2003;
Location/Qualifiers
                                                                                         Length 17;
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87.5%; Pred. No. 9e+02;
tive 0; Mismatches 2; Indels
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Gu,Y. and Shannon,M.E.
Isoforms of human pregnancy-associated protein-E
Patent: US 6656700-A 376 02-DEC-2003;
Location/Qualifiers
                                                                                         Query Match 0.7%; Score 12.8; DB 1; Best Local Similarity 87.5%; Pred. No. 9e+02; Matches 14; Conservative 0; Mismatches 2;
 Patent: US 6617438-A 567 09-SEP-2003;
Location/Qualifiers
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Sequence 824 from patent US 6617438.
AR398443.1 GI:40136260
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Sequence 376 from patent US 6656700.
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0159103-A 512 16-AUG-2001;
RIBOZYME HARMACEUTIALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0159103-A 513 16-AUG-2001;
RIBOSYME PHARMACEUITALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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/mol_type="unassigned RNA"
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/organism="synthetic construct"
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/db xref="taxon:32630"
/noFe="Nucleic Acid"
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Sequence 943 from Patent W00159103.
AX215501
AX215501.1 GI:15525544
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Sequence 512 from Patent W00159103.
AX215070
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Sequence 513 from Patent WO0159103.
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Immunostimulatory nucleic acids
Patent: WO 0122972-A 415 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
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Patent: WO 0159103-A 50 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US)
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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Query Match 0.7%; Score 12.8; DB 1; Length 17; Best Local Similarity 87.5%; Pred. No. 9e+02; Matches 14; Conservative 0; Mismatches 2; Indels
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/noTe="Nucleic Acid"
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/db xref="taxon:32630"
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Sequence 415 from Patent W00122972.
AX104223
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Sequence 50 from Patent WO0159103.
AX214608.1 GI:15524651
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0159103-A 2360 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)
Location/Qualifiers
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nogo gene expression
Patent: WO 0159103-A 2359 16-AUG-2001,
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US)
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
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/organism="synthetic construct"
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/note="Nucleic Acid"
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Sequence 2360 from Patent WO0159103.
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                                                                                          Blatt, L., Mcswiggen, J. and Chowrira, B.M. Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression Patent: WO 0159103-A 943 16-AUG-2001; RIBOZYME PHRAMACEUTICALS, INC. (US); Blatt, Lawrence (US); McSwiggen, James (US); Chowrira, Bharat M. (US)
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illarity 87.5%; Pred. No. 9e+02;
Conservative 0; Mismatches 2;
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/mol_type="unassigned RNA"
/mol_type="taxon:32630"
/nofe="Nucleic Acid"
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/mol_type="unassigned RNA"
/mol_type="taxon:32630"
/nofe="Nucleic Acid"
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Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
Patent: WO 0159103-A 3745 16-AUG-2001;
RIBOZYMS PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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/organism="synthetic construct"
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/noTe="Nucleic Acid"
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/db xref="taxon:32630"
/nofe="Nucleic Acid"
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0153103-A 2168 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
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Method and reagent for the modulation and diagnosis of cd20 anoso gene expression
Patent: WO 0159103-A 2417 16-AUG-2001;
RIBOZYME PHARMACUTICALS, INC. (US) ; Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
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87.5%; Pred. No. 9e+02;
/ative 0; Mismatches 2; Indels
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                                                                     Ouery Match 0.7%; Score 12.8; DB 1; Length 17; Best Local Similarity 87.5%; Pred. No. 9e+02; Matches 14; Conservative 0; Mismatches 2; Indels
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/noce="Nucleic Acid"
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Sequence 2368 from Patent WO0159103.
AX216926
AX216926.1 GI:15526987
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/noTe="Nucleic Acid"
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Matches 14; Conservative
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Best Local Similarity 87.5
Matches 14; Conservative
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AX266660
Sequence 4051 from Patent WO0173002.
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Sequence 4050 from Patent WO0173002.
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/mol_type="unassigned DNA"
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/organism="Homo sapiens"
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
Patent: WO 0173002.A 4046 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
Location/Qualifiers
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RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. Location/Qualifiers
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87.5%; Pred. No. 9e+02;
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17.5%; Pred. No. 9e+02;
.ve 0; Mismatches 2;
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/organism="synthetic construct"
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/db_xref="taxon:32630"
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AX266655
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AX266656
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              AX227355 17 bp 8
Seguence 727 from Patent WO0157206.
AX227355

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synthetic construct
artificial sequences.
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Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Kmiec,E.B., Gamper,H.B. and Rice,M.C.
Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
Patent: WO 0173002-4 4047 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
Location/Qualifiers
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Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
Patent: WO 0173002.A 4050 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
Location/Qualifiers
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Targeted chromosomal genomic alterations with modified single stranded oligonuclectides
Patent: WO 0173002-A 40-OCT-2001;
UNIVERSITY OF DELAWARE (US)
Location/Qualifiers
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SOURCE ORGANISM

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TITLE JOURNAL

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PAT 29-OCT-2001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                   Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Hamblin, P.A. and Ellis, J.H.
Method and reagent for the inhibition of grid
Patent: WO 0162911-A 710 30-AUG-2001;
RIBOZYME PHRAMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
Location/Qualifiers
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Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2;
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/organism="synthetic construct"
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/db_xrefe"taxon:32630"
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                                                                                              Sequence 710 from Patent WO0162911.
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/db_xref="taxon:9606"
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AX355726
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17 CATATTGCGGAGGCTG 2
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Best Local Similarity
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Method and reagent for the inhibition of grid
Patent: WO 162911-A 277 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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Method and reagent for the inhibition of grid
Patent: WO 0162911-A 372 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
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                                                       Query Match 0.7%; Score 12.8; DB 1; Length 17; Best Local Similarity 87.5%; Pred. No. 9e+02; Matches 14; Conservative 0; Mismatches 2; Indels
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Seguence 277 from Patent WO0162911.
AX272708
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/db_xref="taxon:9606"
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Sequence 372 from Patent WO0162911.
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AX272803.1 GI:16545540
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RESULT 1230 AX272803/c LOCUS DEFINITION

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ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

JOURNAL

TITLE

PEATURES

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PAT 18-JUN-2002

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
Patent: WO 0188124-A 1662 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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Method and reagent for the inhibition of erg
Patent: WO 0188124-A 2037 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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Method and reagent for the inhibition of erg
Patent: WO 0188124-A 2034 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (G
                                                                                                                                                       Query Match 0.7%; Score 12.8; DB 1; Length 17; Best Local Similarity 87.5%; Pred. No. 9e+02; Matches 14; Conservative 0; Mismatches 2; Indels
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                                                                                           /mol_type="unassigned RNA"
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/db_xref="taxon:9606"
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/mol_type="unassigned RNA"
/db_xref="taxon:9606"
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/organism="Homo gapiens"
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AX423698.1 GI:21527080
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                                                                             Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                  Haugland, R. and Vesper, S. detail of identifying specific fungi and bacteria batent: WO 0195612-A 3 20-DEC-2001; UNITED STATES ENVIRONMENTAL PROTECTION AGENCY (US)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Method and reagent for the inhibition of erg
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Method and reagent for the inhibition of erg
Patent: WO 0188124-A 1038 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
Location/Qualifiers
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Sequence 1662 from Patent WO0188124.
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  AX402539.1 GI:21387530
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Aspergillus niger
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human kidney tumor overexpressed membrane protein 1
Patent: WO 0224750-A 262 28-MAR-2002,
Aeomica, Inc. (US)
Location/Qualifiers
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Human kidney tumor overexpressed membrane protein
Patent: WO 0224750-A 785 28-MAR-2002;
Aeomica, Inc. (US)
Location/Qualifiers
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 17 bp 1
Sequence 262 from Patent W00224750.
AX475041.
AX475041.1 GI:22214326
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Sequence 785 from Patent W00224750.
AX475564
AX475564.1 GI:22214849
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Sequence 786 from Patent WO0224750.
AX475565
                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Homo sapiens
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AX475564/c
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Method and reagent for the inhibition of erg
Patent: WO 0188124-A 2038 22-NOV-2001,
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
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Human kidney tumor overexpressed membrane protein 1
Patent: WO 0224750-A 261 28-MAR-2002,
Aeomica, Inc. (US)
Location/Qualifiers
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       87.5%; Pred. No. 9e+02;
tive 0; Mismatches
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Sequence 2038 from Patent WO0188124.
AX423702
AX423702.1 GI:21527084
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Sequence 261 from Patent W00224750.
AX475040
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
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Best Local Similarity 87.55
Matches 14; Conservative
        Best Local Similarity 87.5
Matches 14; Conservative
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AX475040/c
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AX423702
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AX475041/c
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human testis expressed patched like protein
Fatent: EP 1229046-A 463 07-AUG-2002;
Acomica, Inc. (US)
Location/Qualifiers
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AX499157
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Sequence 463 from Patent EP1229046.
AX499156

    .17
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    /db_xref="taxon:9606"

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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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DEFINITION Sequence 646 from Patent EP1229046.
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                                     856 CCTGCAGGAAGAGAA
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AX499339/c
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                        Length 17;
Human kidney tumor overexpressed membrane protein 1 Patent: WO 0224750-A 786 28-MAR-2002; Aeomica, Inc. (US)
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Patent: EP 1229046-A 385 07-AUG-2002;
Acomica, Inc. (US)
Location/Qualifiers
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Patent: EP 1229046-A 383 07-AUG-2002;
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Sequence 383 from Patent EP1229046.
AX499076
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Sequence 385 from Patent EP1229046.
AX499078
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Location/Qualifiers
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Homo sapiens
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Aeomica, Inc. (US)
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AX531315/c
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human testis expressed patched like protein
Patent: EP 1229046-A 992 07-AUG-2002;
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Patent: EP 1229046-A 646 07-AUG-2002;
Aeomica, Inc. (US)
Location/Qualifiers
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Patent: EP 1229046-A 993 07-AUG-2002;
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Sequence 992 from Patent BP1229046.
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    .17
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AX499685.1 GI:23381978
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels
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Shannon, M.
Human posh-like protein 1
Patent: EP 1239051-A 824 11-SEP-2002;
Aeomica, Inc. (US)
Location/Qualifiers
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Patent: BP 1239051-A 823 11-SEP-2002;
Aeomica, Inc. (US)
Location/Qualifiers
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Sequence 824 from Patent BP1239051.
AX531315
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Sequence 823 from Patent EP1239051.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                           Zhang, J., Gu, Y. and Nguyen, C.T.
Human udp-galnac.polypeptide n-acetylgalatosaminyltransferase 10
Patent: EP 1243660-A 231 25-SEP-2002;
Acomica, Inc. (US)
Location/Qualifiers
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Whuman udp-galnac.polypeptide n-acetylgalatosaminyltransferase 10
Patent: EP 1243660-A 252 25-SEP-2002;
Aeomica, Inc. (US)
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Human udp-galnac:polypeptide n-acetylgalatosaminyltransferase 10
Patent: EP 1243660-A 251 25-SBP-2002;
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Sequence 251 from Patent EP1243660.

    .17
    forganism="Homo sapiens"
|mol_type="unassigned DNA"
|db_xref="taxon:9606"

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Sequence 252 from Patent BP1243660.
AX544739

    .17
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/mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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                                          Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human udp-galmac:polypeptide n-acetylgalatosaminyltransferase 10
Patent: EP 1243660-A 227 25-SEP-2002;
Aeomica, Inc. (US)
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Patent: EP 1239051-A 1508 11-SEP-2002;
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Sequence 231 from Patent EP1243660.
AX544718 1 GI:25809929
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/db_xref="taxon:9606"
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402 CCCTGCAGACAGGGG 417
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                       16 CCCTGCAGAGCGGGG 1
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Bukaryota, Metazos, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Human udp-galnac:polypeptide n-acetylgalatosaminyltransferase 10
Patent: EP 1243660-A 256 25-SEP-2002;
Aeomica, Inc. (US)
Location/Qualifiers
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Human udp-galnac:polypeptide n-acetylgalatosaminyltransferase 10
Patent: EP 1241660-A 258 25-SEP-2002;
Aeomica, Inc. (US)
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Sequence 256 from Patent EP1243660.
AX544743
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/db_xref="taxon:9606"

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Sequence 258 from Patent BP1243660.
AX544745

    1.17
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16 GGCGTTCAGGACCGC 1
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Human udp-galnac:polypeptide n-acetylgalatosaminyltransferase 10
Patent: EP 1243660-A 654 25-SEP-2002;
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Human udp-galnac:polypeptide n-acetylgalatosaminyltransferase
Patent: BF 1243660-A 653 25-SEP-2002;
Acomica, Inc. (US)
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AX547276
AX547276.1 GI:25812420
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Seguence 654 from Patent BP1243660.
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Sequence 653 from Patent EP1243660.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
Patent: WO 0211674-A 1563 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US); Syntex (U.S.A.) LLC (US)
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                                                                                                                                                                           Query Match 0.7%; Score 12.8; DB 1; Length 17; Best Local Similarity 87.5%; Pred. No. 9e+02; Matches 14; Conservative 0; Mismatches 2; Indels
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Patent: EP 1262488-A 783 04-DEC-2002;
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Human lccl-domain containing protein
Patent: EP 1262488-A 784 04-DEC-2002;
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Sequence 783 from Patent EP1262488.
AX615976
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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'organism="Homo sapiens"
                                          Thompson, James (US)
Location/Qualifiers
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Location/Qualifiers
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Homo sapiens
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                                                             FEATURES
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Method and ragent for the inhibition of calcium activated chloride channel-1 (clca-1)
Patent: WO 0211674-A 1017 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US); Syntex (U.S.A.) LLC (US);
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                     Bratzler, R.L.
Inhibition of angiogenesis by nucleic acids
Patent: WO 02053141-A 415 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                          ch 0.7%; Score 12.8; DB 1; 1 Similarity 87.5%; Pred. No. 9e+02; 14; Conservative 0; Mismatches 2;
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/mol_type="unassigned DNA"
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/noTe="Synthetic Sequence"
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Sequence 1017 from Patent WO0211674.
AX579179
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Sequence 1563 from Patent W00211674.
AX579725.
AX579725.1 GI:27648927
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Location/Qualifiers
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                      artificial sequences.
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  ORGANISM
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AUTHORS
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RESULT 1266
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REFERENCE AUTHORS

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Method and reagent for inhibiting the expression of disease related
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: EP 1273660-A 792 08-JAN-2003;
Aeomica, Inc. (US)
Location/Qualifiers
                                                                                                                RNA
                                                                                                                                                                                                                                                                                                                                                                                                            Patent: EP 1260586-A 1954 27-NOV-2002; RIBOZYME PHARMACEUTICALS, INC. (US) Location/Qualifiers
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Sequence 1954 from Patent EP1260586.
AX634815
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Sequence 792 from Patent EP1273660.
AX648952
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16 GCAAGAGGAAGAGCAG 1
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AX634815/c
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AX648952/c
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Patent: EP 1260586-A 1722 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
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RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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Sequence 1722 from Patent EP1260586.
AX634583.
AX634583.1 GI:28470197
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              Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and their use as
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Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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  Telerman, A., Amson, R. and Tuijnder, M.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Petent: EP 127360-A 793 08-JAN-2003;
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Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2;
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
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AX688740 GI:29411444
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Aeomica, Inc. (US)
Location/Qualifiers
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                                                                                        17 bp DN Sequence 1426 from Patent EP1281758. AX688694
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Sequence 1473 from Patent BP1281758.
AX688741.1 GI:29411445
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
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                                                     Query Match 0.7%; Score 12.8; DB 1; Length 17; Best Local Similarity 87.5%; Pred. No. 9e+02; Matches 14; Conservative 0; Mismatches 2; Indels
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Sequence 1425 from Patent EP1281758.
AX688693
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Sequence 1334 from Patent EP1281758.
AX688602
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AX691283
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Aeomica, Inc. (US)
Location/Qualifiers
Patent: EP 1281758-A 3287 05-FEB-2003;
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′organism≂"Homo sapiens"
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Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
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Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2;
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Aeomica, Inc. (US)
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Sequence 3286 from Patent EP1281758.
AX690554
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Sequence 3287 from Patent EP1281758.
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Sequence 5341 from Patent
AX692609
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                                                                                                                                                                                                                                                                                                               Sequence 5342 from Patent AX692610
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                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                              Aeomica,
                                                                                                                                                                        Patent: EP 1281758-A 5342 05-FEB-2003;
                                                                                                                                                                                                 Four human zinc-finger-containing proteins
                                                                                                                                                                                                              Shannon, M., Gu, Y. and Nguyen, C.T.
                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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ilarity 87.5%;
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                                                                                              /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 87.5%;
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11-4 receptor sequence variation associated with type 1 diabetes
Patent: WO 03010335-A 59 06-FEB-2003;
Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)
Location/Qualifiers
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AX723024
AX723024.1 GI:30423525
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Sequence 59 from Patent W003010335.
AX698570
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chorda
                                                                        AX723728
Sequence 1415 from Patent
AX723728
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                                                             AX723728.1
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Molecular Engines Laboratories (FR)
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                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                           GI:30503071
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Pred. No. 9e+02;
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AX724111/c
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                        Telerman,A., Amson,R. and Tuijnder,M.
Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as
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Sequences involved in phenomena of tumour suppression, tumour sequences and their use as
                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                         Mus musculus
                                                                                                                                                                       AX724397.1
                                                                                                                                                                                      Sequence 2084 from Patent AX724397
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Sequences involved in phenomena of tumour suppression,
reversion, apoptosis and/or virus resistance and their
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                                                                                                                                      Mus musculus (house mouse)
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Location/Qualifiers
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WO 03025176-A 2084 27-MAR-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="unassigned DNJ
/db_xref="taxon:1000"
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/db_xref="taxon:10090"
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87.5%; Pred. No. 9e+02;
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AX724919
                                                                                                                Telerman,A., Amson,R. and Tuijnder,M.
Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as
                                                                                                                                                                                                                                                       17 bp DNA
Sequence 2727 from Patent WO03025176.
AX725040
AX725040.1 GI:30504383
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"
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/db_xref="taxon:10000"
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/mol_type="unassigned DNA"
/db_xref="taxon:10090"
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Pred. No. 9e+02;
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Pred. No. 9e+02;
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Murinae; Mus
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AX725448
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Best Local Similarity 87.5%;
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as
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Location/Qualifiers
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CCCCTTCCAACTGATC 1
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/mol_type="unassigned DNA"
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/mol_type="unassigned DNA"
/db_xref="taxon:10090"
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Location/Qualifiers
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/mol_type="unassigned DNA"
/db_xref="taxon:10090"
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/mol_type="unassigned DNA"
/db_xref="taxon:10090"
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Sequence 1696 from Patent
AX730062
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Sequences involved in phenomena of tumour suppression, tumour
       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                        Homo sapiens
                                                    Homo sapiens (human)
                                                                                 AX730062.1 GI:30509405
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequences involved in phenomena of tumour suppression,
reversion, apoptosis and/or virus resistance and their
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Location/Qualifiers
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/db_xref="taxon:9606"
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/db_xref="taxon:10090"
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Pred. No. 9e+02;
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                                                                              Telerman,A., Amson,R. and Tuijnder,M. Sequences involved in phenomena of tumour suppression, tumour
                                                                                                                                                                Homo sapiens (human)
Homo sapiens
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Sequence 2259 from Patent
AX730625
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Sequence 1748 from Patent W003025175.
AX730114
AX730114.1 GI:30509457
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Sequences involved in phenomena of tumour suppression, tumor reversion, apoptosis and/or virus resistance and their use
Molecular Engines Laboratories (FR)
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                 Patent: WO 03025175-A 2259 27-MAR-2003;
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                                                             reversion, apoptosis and/or virus resistance
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="unassigned DNA"
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/db_xref="taxon:9606"
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Pred. No. 9e+02;
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AX731554
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AX731099/c
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14; Conserv
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Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as
                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequences involved in phenomena of tumour suppression, tumour sequences involved and/or virus resistance and their use as
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                                                                                                  Patent: WO 03025175-A 3188 27-MAR-2003,
Molecular Engines Laboratories (FR)
Location/Qualifiers
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Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                         /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
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AX731963/c
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AX731857
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Best Local Similarity 87.5%;
Matches 14; Conservative
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17 CCCCTACACAGTAGAT 2
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Sequences involved in phenomena of tumour suppression, tume reversion, apoptosis and/or virus resistance and their use
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Sequence 3491 from Patent
AX731857
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                      h 0.7%; Score 12.8; DB 1; Similarity 87.5%; Pred. No. 9e+02;
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                                                                                                                /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 87.5%;
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            AX737293
Sequence 2883 from Patent
AX737293
AX737293.1 GI:30516581
                                                                                                                                                                                                                                                                                                                                     Telerman,A., Amson,R. and Tuijnder,M.
Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments Patent: WO 03025177-A 1697 27-MAR-2003; Molecular Engines Laboratories (FR)
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Patent: WO 03025177-A 1469 27-MAR-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AX736107
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Location/Qualifiers
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                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Pred. No. 9e+02;
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Pred. No. 96
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RESULT 1310
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AX737445
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                                                                         Homo sapiens
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Patent: WO 03025177-A 3035 27-MAR-2003;
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Patent: WO 03025177-A 2883 27-MAR-2003;
                                                                                                                                    Sequence 4203 from Patent AX738613
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Sequence 3035 from Patent
AX737445
AX737445.1 GI:30516733
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Telerman, A.,
Sequences in
                                                                                        Homo sapiens
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                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DN:
/db_xref="taxon:9606"
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87.5%; Pred. No. 9e+02;
                                                                                          (human)
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Pred. No. 9e+02;
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 and Tuijnder, M. phenomena of tu
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AX744200
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Best Local Similarity 87.5%;
Matches 14; Conservative
Query Match
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Best Local Similarity
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                                                                                      A human G protein coupled receptor
Patent: WO 03031621-A 166 17-APR-2003;
Amersham Blosciences (SV) Corp. (US)
Location/Qualifiers
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Sequence 166 from Patent WO03031621.
AX744201
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Patent: WO 03031621-A 165 17-APR-2003;
Amersham Biosciences (SV) Corp. (US)
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 03025177-A 4203 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                             Homo sapiens
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llarity 87.5%;
Conservative (
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                           /organism="Homo sapiens"
/mol_type="genomic DNA"
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Pred. No. 9e+02;
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Pred. No. 9e+02;
 Score 12.8;
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AX745047
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Matches 14; Conservative
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A human G protein coupled receptor
Patent: WO 03031621-A 1012 17-APR-2003;
Amersham Biosciences (SV) Corp. (US)
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                     A human G protein coupled receptor Patent: WO 03031621-A 1013 17-APR-2003; Amersham Biosciences (SV) Corp. (US)
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Sequence 1012 from Patent
AX745047
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 AX757940
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Similarity 87.5%;
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Similarity 87.5%; Pred. No. 9e+
14; Conservative 0; Mismatches
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                                                                                                                     Conservative
                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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tive 0; Mismatches
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Pred. No. 9e+02;
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AX759934
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Sequences involved in tumoral suppression, tumoral reversion,
Sequences involved in temporal suppression, tumoral reversion,
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa;
                                                                          AX783890
Sequence 2221 from Patent
AX783890
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AX757940
AX757940.1 GI:32252556
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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                                                               AX783890.1
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae,
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Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
 Metazoa; Chordata; Craniata; Vertebrata;
                                                              GI:32951739
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Pred. No. 9e+02;
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Best Local Similarity 87.5%;
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Location/Qualifiers
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Sequence 2222 from Patent
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AX783891.1 GI:32951740
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                                                                       Human prostate cancer candidate protein 1 Patent: WO 03050284-A 2411 19-JUN-2003; Amersham Biosciences (SV) Corp. (US)
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Homo sapiens
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Location/Qualifiers
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                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
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Local Similarity 87.5%;
hes 14; Conservative (
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14; Conserv
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Patent: WO 0192572-A 1055 06-DEC-2001;
NISSHINBO INDUSTRIES INC.YSTEM RESEARCH INC,HIDETOSHI INOKO, TI
KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
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synthetic construct
artificial sequences.
1 (bases 1 to 17)
1 (bases 1 to 17)
1 (noko/1., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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WO 0192572-A/1055.
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                                                                                                                    SHOGO MORIYA, MICHIO NISHIDA
C12Q1/68, C12M1/00, C12N15/09, G01N33/53
Description of Artificial Sequence: capture
                                                                                                                                                                                                                                      Artificial Sequence
WO 0192572-A/1055
WO 0192572-A/1055
06-DEC-2001
01-JUN-2001 WO 2001JP004662
01-JUN-2000 JP 00P 164798
HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI
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/organism='Artificial Sequence'
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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87.5%;
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Pred. No. 9e+02;
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RESULT 1322
BD134134
LOCUS
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ACCESSION
VERSION
KEYWORDS
SOURCE
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BD200584
LOCUS
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VERSION
KEYWORDS
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Matches 14
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PF 26-FEB-1999 JP 2000533017

PF 27-FEB-1998 US 66/076325

PI COTTEYA GEORGOPORAS, BLUCE A MORGAN, CLARE KELLY PC

C12N15/09,A01K67/027,A61K31/711,A61K38/00,A61K48/00,A61P35/02, PC

A61P37/02,

PC C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/17

PC C12N15/00,A61K37/02,C12N5/00

PC C12N15/00,A61K37/02,C12N5/00

FT Key

FT Source
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                                                                                                                                                                                                                                                                                                                                                                 source
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                                           molecule participating 1.
BD200584
BD200584.1 GI:33010354
JP 2002509721-A/3610.
Homo sapiens (human)
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                                                                                                       BD200584 17 bp RNA linear PAT 17-JUL-20. Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response.
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Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 17)
                                        Homo sapiens
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 17)
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BD134134
BD134134.1 GI:23229079
JP 2002504357-A/4.
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/mol_type="genomic DNA
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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87.5%; Pred. No. 9e+
tive 0; Mismatches
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             Chordata;
Primates;
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             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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BD201657/c
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TITLE
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Best Local :
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1 (Dases 1 to 17)

Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J.A. Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response patent; JP 2002509721-A 4683 02-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. & Method and reagent for treating diseases or con molecule participating in vasculogenic response Patent: JP 2002509721-A 3610 02-APR-2002; RIBOZYME PHARMACEUTICALS INC
걸표C
                                                                                                                                             C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00,
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PD
PF
PR
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Similarity 87.5%;
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                                                                                                          A61P35/00, A61P43/00, C12N5/10, C12N9/00//A61K35/76, C12N15/00,
                                                                    Method and reagent for treating diseases
                                   participating in vasculogenic response
                                                                                                                                                                                               02-APR-2002
24-MAR-1999 JP 2000541291
27-MAR-1998 US 60/079678
PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
                                                                                                                                                                                                                                                                                   Homo sapiens (human) JP 2002509721-A/4683
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PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT, JAMES A MCSWIGGEN
                                                                                                                                                                                         JAMES A MCSWIGGEN
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27-MAR-1998 US 60/079678
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                                                       concerning molecule
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/mol_type="genomic RNA"
/db_xref="taxon:9606"
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               Location/Qualifiers
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AUTHORS

Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswigg
TITLE

Method and reagent for treating diseases or conditions conc
molecule participating in vasculogenic response
Patent: JP 2002509721-A 5818
PN UP 2002509721-A/5818
PD 02-APR-2002
PP 24-MAR-1999 JP 20^PP 24-MAR-1999 JP 20^PP PR 27-MAR-1999 JP 
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17 bp RNA linear PAT 17-JUL-201 Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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nilarity 87.5%;
Conservative
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27-MAR-1998 US 60/079678
PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
JAMES A MCSWIGGEN
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/mol_type="genomic RNA"
/db_xref="taxon:9606"
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/mol_type="genomic RNA"
/db_xref="taxon:9606"
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Pred. No. 9e+02;
0; Mismatches 2;
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RESULT 1327
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                                                                                                                                                         Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J.A. Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response Patent: JP 2002509721-A 5923 02-APR-2002; RIBOZYME PHARMACEUTICALS INC
                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 17)
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1 (bases 1 to 17)

Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J.A. Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response Patent: JP 2002509721-A 5922 02-APR-2002;

RIBOZYME PHARMACEUTICALS INC
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JP 2002509721-A/5922.
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C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06,
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                                  JAMES A MCSWIGGEN
                                               24-MAR-1999 JP 2000541291
27-MAR-1998 US 60/079678
PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
                                                                                                                           Homo sapiens (human) 
JP 2002509721-A/5923
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Key Location/Qualifiers
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57-MAR-1998 US 60/079678
PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
JAMES A MCSWIGGEN
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/mol_type="genomic RNA"
/db_xref="taxon:9606"
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1734 ACAMAMAMAMAMA 1749
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1 (Dases 1 to 17)

Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J.A. Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response molecule participating in vasculogenic response Patent; JP 2002509721-A 6032 02-APR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.7%;
Similarity 87.5%;
                                                  Similarity
                                                                                                                                                                                                                                                                                      C12N5/00
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                                                                                                                                                                                                                                                                                                     A61P35/00, A61P43/00, C12N5/10, C12N9/00//A61K35/76, C12N15/00,
                                                                                                                                                                                                                                                                                                                                                                  24-MAR-1999 JP 2000541291
27-MAR-1998 US 60/079678
PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
JAMES A MCSWIGGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             participating in vasculogenic response Key Location/Qualifiers
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                                                                                                                                                                                                                    participating in vasculogenic response
Key Location/Qualifiers
                                                                                                                                                                                                                                                                    Method and reagent for treating diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                      JP 2002509721-A/6032
02-APR-2002
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                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
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                                                                                                                                                                                                                                                     concerning
                                                                                               /organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"
                                                                                                                                                              /organism='Homo
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/mol_type="genomic RNA"
/db_xref="taxon:9606"
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                                                  0.7%;
                                                                                                                                                                                                                                                      molecule
                                 Score 12.8; DB 1;
Pred. No. 9e+02;
0; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in vasculogenic response.
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                                                                                                                                                                                    sapiens (human)'.
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RESULT 1330
BD203246/c
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AUTHORS
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ORGANISM
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KEYWORDS
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BD203175
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Best Local Similarity
Matches 14; Conserv
                                                                                                                        TITLE
                                                                                  JOURNAL
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PC A61P35
C12N5/00
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 17)
Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J.A.
Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response
Patent: JP 2002509721-A 6272 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002509721-A/6272
PD 02-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J.A.

Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response
Patent: JP 2002509721-A 6201 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002509721-A/6201
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT
PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT
                                                                                                                                                                                                                                                                                                               Method and reagent for molecule participating
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                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                           JP 2002509721-A/6272.
                                                                                                                                                                                                                                                                           BD203246.1 GI:33013016
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Key Location/Qualifiers
source 1...17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-MAR-1999 JP 2000541291
27-MAR-1998 US 60/079678
PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.7%; Score 12.8; DB
87.5%; Pred. No. 9e+02;
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                                                       Query Match
Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                 OS Synthetic construct
PN JP 2002514903-A/12
PD 21-MAY-2002
PF 16-JAN 1997 JP 1998502904
PF 17-JUN-1996 US 08/65259,01-OCT-1996 US 08/720614 PR
09-DEC-1996 US 08/65259,01-OCT-1996 US 08/720614 PR
09-DEC-1996 US 08/762500
PI GREGORY M LANDES, TIMOTHY C BURN, TIMOTHY D CONNORS, WILLIAM R
PI TERENCE J VAN RAAY, KATHERINE W KLINGER
PC C12N15/12,C12N15/85,C07K14/47,C07K14/475,C07K16/18,A01K67/027
PC Oligonucleotide Primer
CC Oligonucleotide Primer
FT source 1..17
FT source 1..17
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1241 GCTGCTTCACCTGCGT 1256
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Novel human chromosome 16
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C12N5/00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      landes, G.M., Burn, T.C., Connors, T.D., Dackowski, W.R., Raay, T.J.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            artificial sequences.
1 (bases 1 to 17)
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nilarity 87.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            TERENCE J VAN RAAY, KATHERINE W KLINGER C12N15/12, C12N15/85, C07K14/47, C07K14/475, C07K16/18, A01K67/027
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27-MAR-1998 US 60/079678
PAMELA A PAYCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE
                                                          Conservative
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                                                                                                                                                                                                                                                                                                /organism='Synthetic Location/Qualifiers
                                                                                                                                                                           /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/mol_type="genomic RNA"
/db_xref="taxon:9606"
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Patent: JP 2002514903-A 25 21-MAY-2002;
GENZYME CORP
OS Synthetic construct
PN JP 2002514903-A/25
PD 21-MAY-2002
PF 16-JAN-1997 JP 1998502904
PR 17-JUN-1996 US 08/665259,01-OCT-15
O9-DEC-1996 US 08/762500
PI GREGORY M LANDES, TIMOTHY C BURN, TIMOT
PI DACKOWSKI,
PI TERENCE J VAN RAAY, KATHERINE W KLINGE
PC C12N15/12,C12N15/85,C07K14/47,C07K14/
CC Oligonucleotide Primer
FH Key LOCAL STANDER SONTEN CONTROLOGUE
FT SOURCE J VAN GRANGE STANDER SONTEN CONTROLOGUE
PO C12N15/12,C12N15/85,C07K14/47,C07K14/
CC Oligonucleotide Primer
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Sequence 658 from Patent WO0244994.
AX598384
                                                                                                                                   Brower, A., Brow, M.A., Cracauer, R.F., Fore, L., Granske, R., de arruda Indig, M., Kurensky, D., Luedtke, C., Lukowiak, A.A., Lyamichev, V., Neri, B.P., Reimer, N.D., Roeven, R.T., Skrzypczynski, Z., Ziarno, W.A., Comerford, J., Stump, S. and Viegut, D.D. Skrzypczynski, Z., Ziarno, W.A., Systems and method for detection assay production and sale Patent: WO 024494-A 658 06-UUN-2002; THIRD WAVE TECHNOLOGIES, INC. (US)
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synthetic construct
artificial sequences.
1 (bases 1 to 17)
1 (bases 1, to 17)
1 (bases 3, Burn, T.C., Connors, T.D., Dackowski, W.R., Raay, T.J.V.
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TERENCE J VAN RAAY, KATHERINE W KLINGER
C12N15/12,C12N15/85,C07K14/47,C07K14/475,C07K16/18,A01K67/027
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                   Location/Qualifiers
organism="synthetic construct"/mol_type="unassigned DNA"
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Pred. No. 9e+02;
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Search completed: August 16, 2004, 15:19:39
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                                                                                                                                                                                                                                                                              Method and reagent for the inhibition of erg Patent: WO 0188124-A 838 22-NOV-2001; RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED
                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AX422502 17 bp
Sequence 838 from Patent WO0188124.
AX422502
                                                                                                                                                                                                                                                                                                                              Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Mclaughlin,F.G. and Randi,A.M.
                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
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Similarity 92.9%; Pred. No. 9.4e+02;
13; Conservative 0; Mismatches 1
                                                                                                                                             0.7%;
Similarity 92.9%;
                                                                                                                               Conservative
                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"
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Pred. No. 1e+03;
0; Mismatches 1;
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Bovine viral diarr Human saig63 PCR/s Nucleoride sequenc Murine SCGE 5'-RAC Coxsackte B virus 2',5'-linked tetra	oligomer IL6803 fo Oligomer IL6804 fo Cleavage of nuclei	Cleavage of nucles Human MSH2 (hWSH2) POLYA, a competito Nucleotide sequenc	pBluescriptSK+ pha	Immunostimulatory	Immunostimulatory Human prostate exp	Angiogenesis inhib Angiogenesis inhib	Immunostimulatory A24 oligonucleotid Human phosphatidyl	A24 oligonucleotid RNA-PCR procedure	Gastric ulcer trea	Immunostimulatory Oligo (dT)24 RT-PC Immunostimulatory	Immunostimulatory	mRNA poly A. Unid	Immunostimulatory Immunostimulatory Imminostimulatory	Butterfly biliverd	Kolling circle amp Oligonucleotide bi	PCR primer for hum Rapid capture prob	Capture probe CP12	Example oligonucle	Oligonucleotide of	Sequence of scissi Sequence of scissi	SS probe MRCO59.	CDNA library produ	Scaffold oligonucl	Human zalphall Lig Primer #2 used to	LS147-specific pol	Oligodeoxynucleic Oligo (dT) primer	Sequence of scissi	Sequence of scissi SS probe MRCO46.	SS probe MRCO71.	DNA sequence used M. tuberculosis rp	Immunostimulatory	Anglogenebis innib Immunostimulatory	Human androgen rec Human ARCAP associ
1 AAD55692 1 ABX93598 1 ACF36382 1 ABX12469 1 ABX12469 1 AAQ64724	1 AAQ30430 1 AAQ30431 1 AAC62450	1 AAC62451 1 ABL01773 1 AAT99286 1 AAV31743	1 AAA40359 1 AAA40359 1 AAA40353	1 AAF99756	1 AAF99757 1 ABV14842 1 ABS78477	1 ABS77949 1 ABS78478	1 ABL39405 1 ABA98840 1 AAI66361	1 AAS17869 1 ABK15639	1 ACA58802	1 ABZ80181 1 ACA62284 1 ACD99729	1 ACH03285	1 ADA66379	1 ADB3/258 1 ADB36806 1 ADB37259					1 ABK49986			1 AAN92241 1 AAN92242			1 AAS20672		1 ABZ24784 1 ACA62282		1 AAN70274 1 AAN92240	AAN9224	1 AAQ40854 1 AAZ43904			1 ABS53863 1 ABS54324
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compun nucleic search, using sw model	August 16, 2004, 15:23:23 ; Search (withou	us-10-008-789-3 1755 1 cgcccgggcaggtcccaaaa	e: IDENTITY_NUC Gapop 10.0 , Gapext 0.5	1487 segs, 28657 residues	of hits satisfying chosen parameters:	seq length: 8 seq length: 50	: Minimum Match Maximum Match		rngdb:*	No. is the number of results predicted by greater than or equal to the score of the derived by analysis of the total score d	STIMMARTES		dueiy re Match Length DB ID	1.5 27 1	1.3 23 1	1.3 24 1	1.3 28 1	1.2	1.2 25 1	1.2 26 1	1.2 26 1	1.2	1.2 24 1	1.2 21 1	1.2 25 1	1.2 25 1	1.2 25 1	1.2 26 1	1.2 26 1	1.2 26 1	1.2 28 1	1.2 24 1	.6 1.2 26 1 ABS52637 .6 1.2 26 1 AAD45054
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Vaccinia virus thy TK gene specific f Hereditary haemoch Antisense primer f Mouse flt-1 VEGF r Vaccinia virus thy Clonotypic IgH CDR Forward PCR Primer	Secretory peptide Oligonucleotide d Antisense PCR pri PCR primer Mk17 u	Antifense oligonu Antisense oligonu Heltest4 cleavage	Shrimp white spot Grand fir monoter	Sample origonucle Cleavage product	DNA probe #22 for Human tumour supp	End-labelled probe Siglec-BMS, PCR pr	Siglec-BMS, PCK po Cleavage product	Synthetic DNA sell	Vaccinia virus TK	Human humanin CDNA Waccinia virus thv	Beer spoilage-asso Human ORIG1 gene n	Human GSR allele 6 ASO primer #4 to d	Human CDK4 gene po HIV-1 proviral DNP	Uligomucieotue se Human MIF gene D5k IGFBP3 oligonucleo	IGF-I oligonucleot IGFBP2 oligonucleo	IGFBP3 oligonuclec	IGFBP3 oligonucled IGFBP3 oligonucled	Nucleotide sequen	Triple helix form	Nucleic acid cloni	Single-base misma	Purine rich HIV to Cryptosporidium po	Forward primer #66 Molecular beacon t	Human Ghrelin ant	septoria tritici	Plasmodium raicipa Human c-myb hammer	Bumper primer 2 fo Human flt1 VEGF re	Human flt1 VEGF re Human flt1 VEGF re	toria	Integrin subunit 1 HIV gag bumper pr:
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	.8 17 1 AAX63006 .8 17 1 AAA20382 .8 17 1 AAA20383 .8 17 1 AAAA8867	.8 17 1 AAA36380 .8 17 1 AAA36382 .8 17 1 AAZ44068	.8 17 1 AAA25445 .8 17 1 AAA25182 . 17 1 AAA35182	.8 17 1 AAA25180 .8 17 1 AAA25181	.8 17 1 AAF02549 .8 17 1 AAF06382	.8 17 1 AAF06381 .8 17 1 AAF03345	.8 17 1 AAF03382 .8 17 1 AAF03473	.8 17 1 AACGZGS	.8 17 1 ABK013/5 .8 17 1 ABK02358	.8 17 1 ABK02357 .8 17 1 ABK02344 8 17 1 ABK0347	.8 17 1 ABL46642 .8 17 1 ABL46642	.8 17 1 ABL46643 .8 17 1 ABL46459	.8 17 1 ABL46888 .8 17 1 AAC89333	.8 17 1 ABN10512 .8 17 1 ABN00987 .8 17 1 ABN00904	.8 17 1 ABN10513 .8 17 1 ABN10514	.8 17 1 ABN10030 .8 17 1 ABN10510	.8 17 1 AAD33183 .8 17 1 ABV85236	.8 17 1 ABV85237	.8 17 1 ABV95264 .8 17 1 ABV79401	.8 17 1 ABK18613	.8 17 1 ABK18192	.8 17 1 ABS74958 .8 17 1 ABV90794	.8 17 1 ACC59531 .8 17 1 ABO80178	.8 17 1 ABT36841	.8 17 1 ADB00093 Human	.8 17 1 ABZ64549 Huma .8 17 1 ABZ61439 Huma	.8 17 1 ABZ61374 .8 17 1 ABZ65369	.8 17 1 ACD62029 .8 17 1 ACD62960	.8 17 1 ACD56960 .8 17 1 ACC68140	.8 17 1 ADD42044 .8 18 1 AAN97167
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The simple and searches a novel genetically modified glucocofficions and is transactivation deficient. The invention also describes (1) a gene construct comprising at least a nucleic acid encoding the glucocorticoid receptor, operably linked with regulatory sequences of a reporter gene, preferably a DNA-binding domain for a reporter gene; (2) identifying a gene encoding a cofactor involved in glucocorticoid receptor modulation of at least another transcription factor comprising; (a) using the above construct with an expression bank of a eukaryotic cell expressed in a yeast two hybrid system; (b) detecting a specific protein-protein complex control exceptor and a cofactor through growth in a selective medium for the reporter and (c) isolating and characterising the nucleic acid characteristic for the glucocorticoid receptor with a cofactor in the cDNA clone; (3) a cofactor with control exceptors are bound; (4) identifying an agent which affects the reciprocal effect of the glucocorticoid receptor with other transcription achieves a reciprocal effect of the glucocorticoid receptor with other transcription factors and/or cofactors, whereby the receptor with other transcription creciprocal effect of the glucocorticoid receptor or construct is contacted with a potential agent and modulation of the interaction of the protein complex binding; (5) an agent for modulating interaction of the glucocorticoid receptor with a cofactor which binds either at the binding site of a physical lormone or at a separate binding place or detecting and (6) a compound with an inflammation-inhibiting or immunosuppressive receptors are used constructed receptors is used transcription or is useful to identify coreceptors when transmined the construction of effect comprising the above agent. The genetically modified the provence of the response or at a separate binding place of a physical permentation of the interaction of effect comprising the above agent. The genetically receptor is used transcriptors where the parament of the provence or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to produce an inflammation-inhibiting or immunosuppressive treatment.
This sequence represents a PCR primer #198rev used to amplify a Renilla reniformis luciferase gene which is then cloned into a reporter construct behind a ubiquitin promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A genetically modified glucocorticoid receptor which is transactivation deficient is used to identify cofactors which will be useful to provide inflammation-inhibiting and immunosuppressive treatment.
                                                                                                                                                                                                                                                            Luciferase, ubiquitin promoter, glucocorticoid receptor, PCR; primer, transrepression protein-protein reciprocal effect; immunosuppressive, transactivation deficient inflammation; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel genetically modified glucocorticoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Boettlicher M, Heilbock C, Herrlich P, Litfin M, Schneider S;
                                                                                                                                                                                                                    Renilla luciferase associated PCR primer #198rev.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GESL ) FORSCHUNGSZENTRUM KARLSRUHE GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Col 12; 12pp; German.
                                                             ABX94934 standard; DNA; 27 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAY-2002; 2002DE-01022714.
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                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                        Renilla reniformis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JAN-2003.
                                                                                                                                                              25-AUG-2003
                                                                                                              ABX94934;
                                     ABX94934/c
RESULT
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Sequence 27 BP; 5 A; 6 C; 11 G; 5 T; 0 U; 0 Other;
Query Match
Best Local Similarity 100.0%; Pred. No. 23;

ALIGNMENTS

1046 TTGATCGCGTCTTTCACGTGGGC 1068

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Gaps

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Mon Aug 16 16:46:36 2004

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The invention relates to antisense compounds targetted to a nucleic acid encoding thyroid hormone receptor interactor 6 (TRIE6) to inhibit its expression. TRIP6 is also known as OPA-interacting protein-1 (OID-1) and zyxin-related protein-1 (CRP-1). TRIP6 DNA is located on chromosome 7q22. Antisense compounds of the invention are useful for modulating the expression of TRIP6 and for treating diseases or conditions associated with the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as research reagents and kits and in distinguishing between functions of various amembers of a biological pathway. The are also useful in antisense therapy. The present sequence is human TRIP6 DNA specific PCR probe, used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.
                                                                                                                                                                                                                                                                         Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour; OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis; inflammation; therapy; hyperproliferative disorder; infection; cancer; chromosome 7q22; ZRP-1; PCR; probe; ss.
Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 23 BP; 2 A; 6 C; 7 G; 8 T; 0 U; 0 Other;
Mismatches
                                1567 GCCACCGTCACCACTGACTGCTGAGTC 1593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mod_base= OTHER
/note= "TAMRA labelled"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /mod_base= OTHER
/note= "FAM labelled"
                                                               27 GCCACCGTCACCACTGACTGAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 13; Page 74; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                              Human TRIP6 DNA specific PCR probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          base= OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-NOV-2002; 2002WO-US035479
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                                                                                                                                               ACC82883 standard; DNA; 23
                                                                                                                                                                                                               (first entry)
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Best Local Similarity 100...
Loca 23; Conservative
27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bennett CF, Dobie K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-430662/40.
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                                                                                                                                                                                                                                                                                                                                                                                                             modified base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified_base
                                                                                                                                                                                                              27-AUG-2003
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-MAY-2003
                                                                                                                                                                               ACC82883;
Matches
                                                                                                              RESULT 2
                                                                                                                               ACC82883
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The invention relates to systems for identification and characterisation of gene expression in one or more samples, comprising an identimer having a specific oligo-dr primer sequence, where the identimer comprises a detectable marker at its 5' end. The system is useful for identifying any correctable marker at its 5' end. The system is useful for identifying any correctable marker at its 5' end. The system is useful for identifying any set the relative differences in mRNA between 2 or more sample, as well as the relative difference in mRNA between 2 or more samples. Where the desired, for supporting discovery of new genes, and for identifying mRNA system or method addresses limitations of prior methods by comprising compositions and systems that incorporate new strategies where molecular compositions and systems that incorporate new strategies where molecular expression. The system has the following advantages over existing expression. The system has the following advantages over existing nethods: (a) prior sequence information or clone library construction is not needed to enable the assay; (b) provides immediate sequence information in addition to information construction divides in mRNA level, to determine mRNA expression level and mRNA identification in many assay; (c) generates cDNA fragment from all mRNAs present in the sample for subsequent investigation by common molecular biology techniques; and (d) does not require prior knowledge of the sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organisms lacking significant genomic sequence in formation. The present sequence represents an oligo dT primer used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying and characterizing gene expression in samples, for identifying mRNAs expressed at different levels, comprises employing an identimer having a oligo-dT primer of a specific sequence and a detectable marker at its 5 end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the organism under investigation and can be employed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 24;
                                                                                                                                           Oligo dT primer #2 used in method to study gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                     Oligo dT primer; gene expression analysis; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24 BP; 20 A; 0 C; 1 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.3%; Score 22.4; D
95.8%; Pred. No. 87;
tve 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1730 GTTTACAAAAAAAAAAAAAAAAA 1753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nagel AC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 11; 45pp; English.
                 ABK86169 standard; DNA; 24 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                              GENO-) GENOMIC SOLUTIONS INC
                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-2000; 2000US-0244933P.
                                                                                                                                                                                                                                                                                                                                                          01-NOV-2001; 2001WO-US045401.
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                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kane MD, Dombkowski AA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-508123/54.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the genome of
                                                                                                   24-SEP-2002
                                                                                                                                                                                                                                                                                                                  10-MAY-2002
                                                                                                                                                                                                                                 Synthetic
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Matches
ABK86169
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Gaps

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1.3%; Score 23; DB 1; Length 23; 100.0%; Pred. No. 69; tive 0; Mismatches 0; Indels

a specific oligo-dr primer sequence, where the identimer comprises a specific oligo-dr primer sequence, where the identimer comprises a detectable marker at its 5' end. The system is useful for identifying any or all genes expressed in a given in vivo or in vitro RNA sample, as well as the relative differences in mRNA between 2 or more samples, where that are expressed at different levels between 2 or more samples, where that are expressed at different levels between 2 or more samples. The new system or method addresses limitations of prior methods by comprising compositions and systems are linked to DNA or RNA sequence databases for optimal resource efficiency in assaying gene compositions and systems and systems are linked to DNA or RNA sequence databases for optimal resource efficiency in assaying gene corpression. The system has the following advantages over existing methods: (a) prior sequence information or clone library construction is not needed to enable the assay; (b) provides immediate sequence information in addition to information concerning changes or differences in many level, to determine mRNA expression level and mRNA identification in one assay; (c) generates CDNA expression level and mRNA identification in many level, to determine mRNA expression level and mRNA identification in earlier sequence in formation in determine mRNA expression level and mRNA identification conforming addition and can be employed in companies and (d) does not require prior knowledge of the sequence of the genome of the organism under investigation and can be employed in companies. The invention relates to systems for identification and characterisation Identifying and characterizing gene expression in samples, for identifying mRNAs expressed at different levels, comprises employing an identimer having a oligo-dT primer of a specific sequence and a detectable marker at its 5' end. sequence represents an oligo dT primer used in the method of the Oligo dT primer #1 used in method to study gene expression. Oligo dT primer; gene expression analysis; primer; ss 1 GTTTAAAAAAAAAAAAAAAAAA 24 Disclosure; Page 11; 45pp; English. Dombkowski AA, Nagel AC; (GENO-) GENOMIC SOLUTIONS INC. ABK86168 standard; DNA; 24 BP 01-NOV-2000; 2000US-0244933P. 01-NOV-2001; 2001WO-US045401. 24-SEP-2002 (first entry) WPI; 2002-508123/54. WO200236828-A2 10-MAY-2002 Synthetic invention ABK86168; Kane MD, 

ö DB 1; Length 24; 1; Indels Sequence 24 BP; 3 A; 1 C; 0 G; 20 T; 0 U; 0 Other; Score 22.4; DB Pred. No. 87; 0; Mismatches 1730 GTTTACAAAAAAAAAAAAAAA 1753 1.3%; 23; Conservative Local Similarity Query Match Matches

GTTTAAAAAAAAAAAAAAAA 1

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Normalised, cDNA library, mRNA cloning, reverse transcription, immobilise, screening, hybridisation, nucleic acid amplification, expression pattern, drug development, PCR primer, RT-PCR; ss. (DISP-) DISPLAY SYSTEMS BIOTECH APS. Anchored poly T RT-PCR primer. AAV71935 standard; DNA; 27 BP 98WO-DK000186. 97DK-00000547. 97US-00871030. 98DK-00000432. (first entry) WO9851789-A2 13-MAY-1998; 13-MAY-1997; 19-MAY-1997; 27-MAR-1998; 18-FEB-1999 19-NOV-1998 Warthoe PR; Synthetic. AAV71935; 

reverse transcription and amplification, used to screen for new genes and interacting proteins, potential drugs, and for diagnosis. Preparation of normalised, subdivided cDNA libraries from mRNA - by WPI; 1999-009772/01.

Example 1; Page 29; 71pp; English.

The invention relates to preparation of a normalised, subdivided library of amplified cDNA from the coding regions of mRNA in a sample. The method involves reverse transcription, with at least one cDNA primer of formula 5'-Conl-dTn2-Vn3-Nn4 to form first strand cDNA where COnl = any sequence of 1-100 nucleotides; of = deoxythymidiny!; n2 is at least 1; n3 and n4 are both 0, or n3 is 1 and n4 is at least 1; followed by second strand cDNA synthesis using the first strand as template and a second cDNA primers Comparation of Gouble-stranded by second cDNA primers of as similar formula, in the presence of DNA polymerase I (or its Klenow fragment) and amplification of Gouble-stranded cDNA with a set of antendase (a computer-generated list of molecular weights of restricted DNA fragments of known sequence) is used to determine presence of an carpassed protein in a cell, also to detect changes in such expression (particularly for diagnosis of disease). Surfaces (chip) having amplified condition the presence of an careen for genes of a particular family, by hybridisation with nucleic acid from the family (to identify new genes) and to detect differences in expression patterns between cells. The polypeptides expressed by the libraries can be used for dray development. Sequences by the libraries can be used for drug development. Sequences AAV11935 to AAV71946 represent primers used to exemplify the method of the invention

1.3%; Score 22.4; DB 1; Length 27; 95.8%; Pred. No. 96; 1; Indels 0; Mismatches 23; Conservative Similarity Query Match Local Matches

Sequence 27 BP; 2 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

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Gaps

RESULT

us10008789-3.rng

is created from the inforamtion given on page 11

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SXS
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The method comprises providing a nucleic acid sequence which is initially catalytically inactive, but which becomes catalytically antitive in the effector); providing a nucleic acid substrate for presence of an analyte (the effector); providing a nucleic acid substrate for the catalytic activity of the nucleic acid sequence and the substrate with the sample under.

Conditions allowing catalytic activity of nucleic acid sequences. The conditions allowing catalytic activity of nucleic acid sequence will be able to convert the nucleic acid sequence will be able to convert the nucleic acid sequence will be able to convert the nucleic acid sequence will be able to convert the nucleic acid catalytic product if the analyte of interest is ubstrate intro a nucleic acid product only if the analyte of interest is significant increase in the amount of product is then amplified, and a significant increase in the amount of product indicates the presence of significant increase in the amount of product indicates the presence of significant increase in the method is useful for the qualitative or quantitative determination of an analyte in a sample in diagnostic assays. The invention describes the in vitro selection of a ribozyme ligase was selected from a pool of RNA molecules comprising a central randomised regions (the N90 RNA pool; AAA57851). In the presence of the effector, selection 90 nucleotides in length flanked on both sides by constant sequence regions (the N90 RNA pool; AAA57851). In the presence of the effector and a bNA primer identical in sequence to the substrate used for the selection. A ribozyme ligase, L1, was selected via this procedure. L1 can only adopt its active conformation (AAA57869) and then PCR amplified using the effector oligo (analyte). In the absence of the effector, L1 adopts an inactive conformation (AAA57860). The present sequence regioned usplanted using the present sequence is not given in the specification, but present 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting an analyte in a sample comprises providing nucleic acid sequence which is catalytically active in presence of analyte, contacting catalytic nucleic acid with substrate and amplifying catalytic product.
                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= b
/bound_moiety= "Bases 13-17 of N90 RNA pool (AAA57851)"
                                                                                                                                                                                    Ribozyme, catalytic RNA; analyte detection, effector molecule, nucleic acid substrate; in vitro selection; ribozyme ligase, conformation dependent activity; allosteric activation; ss.
                                                                                                                                               Deoxy-T22-tagged substrate oligonucleotide.
                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                          BP.
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                     AAA57856 standard; DNA; 28
                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                     23. .28
/*tag= a
24. .28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nathan A, Ellington A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200024931-A2
                                                                                                        11-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                            misc binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-OCT-1998;
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                                                                                                                                                                                                                                                                        Synthetic.
                                                            AAA57856;
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AAA57856/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting minority genomes in viral quasi-species, useful for identifying mutants responsible for drug resistance and to individualize therapy.
                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                              Minority genome method; viral quasi-species; majority genome; genetic diagnosis; viral infection; human immune deficiency virus; hepatitis B; hepatitis C; antiviral therapy; ss.
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                               1.3%; Score 22.2; DB 1; Length 28; 88.9%; Pred. No. 1.1e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 22.2; DB 1; Length 28;
Pred. No. 1.18+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arias Esteban A, Baranowski E, Briones Llorente C;
Domingo Solans E, Escarmis Homs C, Gomez Castilla J;
Martin Ruiz- Jarabo C, Parro Garcia V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 28 BP; 3 A; 1 C; 4 G; 19 T; 0 U; 1 Other;
Sequence 28 BP; 1 A; 2 C; 1 G; 22 T; 2 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "C6 aminolinker sequence"
                                                                                                                                                                                                                                                                                                               Minority genome method VIH-MUT-12 DNA sequence.
                                                                                                1729 AGTTTACAAAAAAAAAAAAAAAAAAAAAAAAA 1755
                                                                                                                   28 AGTGCAAAAAAAAAAAAAAAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'label= unknown
                                                                                                                                                                                                                ABK52626 standard; DNA; 28 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-APR-2001; 2001WO-ES000165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-APR-2000; 2000ES-00001068
                                                                                                                                                                                                                                                                                27-AUG-2002 (first entry)
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                                                               24; Conservative
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Best Local Similarity
Matches 24; Conserv
                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200183815-A1
                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified
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                               Query Match
                                                               Matches
                                                                                                                                                                                               ABK52626/
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incyte clone 1; fluorescent label; probe; primer; DNA sequencing; ss.

Sequencing primer used to exemplify the invention.

(first entry)

16-OCT-1998

/*tag= a /note= "labelled with the donor carboxyfluoscein"

Location/Qualifiers

modified_base

Synthetic

modified_base

/*tag= b /note= "optionally laballed with the acceptor

carboxyrhodamine"

modified base

modified base

/*tag= b /note= "optionally laballed with the acceptor 6-carboxyrhodamine"

/*tag= a /note= "optionally labelled with the donor

carboxyfluoscein"

nodified base

/*tag= b /note=_"optionally laballed with the acceptor 6-

carboxyrhodamine'

W09831834-A1

97WO-US022914.

12-DEC-1997; 23-JUL-1998.

(INCY-) INCYTE PHARM INC.

15-JAN-1997;

WPI; 1998-414127/35.

Ju J.,

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The invention relates to a mammalian PGI gene and protein, and a set of PGI biallelic markers. The PGI polynucleotide and biallelic markers are used in a hybridisation assay, a sequencing assay, or in an allele-specific amplification assay for determining the identity of a nucleotide at a PGI-related biallelic marker. The methods can be used to detect and to assess the risk of developing cancer or prostate cancer. Early-stage diagnosis of prostate cancer relies on prostate specific antigen (PSA) coasse. However, the effectiveness of this is limited due to its inability to discriminate between malignant and non-malignant affections of the organ. A need exists for both a reliable diagnostic procedure which would enable early-stage diagnosis, and for preventative and curative treatments of the disease. The PGI gene can be used for detection of prostate cancer, and the risk of developing it in the future, and can also be used to determine therapies for the disease
                                                                                                                                                                                                                                           PG1 gene; biallelic marker; PCR primer; PG1-related biallelic marker; cancer; prostate cancer; diagnosis; therapy; prostate specific antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of a prostate cancer associated gene and biallelic markers derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chumakov I, Bougueleret L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 24 BP; 3 A; 0 C; 1 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                           PCR primer PGRT32 for PG1 coding sequence.
Example 6; Page 42; 385pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-IB002133.
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98US-0099658P.
                                                                                                877/c
AAZ00877 standard; DNA; 24
                                                                                                                                                                           27-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cohen D, Blumenfeld M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-405178/34.
                                                                                                                                                                                                                                                                             PSA; human; 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                            WO9932644-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-DEC-1997;
09-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                           22-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1999.
1728
                                                                                                                                            AAZ00877;
                                                                                                                                                                                                                                                                                                             Synthetic
                                28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from it.
                                                                                             RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence exxemplified the primer of the invention, and is used to sequence Incyte clone 1 (AAV42737). The primer of the invention is labelled with a set of at least 2 different fluorescent labels. The set comprises an energy-transfer fluorescent label with at least 1 each of a donor fluorophore and an acceptor fluorophore capable of energy transfer, and separated by a distance x, and a second similar fluorescent label in which the separation distance is y, x and y being sufficiently different for the two fluorescent labels to produce distinct fluorescent signals. Fluorescent labels are useful in multicomponent analyses, e.g. as probes for fluorescent in situ hybridisation or especially as primers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Set of energy-transfer fluorescent labels with donor and acceptor at different separations – useful for DNA sequencing allows use of fewer analysing wavelengths or an increased throughput.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.2%; Score 21.4; DB 1; Length 25; 95.7%; Pred. No. 1.2e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 25 BP; 1 A; 1 C; 0 G; 23 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1733 TACAAAAAAAAAAAAAAAAAA 1755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 14; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 95.7
ses 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Gaps

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1; Indels

0; Mismatches

22; Conservative

Matches

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Local Similarity

Query Match

1732 TTACAAAAAAAAAAAAAAAAAA 1754

TTTCAAAAAAAAAAAAAAA 1

RESULT 9 AAV42215/c ID AAV42215 standard; DNA; 25 BP. AC AAV42215;

1.2%; Score 21.4; DB 1; Length 24; 95.7%; Pred. No. 1.2e+02;

us10008789-3.rng

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The parent discloses nover nument problemics to the parent discloses nover numen problemics and its corresponding protein. Zeycoris year to identify modulators (e.g. agoniets or antagonists). Zeycoris, its agoniets or antagonists are useful in the treatment of inflammation, the agonists or antagonists are useful in the treatment of inflammation during or cardiovascular conditions, muscle inflammation, inflammation during and after surgery, arthritis, asthma, inflammation, inflammation during and after surgery, arthritis, asthma, inflammation, one disease or diverticulitis, for modulating spermatogenesis, sperm capacitation, as immunocontraceptive or anti-fertility vaccine and for treating male infertility. Zeytori3 protein and its antibodies are used to diagnose cancer, repertivation ischaemia, asthma, iperiasis and melanoma. Zeytori3 proteins are used to enhance fertilisation. Zeytori3 antagonists are used to treat myocarditis, atherosclerosis, pelvic inflammatory diseases (PID), peoriasis, eczema, scleroderma and other inflammatory diseases. Zeytori3 sequences and/or its antibodies are useful for treatment of disorders associated with vasconstriction, heart arrhythmia, congestive heart classase, muscle spasms and fatigue. They are used for detecting human chromablities. Zeytori3 colby are used in gene therapy.

Zeytori3-cytoria-cytoria fusion proteins are useful for enhancing in vivo killing of target tissue. The present are useful for enhancing in vivo killing of target tissue.
                                                                                                                                                                                                                                                                                                  Novel human phosphodiesterase polypeptide, zcytor13 and polynucleotide encoding it, for detecting human chromosomal abnormalities, identifying modulators and treating inflammatory and cardiovascular diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                are useful for enhancing in vivo killing of target tissue. The present sequence is a polyA PCR primer, 2C7764b which is used to isolate full length zcytor13 cDNA by screening human placental cDNA library
                                                                                                                                                                                                                                                                                                                                                                                     Example 1C; Page 118; 122pp; English.
                                                                                                 06-OCT-2000; 2000WO-US027734.
                                                                                                                                                                                                                        Presnell SR, Novak JE,
                                                                                                                                                                                                                                                                WPI; 2001-266312/27.
                   WO200125444-A2
                                                                                                                                         07-OCT-1999;
                                                           12-APR-2001
This sequence represents a PCR primer used to isolate DNA encoding the human Nck associated protein 1 (Napl) of the invention. Napl inhibits apoptosis. The protein can be used in the investigation, diagnosis and treatment (e.g. by gene therapy) of Alzheimer's disease
                                                                                                                                                                                                   Nck associated protein 1; Napl; human; apoptosis; Alzheimer's disease;
therapy; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein inhibiting apoptosis, useful in the diagnosis and treatment of
                                                                                                                                                          PCR primer for human Nck associated protein 1 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.2%; Score 21.4; DB 1; Length 25; 95.7%; Pred. No. 1.2e+02; iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25 BP; 1 A; 0 C; 0 G; 24 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Page 76; 90pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                          98WO-JP005646
                                                                                                                                                                                                                                                                                                                                                                                                                                              97JP-00363183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KYOW ) KYOWA HAKKO KOGYO KK.
                                      AAX84259 standard; DNA; 25
                                                                                                                  08-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-395181/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SAKA/) SAKAKI Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1997;
                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                          14-DEC-1998;
                                                                                                                                                                                                                                                                                                                         WO9931239-A1
                                                                                                                                                                                                                                                                                                                                                                  24-JUN-1999.
                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sakaki Y;
                                                                            AAX84259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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patent discloses novel human phosphodiesterase (PDE), zcytor13 cDNA

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99US-00414025

(ZYMO ) ZYMOGENETICS INC

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                                                                                                                                                                                                                                                                                                                                                                                                         Human, zsig63; chromosome 4q12-4q13; salivary protein; antimicrobial; ss; microbial infection; tooth decay; periodontal disease; thrush; emphysema; gastrointestinal disease; urinary tract infection; vaginal infection; skin infection; epithelial wound; chronic tissue damage; cystic fibrosis; acquired immunodeficiency syndrome; AIDS; lung infection; sarcoidosis; chronic bronchitis; gene therapy; protein therapy; primer; 2C7764a.
                                                                           Gaps
                                                                           ;
0
                                1.2%; Score 21.4; DB 1; Length 26; 95.7%; Pred. No. 1.3e+02; ive 0; Mismatches 1; Indels
Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                       Human zsig63 cDNA sequencing primer ZC7764a.
                                                                                                                 1733 TACAAAAAAAAAAAAAAAAAA 1755
                                                                                                                                        26 TAAAAAAAAAAAAAAAAA 4
                                                                                                                                                                                                                                                       AAS20596 standard; DNA; 26 BP
                                                                                                                                                                                                                                                                                                                                  23-APR-2002 (first entry)
                                                        Local Similarity 95.7
nes 22; Conservative
                                      Query Match
                                                                           Matches
                                                                                                                                                                                                                                     AAS20596/
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Gaps

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1733 TACAAAAAAAAAAAAAAAAAA 1755

Local Similarity 95.7 nes 22; Conservative

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25 TAAAAAAAAAAAAAAAAAA 3

AAD03682 standard; DNA; 26

RESULT 11 AAD03682/

Homo sapiens

Human; phosphodiesterase; PDE; zcytorl3; antiasthmatic; antiarthritic; antipscriatic; cytostatic; antiatherosclerotic; antinfertility; cardiant; antinflammatory; dermatological; wound healing; antiviral; antibacterial; therapy; inflammatory bowel disease; diverticulitis; spermatogenesis; sperm capacitation; immunocontraceptive; vaccine; cancer; reperfusion ischaemia; psoriasis; melanoma; wyccarditis; PID; pelvic inflammatory disease; eczema; scleroderma; vasoconstriction; heart arrhythmia; congestive heart disease; muscle spasm; fatigue; chromosomal abnormality; gene therapy; PCR primer; ss.

Homo sapiens

Human full length zcytor13 cDNA isolating polyA PCR primer, ZC7764b

(first entry)

19-JUN-2001

AAD03682;

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The invention relates to a polynucleotide derived from the 4q12-4q13 region of human chromosome 4 and encoding a zsig63 polypeptide, a secreted salivary protein with anti-microbial activity. Due to their microbial activity, the sequences can be used in the study of microbial infections, e.g. for recombinant production of anti-microbial proteins. The sequences can be used in the treatment of tooth decay, periodontal disease, thrush, gastrointestinal disease, uninary tract infections, vaginal infections, skin infections, epithelial wounds, chronic tissue diamage, acquired immunodeficiency syndrome (AIDS), cystic fibrosis, lung infections, sarcoidosis, emphysema and chronic bronchitis. This sequence represents a sequencing primer for cDNA encoding human zsig63
                                                                                                                                                                                                                                                                            Polynucleotides encoding salivary proteins useful as anti-microbial
                                                                                                                                                                                                                                                                                                                                    Example 1; Col 53; 29pp; English.
                                                                                                                             99US-0124820P
                                                                                        17-MAR-2000; 2000US-00527345
                                                                                                                                                              (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                   Adler DA, Sheppard PO;
                                                                                                                                                                                                                                         WPI; 2002-096707/13
                                                                                                                             17-MAR-1999;
                   US6331413-B1
                                                      18-DEC-2001
                                                                                                                                                                                                                                                                                               agents.
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Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

Gaps ö 1.2%; Score 21.4; DB 1; Length 26; 95.7%; Pred. No. 1.3e+02; 1; Indels 0; Mismatches Local Similarity 95.7 tes 22; Conservative Query Match Best Loca Matches

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1733 TACAAAAAAAAAAAAAAAAAA 1755 TAAAAAAAAAAAAAAAAAA 4

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ABS52638 standard; DNA; 26 BP 15-NOV-2002 ABS52638; 

(first entry)

Human secreted salivary protein zsig63 PCR primer ZC7764a.

Human; secreted salivary protein; zsig63; immunogen; zsig63-cytokine; antibody-cytokine; in vivo killing; pathological microbe; bacteria; fungal; viral; infection; salivary gland; anti-microbial; dental caries; tooth decay; periodontal disease; thrush; gastrointestinal disease; urinary tract infection; vajnal infection; skin infection; microflora; epithelial wound; pathogenic colonisation; invasion; pro-inflammatory; enfront cissue danage; vascular system; diabetes; anti-inflammatory; incompetent immune system; AIDS; acquired immunodeficiency shordcome; chemotherapy; radiation treatment; lung infection; cystic fibrosis; digestion; PCR; primer; ss.

Homo sapiens.

US2002081701-A1

27-JUN-2002

03-AUG-2001; 2001US-00922480.

99US-0124820P. 17-MAR-1999;

17-MAR-2000; 2000US-00527345.

(SHEP/) SHEPPARD P (ADLE/) ADLER D A.

Adler DA, Sheppard PO;

WPI; 2002-635468/68

Novel secreted salivary protein, zsig63 and polynucleotide encoding it useful for treating microbial infections, inflammatory conditions, dental caries and lung infections associated with cystic fibrosis.

Example 1; Page 29; 33pp; English.

The present invention relates to a new secreted salivary protein, zaig63.

The invention is useful for detecting in a test sample, the presence of
an antagonist or agonist of zaig63 protein activity. The invention is
also useful as an immunogen for proteins an antibody to zaig63
also useful as an immunogen for producing an antibody to zaig63
co polypeptide. zaig63-cytokine fusion proteins or antibody-cytokine fusion
co protein are useful for enhancing in vivo killing of target tissues.

Pharmaceutical composition comprising purified zaig63 polypeptide are
useful in the treatment of conditions associated with pathological
confictors, including bacterial, fungal and viral infections. High
corporates are useful for treatment of dental caries (cooth decay),
confictorial disease, thrush and gastrointestinal disease. Other
copplications can be used in uninary tract infections, vaginal infections,
periodontal disease, thrush and gastrointestinal disease. Other
copplications can be used in uninary tract infections and protect
copplyceptides can be used to establish normal microflora and protect
copplyceptides can be used to establish normal microflora and protect
copplyceptides can be used to establish normal microflora and protect
copplyceptides can be used to establish normal microflora and protect
copplications can be used to establish normal microflora and protect
copplications can be useful as anti-inflammatory agents. The invention is
copplicationly in areas having a limited or damaged vascular system e.g.
copplyceptides may be useful as anti-inflammatory agents. The invention is
conferent for the treatment of patients having incompetent immune system
could as AIDS (acquired immunodeficiency syndrome) patients or individuals
could be a AIDS (acquired immunodeficiency syndrome) patients or individuals
could be present nucleic acid sequence represents a useful for aiding digestion.
The present nucleic acid sequence represents a cyling infections of zsig63
in the methods of the invention for identification of zsig63

Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

Gaps ö 1.2%; Score 21.4; DB 1; Length 26; 95.7%; Pred. No. 1.38+02; tive 0; Mismatches 1; Indels Query Match
Best Local Similarity 95.7
Matches 22, Conservative

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1733 TACAAAAAAAAAAAAAAAAAA 1755 

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AAD45055 standard; DNA; 26 BP AAD45055; AAD45055/

RESULT 14

(first entry) 27-DEC-2002

Human; secreted salivary protein; zsig61 protein; host defense protein; immune modulating factor; antipathogenic; cell-cell signalling molecule; growth factor; cytokine; growth factor hormone activity; dental carries; infection; tooth decay; periodontal disease; gastrointestinal disease; thrush; urinary tract infection; vaginal infection; diabetes; obesity; anti-inflammatory; chronic tissue damage; lung dysfunction; restenosis; gene therapy; salivary gland dysfunction; prostate gland dysfunction; forensic DNA profiling; chondrosarcoma; atherosclerosis; primer; ss. 2C7764a primer used in the identification of human zsig63 DNA. MARKE MARKEY SAXD

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The invention relates to human secreted salivary polypeptide designated as zsig63 and nucleic acid molecules encoding such polypeptides. zsig63 can be used in detecting agonists and antagonists of its activity, and is also useful as a host defense polypeptide, immune modulating factor, antipathogenic polypeptide, cell-signalling molecule, growth factor, cytokine, or as secreted extracellular matrix associated proteins with growth factor hormone activity. It is useful for treating conditions associated with pathological microbes, including bacterial, fungal and viral infections, for treating dental carries (tooth decay), periodontal cification, vaginal infection and for preventing infection in skin and other epithelial wounds. zsig63 is useful for establishing normal currenting chronic tissue damage e.g. damage in extremities associated with cidabetes and useful as anti-inflammacory agents. It is useful as a marker of lung dysfunction, salivary gland dysfunction, or dysfunction of propeated gland. It is also therapeutically useful for aiding digestion. Polymucleotides of the invention are used in gene therapy for increasing or inhibiting zsig63 activity, for detecting abnormalities on human chromatoms. Subsociated with disease or other human traits and as diagnostics in forensic DNA profiling. Sequences of the invention are used diagnostics in forensic DNA profiling. Sequences of the invention are used the invention of diapocytes and for shrinking relation or differentiation of adapocytes and for invity in the mycoytes and set in shrinking relation or differentiation of adapocytes and for invity in the mycoytes and set in the profileration or differentiation of adapocytes and for invity in the disease or other human traits and as marker when the mycoytes and set in the profileration or differentiation of adapocytes and for increasing the mycoytes and set in the part of the profileration or differentiation or differentiation or differentiation or differentiation or differentiation or differentiation or differenti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present sequence is a primer used in the identification of human zsig63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel secreted salivary polypeptide, zsig63, useful as antimicrobial agent for treating microbial infection, dental carries, periodontal disease, thrush gastrointestinal disease, and for aiding digestion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inhibiting chondrosarcomas, atherosclerosis, restenosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 30; 33pp; English
                                                                                                                                                                                                                                                17-MAR-1999; 99US-0124820P.
                                                                                                                                                                                        03-AUG-2001; 2001US-00923236
                                                                                                                                                                                                                                                                                                                                                                                                                      Adler DA, Sheppard PO;
                                                                                                                                                                                                                                                                                                                                 (ADLE/) ADLER D A. (SHEP/) SHEPPARD P O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-642378/69
                                                                               US2002090677-A1.
                             Homo sapiens.
                                                                                                                                      11-JUL-2002
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Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

Gaps ; 0 Score 21.4; DB 1; Length 26; Pred. No. 1.3e+02; 0; Mismatches 1; Indels 1.2%; Local Similarity 95.7 Les 22; Conservative Query Match Matches

1733 TACAAAAAAAAAAAAAAAAA 1755 TAAAAAAAAAAAAAAAAAA 56

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RESULT 15

Human zalphall Ligand sequencing primer 2C7764a.

Cytokine; zalphall Ligand; zalphall receptor; NK cell progenitor; natural killer cell proliferation; T-cell proliferation; B-cell proliferation; anti-tumour response; immune system; immunostimulant; cytostatic; human; sequencing primer; ss

Homo sapiens

US6307024-B1

23-OCT-2001

09-MAR-2000; 2000US-00522217

09-MAR-1999; 11-MAR-1999;

99US-0123547P. 99US-0123904P. 99US-0142013P. 01-JUL-1999;

(ZYMO ) ZYMOGENETICS INC.

Sprecher CA, Foster DC, Holly RD; Nelson AJ, Dillon SR, Hammond AK; Presnell SR, Johnston JV, Novak JE, Gross JA,

WPI; 2002-040208/05.

New zalphall ligand polypeptides and polynucleotides, useful for stimulating proliferation, activation, differentiation and/or induction of inhibition of specialized cell function, or for stimulating an antigenic response

Example 7; Col 139; 105pp; English.

calphall Ligand and the polymucleotide encoding it. The invertion also gives the sequence for the zalphall receptor and the polymucleotide encoding it. The zalphall Ligand polypeptide stimulates proliferation of encoding it. The zalphall Ligand polypeptide stimulates proliferation of natural killer (NK) cells or NK cells, proliferation of B-cells stimulated with anti-cells, proliferation of T-cells, proliferation of B-cells stimulated with anti-ceduces proliferation of B-cells stimulated with anti-ligh antibodies. The zalphall Ligand polypeptide is also useful in preparing antibodies that bind to zalphall Ligand epitopes. The zalphall Ligand polymucleotides can be used as probes or primers to clone regions of a zalphall Ligand gene, and in gene therapy. Zalphall Ligand may also be used to identify inhibitors of its activity, to enhance the generation of anti-tumour responses with or without the infusion of donor lymphocytes, and to a sequence or stimulate the infusion of donor lymphocytes, and to a sequence control properson of a sequence represents present invention relates to the isolation of a novel cytokine, 

Seguence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

obesity.

Gaps ö 1.2%; Score 21.4; DB 1; Length 26; 95.7%; Pred. No. 1.3e+02; ive 0; Mismatches 1; Indels Conservative Local Similarity 22; Query Match Matches

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ABX93599 standard; DNA; 26 BP (first entry) 28-MAY-2003 ABX93599; ABX93599/c

RESULT 16

Human zsig63 PCR/sequencing primer ZC7764a.

ss; PCR; zsig63; adhesin; salivary gland; dental carries; periodontal disease; thrush; gastrointestinal disease; epithelial wound; urinary tract infection; vaginal infection; skin infection; primer; 

1733 TACAAAAAAAAAAAAAAAAAAAAAAAAAA 1755

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pro-inflammatory; chronic tissue damage; vascular system; diabetes; AIDS; lung infection; cystic fibrosis; lung dysfunction; digestive; salivary gland carcinoma; Pneumocystis carinii infection; emphysema; chronic bronchitis; prostate dysfunction; prostate adenocarcinoma; cell culture media; gene therapy; human chromosome 4q12-4q13; dentinogenesis imperfecta; dentin dysplasia type II.
                                                                                            03-AUG-2001; 2001US-00922469.
                                                                                                          17-MAR-1999; 99US-0124820P.
17-MAR-2000; 2000US-00527345.
                                                                                                                                                     Adler DA, Sheppard PO;
                                                                                                                               (ADLE/) ADLER D A. (SHEP/) SHEPPARD P O.
                                                                                                                                                                    WPI; 2003-328428/31.
                                                               US2002173027-A1.
                                                                                                                                                                                                       skin infections.
                                                                                                         17-MAR-1999;
                                                                              21-NOV-2002
                                                  Synthetic
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The invention relates to an isolated zeig63 polypeptide comprises domain 3, mature zeig63 and full length zeig3. Also zeig63, domain 3, mature zeig63 and full length zeig3. Also included are the polyuncleotide encoding zeig63, a zeig63 expression controlled are the polyuncleotide encoding zeig63, a zeig63 expression included are the polyuncleotide encoding zeig63, a zeig63 expression comprising the vector and expression the protein (comprising amino acids 1-15, 18-37, 38-22, 127-219 or 16-219 of zeig63 and an additional protein, using a carging sene construct to identify zeig63 agonists, and producing an anti-zeig63 antibody using zeig63 immunogenic peptides, zeig63 is natioody using zeig63 immunogenic peptides, zeig63 is carging protein activity. Zeig63 has antimicrobal accivity, and since exhibits high expression in sallvary gland, can be used for treating dental carries, periodontal disease, thrush, and gaatrointestinal disease, uninary tract infections, vajanal infections, seig63 is and other epithelial wounds. The polypeptides can be used to establish cornal infections and protect against pathogenic colonization and other epithelial sounds. The polypeptides can be used to retablish cornal infections and protect against pathogenic colonization and crowing chronic, tissue damage particularly in areas having limited invasion. Zeig63 can also be used for providing pro-inflammatory activity for treating chronic, tissue damage particularly in areas having limited chemotherapy, radiation treatment, for treating lung infections e.g. in cystic fibrosis. Detection of zeig63 is polypeptides ar relatively high conditions associated with sallvary gland carcinoma, headen any indicate that such polypeptides may be used to replace serum that is commonly used in the traches may indicate that such polypeptides may be used to replace serum that is commonly used in culture media and may be used to replace serum that is commonly and encoding human zeig63 activity, and for detecting abnormalities on human zeig63 primer used to 
                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated zsig63 polypeptide, member of the adhesin family, useful for treating dental carries, periodontal disease, thrush, gastrointestinal disease, urinary tract infections, vaginal infections,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 29; 32pp; English.
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The invention discloses a method for identifying a candidate polymorphic repeat within a coding sequence (expressed sequence tag, EST), which comprises detecting tandem repeats in a target coding sequence, scoring the repeats for polymorphic probability and generating a dataset candidate polymorphic probability and generating a dataset correlating the repeats with polymorphic probability to identify a candidate polymorphic repeat. The computational methods (polymorphic marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are useful for identifying and detecting candidate polymorphic repeats in them agence, which can be used to understand, treat or eliminate genetic diseases, predispositions or adverse drug-treatment reactions. Examples of diseases linked to nucleotide repeats are Machado-Joseph, Haw River syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis, myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are the polymorphic repeats identified for a search of human ESTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat; polymorphic marker prediction of ubiquitous simple sequences; POMPOUS; Rep.X; human; genetic disease; drug-treatment; Machado-Joseph; Haw River syndrome; Huntington's disease; fragles x syndrome; Predreich's ataxis; myotonic dystrophy; hyperandrogenaemia; spinal atrophy; bulbar atrophy; spinocerebellar ataxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying a candidate polymorphic repeat within a coding sequence, funderstanding or treating genetic disease, comprises detecting tandem repeats in a target coding sequence and scoring the repeats for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence 27 BP; 1 A; 0 C; 0 G; 26 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                             EST polymorphic DNA repeat polynucleotide #153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fondon JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1733 TACAAAAAAAAAAAAAAAAA 1755
|| || || || || || || || || || || || ||
   24 TAAAAAAAAAAAAAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example; Col 717; 588pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minna JD,
                                                                                                                                                                                   ABX79828 standard; cDNA; 27 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-00475947.
                                                                                                                                                                                                                                                                                                                                     17-APR-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polymorphic probability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sarner HR, Wren JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-208818/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US6472154-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                            ABX79828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                 ABX79828,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
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Best Local Similarity Matches 22; Conserv

Query Match

1.2%; Score 21.4; DB 1; Length 26; 95.7%; Pred. No. 1.38+02;

AAQ75644;

RESULT 18

AAQ75644,

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New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.
                                                                                                                                                                                                                                                                                                                            The invention relates to antisense compounds targetted to a nucleic acid encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22. Antisense compounds of the invention are useful for modulating the expression of TRIP6 and for treating diseases or conditions associated with the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as tresearch reagents and kits and in distinguishing between functions of various members of a biological pathway. The are also useful in antisense therapy. The present sequence is human TRIP6 DNA specific PCR primer, used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein inhibiting apoptosis, useful in the diagnosis and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nck associated protein 1; Nap1; human; apoptosis; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR primer for human Nck associated protein 1 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.2%; Score 21; DB 1; Length 21; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21 BP; 7 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                           Example 13; Page 74; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1074 TGTATGTTCTACATGCCGGGC 1094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 TGTATGTTCTACATGCCGGGC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KYOW ) KYOWA HAKKO KOGYO KK.
(SAKA/) SAKAKI Y.
                                         08-NOV-2001; 2001US-00008789.
05-NOV-2002; 2002WO-US035479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-JP005646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX84258 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapy; PCR primer; ss.
                                                                                  PHARM INC
                                                                                                                         Dobie K;
                                                                                                                                                                  WPI; 2003-430662/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VPI; 1999-395181/33.
                                                                                  SISI (-SISI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .5-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9931239-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-SEP-1999
                                                                                                                         Bennett CF,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sakaki Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX84258;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       턩
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - by amplification of mRNA followed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            whethod can be used to analyse gene expression rapidly and easily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A method for the analysis of cDNA comprises (a) preparing an aggregate double-stranded cDNAs by using an aggregate of mRNAs and a plural type of abolied reverse transcription primers (GBNESEQ files AAQ7554-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with estimated compared aggregates of electrophoresing the digested aggregate of cDNAs in seperate lanes. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour; OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis; inflammation; therapy; hyperproliferative disorder; infection; cancer; chromosome 7q22; ZRP-1; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                       Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.2%; Score 21; DB 1; Length 21; 00.0%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human TRIP6 DNA specific reverse PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Analysis of cDNA and gene expression - by digestion with restriction enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1732 TTACAAAAAAAAAAAAAA 1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 6; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 TTACAAAAAAAAAAAAAA 1
                                         BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВР
                                                                                                                                                                                                                                                                                                                                                                                               93JP-00112515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACC82882 standard; DNA; 21
                                    AAQ75644 standard; DNA; 21
                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-AUG-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-018287/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003040328-A2
                                                                                                                       04-AUG-1995
                                                                                                                                                                                                                                                                                                             JP06303997-A.
                                                                                                                                                                                                                                                                                                                                                                                             16-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                    16-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                      Synthetic.
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ACC82882;

RESULT 19
ACC82882/C
ID ACC8.
XX
AC ACC8.
XX
DT 27-AI
XX
HUMA:
KW HUMA:
KW OPAKW OPAKW Chro
XX
HOMO
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YX
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Query Match Matches

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Length 25;

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The invention relates to sequence determination oligonucleotides for detecting polymorphic sites in a 5' flanking region of cytochrome P450 2D6 (CYP2D6) gene. CYP2D6 enzymes are involved in the metabolism of many different xenobiotics. Human CYP2D6 gene is located on chromosome 22. The oligonucleotides may be used as in situ hybridisation probes, in ligase-based sequenced determination, as components of diagnostic assays, as probes in sequence determination methods based on mismatches, as hybridisation-based diagnostic assays, and as components of diagnostic microarray. CYP2D6 is useful to predict variations in an individual's ability to metabolise certain drugs. The present sequence is a sense oligonucleotide used for detecting of human CYP2D6 gene 5' flanking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, cytochrome P450 2D6; CYP2D6; enzyme; detection; xenobiotic;
ligase-based sequenced determination; drug metabolism; chromosome 22; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polymorphic sites in a 5' flanking region of a CYP2D6 gene, as
hybridization probes, as components of diagnostic assays, or in ligase-
                                                                            This sequence represents a PCR primer used to isolate DNA encoding the human Nck associated protein i (Napl) of the invention. Napl inhibits apoptosis. The protein can be used in the investigation, diagnosis and treatment (e.g. by gene therapy) of Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human CYP2D6 gene polymorphic site 385 detecting sense 5' oligo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Risinger C, Andersson MK, Lewander T, Oliasson E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New sequence determination oligonucleotides, useful
                                                                                                                                                                           Seguence 25 BP; 0 A; 0 C; 1 G; 24 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 25 BP; 22 A; 2 C; 1 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                              1.2%; Score 21; DB 1; Le
100.0%; Pred. No. 1.4e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     region single nucleotide polymorphism (SNP)
                                                                                                                                                                                                                                                                                             1735 CAAAAAAAAAAAAAAAAA 1755
                                      Example 1; Page 76; 90pp; Japanese.
                                                                                                                                                                                                                                                                                                                       CAAAAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 23; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-AUG-2001; 2001WO-IB001544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          based sequence determination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-AUG-2000; 2000GB-00021286
                                                                                                                                                                                                                                                                                                                                                                                                                                AAD34264 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GEMI-) GEMINI GENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-329785/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ношо варіепв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD34264;
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for detecting

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Generating mutation in gene using cells which contain defective mismatch repair gene, useful to generate genetically altered mutations with new output traits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The patent discloses a method for generating hypermutable organisms. Dominant negative alleles of human mismatch repair genes can be used to generate hypermutable cells and organisms. They increase the rate of spontaneous mutations by reducing the effectiveness of DNA repair and thereby render the cells or animals hypermutable. The method is used to produce genetically altered organisms to produce new output traits. The present sequence is a bacterial poly purine nucleotide phosphorylasse (polypwPP) DNA fragment containing an in-frame polyA tract. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                   Hypermutable organism; dominant negative allele; mismatch repair gene; spontaneous mutation; DNA repair; purine nucleotide phosphorylase; PNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grasso L, Vogelstein B, Kinzler KW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.2%; Score 21; DB 1; Length 25; 100.0%; Pred. No. 1.4e+02;
                                                                                                                                                                                                          Bacterial PNP DNA fragment with an in-frame polyA tract.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25 BP; 21 A; 1 C; 2 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/note= "In-frame polyA tract"
                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/note= "Bacterial PNP gene"
                                1735 CAAAAAAAAAAAAAAAAAA 1755
                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                          22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 5; Fig 7; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAY-2001; 2001WO-US015376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-MAY-2000; 2000US-0204769P.
                                                                                                                          25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNIV JOHNS HOPKINS
                                                                                                                                                                               (first entry)
21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sass PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NICOLAIDES N C.
SASS P M.
GRASSO L.
                                                                                                                          AAD26900 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                           ..5
*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MORPHOTEK INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KINZLER K W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-083004/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nicolaides NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200188192-A2
                                                                                                                                                                                                                                                              bacteria, ss.
                                                                                                                                                                                                                                                                                                  Unidentified.
Chimeric.
                                                                                                                                                                               09-APR-2002
                                                                                                                                                                                                                                                                                                                                                          misc feature
                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-NOV-2001
                                                                                                                                                      AAD26900;
                                                                                                                                                                                                                                                                                        Bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UYJO )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NICO/)
(SASS/)
(GRAS/)
(VOGE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KINZ/)
                                                                                                   RESULT 22
                                                                                                               AAD26900
                                                                                                                                        6.4
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Best Local Similarity

Length 25;

1.2%; Score 21; DB 1; Lv 100.0%; Pred. No. 1.4e+02;

Query Match Best Local Similarity

1735 CAAAAAAAAAAAAAAAAA 1755

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Gaps

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The invention relates to systems for identification and characterisation of gene expression in one or more samples, comprising an identimer having a specific oligo-dT primer sequence, where the identimer comprises a categoristic oligo-dT primer sequence, where the identimer comprises a categorist cast the relative differences in mRNA between 2 or more samples, where differences in mRNA between 2 or more samples, where captered, for supporting discovery of new genes, and for identifying mRNAs that are expressed at different levels between 2 or more samples. The new system or method addresses limitations of prior methods by comprising compositions and systems that incorporate new strategies where molecular or biochemical assay compositions and systems are linked to DNA or RNA sequence databases for optimal resource efficiency in assaying gene corpositions and systems are linked to DNA or RNA sequence databases for optimal resource efficiency in assaying gene corposition and the following advantages over existing methods: (a) prior sequence information or clone library construction is not needed to enable the assay; (b) provides immediate sequence in formation and differences in mRNA level, to determine mRNA expression laborates cDNA fragments from all mRNAs present in the sample for subsequent investigation by common molecular biology contenting subsequent investigation by common molecular biology contenting allowing advantages or differences of the genome of the organism under investigation and can be employed in consequence represents an oligo off primer used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying and characterizing gene expression in samples, for identifying markha expressed at different levels, comprises employing an identimer having a oligo-dT primer of a specific sequence and a detectable marker at its 5' end.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligo dT primer #3 used in method to study gene expression.
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligo dT primer; gene expression analysis; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25 BP; 0 A; 0 C; 2 G; 23 T; 0 U; 0 Other;
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Mismatches
                                                                          1735 CAAAAAAAAAAAAAAAAAAAAAA 1755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Page 21; 45pp; English.
                                                                                                                                                 5 САВАВАВАВАВАВАВАВАВ 25
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                                                                                                                                                                                                                                                                                                                                          BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-2001; 2001WO-US045401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-2000; 2000US-0244933P
                                                                                                                                                                                                                                                                                                                                          ABK86170 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-508123/54.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                ABK86170;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kane MD,
Matches
                                                                                                                                                                                                                                                                                                  ABK 86170/ABK 86170/ABK 86170/ABK 87X ABK 87X 
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detecting,
                                                                                                                                                                                                                     BS124; breast; cancer; detection; diagnosis; prevention; treatment; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated BS124 polynucleotides and polypeptides - used for detecting diagnosing, preventing or treating diseases or conditions of the breast, such as breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gordon J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence is that of an oligonucleotide used in the isolation of 8214-specific SET clone. It is useful for detecting, diagnosing, staging, preventing or treating, or determining predisposition to diseases or conditions of the breast, such as breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pancreatic disease, PA153; human; cytostatic; detection; antigen; anti-PA153; antagonist; therapy; treatment; tumour; metastasis; gene therapy; EST; expressed sequence tag; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Russell JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.2%; Score 21; DB 1; Length 26; 100.0%; Pred. No. 1.4e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Friedman PN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Billing-Medel PA, Cohen M, Colpitts TL, Friedman |
Granados EN, Hodges SC, Klass MR, Kratochvil JD,
Scheffel CP, Stroupe SD, Yu H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human pancreatic PA153 EST-specific clone primer 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 26 BP; 0 A; 0 C; 1 G; 25 T; 0 U; 0 Other;
                                                                                                                                                                                      Human BS124 specific EST clone oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 97; 125pp; English.
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AAX78723 standard; DNA; 26 BP.
XX
AC AAX78723;
XX
DT 03-SEP-1999 (first entry)
XX
C Human pancreatic PA153 EST-speci
XX
KW Pancreatic disease; PA153; human
KW anti-PA153; antagonist; therapy;
KW gene therapy; EST; expressed seq
XX
C Synthetic.
98WO-US012862.
                                                                                                                                                                                                                                                                                                                                                                                           97US-00879354.
                                                                              '466/c
AAX07466 standard; cDNA; 26
                                                                                                                                                       (first entry)
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Best Local Similarity
Matches 21; Conserva
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                                                                                                                                                                                                                                                                                                  WO9859049-A1
                                                                                                                                                                                                                                                                                                                                                              19-JUN-1998;
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                                                                                                                                                                                                                                                                                                                               30-DEC-1998
                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                          AAX07466;
                                                                          AAX07466/
ID AAX0
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Gaps

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1.2%; Score 21; DB 1; Length 25; 100.0%; Pred. No. 1.4e+02; rative 0; Mismatches 0; Indels

Query Match
Best Local Similarity 100.
Matches 21; Conservative

us10008789-3.rng

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Generating mutation in gene using cells which contain defective mismatch repair gene, useful to generate genetically altered mutations with new output traits.
                                                                                                                                                                                                                                                                                                                                                                                                                                      The patent discloses a method for generating hypermutable organisms. Dominant negative alleles of human mismatch repair genes can be used to generate hypermutable cells and organisms. They increase the rate of spontaneous mutations by reducing the effectiveness of DNA repair and thereby render the cells or animals hypermutable. The method is used to produce genetically altered organisms to produce new output traits. The present sequence is a bacterial poly purine nucleotide phosphorylase (polyPNP) DNA fragment containing an out-of-frame polyA tract. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dominant negative allele; mismatch repair gene; D-MMR; gene discovery; ITRE; inducible transcriptional regulatory element; recombinant gene mutagenesis; recombinant protein production; drug target discovery; ds.
                                                                                                                                                                                                                                               Grasso L, Vogelstein B, Kinzler KW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.2%; Score 21; DB 1; Length 26; 100.0%; Pred. No. 1.4e+02; tive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 26 BP; 22 A; 1 C; 2 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PolyPNP out-of-frame polyA tract DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                        Sxample 5; Fig 7; 59pp; English.
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                14-MAY-2001; 2001WO-US015376.
                                                      17-MAY-2000; 2000US-0204769P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-MAY-2001; 2001US-00853646.
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17-MAY-2000; 2000US-0204769P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD39650 standard; DNA; 26
                                                                                          UNIV JOHNS HOPKINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                               Vicolaides NC, Sass PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NICO/) NICOLAIDES N.C.
(SASS/) SASS P.M.
(GRAS/) GRASSO L.
                                                                                                            MORPHOTEK INC.
NICOLAIDES N C.
                                                                                                        (MORP-) MORPHOTEK INC.
(NICO/) NICOLAIDES N C
(SASS/) SASS P M.
(GRAS/) GRASSO L.
(VOGE/) VOCELSTEIN B.
(KINZ/) KINZLER K W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                     WPI; 2002-083004/11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD39650;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes novel contiguous and partially overlapping cDNA sequences and their encoded polypeptides, designated PA153, transcribed from human pancreatic tissue and which have cytostatic activity. The PA153 polynucleotides, proteins and antibodies are all useful in methods of detection. Detection of PA153 polynucleotide, antigens or anti-PA153 antibodies in a sample is indicative of pancreatic disease. PA153 antibodies (antagonists) can also be used in vivo for therapeutic use, e.g. treatment of pancreatic disease, tumours or metastases. Antisense PA153 polynucleotides can be used in gene therapy of pancreatic diseases. AAX78712-X78725 represent primers used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypermutable organism; dominant negative allele; mismatch repair gene;
spontaneous mutation; DNA repair; purine nucleotide phosphorylase; PNP;
bacteria; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                           il PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;
Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacterial PNP DNA fragment with an out-of-frame polyA tract.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.2%; Score 21; DB 1; Length 26; 100.0%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 26 BP; 0 A; 0 C; 1 G; 25 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6. .26
/*tag= a
/note= "Out-of-frame polyA tract"
                                                                                                                                                                                                                                                                                                                                               PA153 cDNA transcribed from pancreatic tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l. .5
/*tag= a
/note= "Bacterial PNP gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Page 121; 123pp; English
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                                                                                                              98WO-US026441.
                                                                                                                                                  97US-00990568
                                                                                                                                                                                                                             Billing-Medel PA, Cohen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD26899 standard; DNA; 26
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hes 21; Conservative
                                                                                                                                                                                                                                                                                                         WPI; 1999-405041/34.
                                                                                                                                                                                       (ABBO ) ABBOTT LAB
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Unidentified.
Chimeric.
                                                                                                                                                                                                                                                 Granados EN,
Russell JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
Homo sapiens
                                  WO9931274-A2
                                                                                                              11-DEC-1998;
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                                                                        24 - JUN - 1999
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Best Loca Matches

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cells
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                                                                                                                                                                     The invention relates to methods for generating a mutation in a gene of interesting using a dominant negative allele of a mismatch repair gene (D-MMR) under control of an inducible transcriptional regulatory element (TTRE). The invention is useful to provide new call lines that can be used for gene discovery, drug target discovery, recombinant gene mutagenesis or recombinant protein production. The present sequence is a polyPNP (purine phosphorylase) out-of-frame polyA tract DNA
                                                                                  Generating a mutation in a gene using a dominant negative allele of a mismatch repair gene which results in mismatch repair deficiency in ce containing the allele is useful in gene and drug target discovery and
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Normalised; cDNA library; mRNA cloning; reverse transcription; immobilise; screening; hybridisation; nucleic acid amplification; expression pattern; drug development; PCR primer; RT-PCR; ss.
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0
                                     Kinzler KW;
                                                                                                                                                                                                                                                                                                  Length 26;
                                                                                                                                                                                                                                                                                                                           0; Indels
                                     Vogelstein B,
                                                                                                                                                                                                                                                                           Sequence 26 BP; 22 A; 1 C; 2 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                               1.2%; Score 21; DB 1; Le
100.0%; Pred. No. 1.4e+02;
:ive 0; Mismatches 0;
                                     Grasso L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DISP-) DISPLAY SYSTEMS BIOTECH APS.
                                                                                                                                                                                                                                                                                                                                                   CAAAAAAAAAAAAAAA 1755
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                                                                                                                                                                                                                                                                                                                                                                         5 CAAAAAAAAAAAAAAAAAA 25
                                                                                                                                                 Example 5; Fig 7; 25pp; English.
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97US-00871030.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                           21; Conservative
                                     Nicolaides NC, Sass PM,
                                                                                                                         recombinant technology.
(VOGE/) VOGELSTEIN B.
           (KINZ/) KINZLER K W.
                                                            WPI; 2002-499469/53.
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                                                                                                                                                                                                                                                                                                              Local Similarity
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27-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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The invention relates to preparation of a normalised, subdivided library of amplified cDNA from the coding regions of mRNA in a sample. The method

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involves reverse transcription, with at least one cDNA primer of formula 5'-Conl-dTn2-Vn3-Nn4 to form first stand cDNA where Conl = any sequence of 1-100 nucleotides; dT = deoxythymidinyl; n2 is at least 1; n3 and n4 are both 0, or n3 is 1 and n4 is at least 1; followed by second strand con both 0, or n3 is 1 and n4 is at least 1; followed by second strand primer of a similar formula, in the presence of DNA polymerase I (or its Klenow fragment) and amplification of double-stranded cDNA with a set of atsabase (a computer-generated list of molecular weights of restricted DNA fragments of known sequence) is used to determine presence of an expressed protein in a cell, also to detect changes in such expression (particularly for diagnosis of disease). Surfaces (chip) having amplified CDNA stably immobilised on it, obtained by a similar method, are used to screen for genes of a particular family, by hybridisation with nucleic conditions the first of disease). Surfaces (chip) having amplified con the family (coidentify new genes) and to detect differences in expression patterns between cells. The polypeptides expressed by the control of the ford of the control of t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV71946 represent primers used to exemplify the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide-based cDNA characterisation; haemoglobin alpha 2; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transcript, genetic, and especially nucleic acid sequence analysis comprises analysis of hybrid peptide products.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.2%; Score 21; DB 1; Length 27; 100.0%; Pred. No. 1.5e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human haemoglobin alpha 2 transcript (extreme 3' end).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 27 BP; 0 A; 1 C; 1 G; 25 T; 0 U; 0 Other;
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Best Local Similarity
Matches 21; Conserve
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peptide is considerably smaller than the DNA molecule that encodes it (individual amino acids averages about 110 Daltons each whereas the trinucleorides (triplets) that encode them average N Daltons each). Also, the peptides are much more diverse in composition than nucleic acids, as they are composed of combinations of 20 different amino acids instead of combinations of 4 different nucleotides, e.g., two random DNA fragments of identical composition (e.g., with 10 adenines, 10 thymines, 15 guanines, and 15 cytosines) are extremely unlikely to encode peptides of identical composition. This means that whereas the two nucleic acids have identical masses and cannot be distinguished on the basis of mass, the peptides that they encode will, except in statistically very rare cases, have different masses and can be readily distinguished in the basis of mass. The present sequence represents the coding sequence of human haemoglobin alpha 2 transcript (extreme 3' end) used in an example to demonstrate the method of the invention 

Sequence 28 BP; 23 A; 2 C; 3 G; 0 T; 0 U; 0 Other;

Gaps ö 1.2%; Score 21; DB 1; Length 28; 100.0%; Pred. No. 1.5e+02; ive 0; Mismatches 0; Indels Query Match
Best Local Similarity luv...
Best 21; Conservative

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ABK48140/c RESULT 30

ABK48140 standard; DNA; 24 BP 

18-JUN-2002 (first entry) ABK48140;

Aspergillus niger aminopeptidase RT-PCR primer poly-T.

Aminopeptidase; primer; ss; food composition; dough; flavour enhancer; baked product; cheese; poly-T; reverse transcriptase PCR.

Synthetic.

WO200216618-A1.

22-AUG-2001; 2001WO-EP009925.

23-AUG-2000; 2000EP-00202995

(STAM ) DSM NV

Basten D, Dekker PJT, Schuurhuizen PW, Schaap PJ, Visser J;

WPI; 2002-257917/30.

An isolated polypeptide with aminopeptidase activity, for preparing food compositions, such as bread and cheese, with enhanced flavoring.

Example 5; Page 40; 94pp; English.

The invention relates to an isolated polypeptide with aminopeptidase activity and the gene encoding it (including sequences complimentary to the gene and which hybridise to it at high stringency). From Appergillus niger. Also included are a nucleic acid construct comprising the above polynucleotide operably linked to one or more control sequences that direct the production of the polypeptide in a suitable expression host, a recombinant expression vector comprising the above nucleic acid construct, a recombinant host cell comprising the above construct or vector, and producing the protein comprising cultivating an above strain/recombinant host cell to produce a supernatant and/or cells comprising the polypeptide and recovering the polypeptide. The aminopeptidase is used to prepare a food composition such as dough to enhance the flavour

ö of. a baked product from the dough and for preparing a cheese to enhance the flavour. The invention provides a bacterial enzyme for protein hydrolysis i.e. with aminopeptidase activity, to produce flavouring agents, and the enzyme has been isolated ancharacterised, compared to previously observed weak aminopeptidase activity which was detected in an Aspergillus niger culture filtrate but the source was never isolated or identified. The use of enzymes to produce flavouring agents from proteinaceous material is better than use of strong acids which can severely degrade the amino acids obtained. The present sequence is a reverse transcriptase (RT)-PCR primer used to investigate the intron-exon Gaps ö Match 1.2%; Score 20.6; DB 1; Length 24; Local Similarity 91.3%; Pred. No. 1.5e+02; les 21; Conservative 1; Mismatches 1; Indels Sequence 24 BP; 0 A; 0 C; 0 G; 23 T; 0 U; 1 Other; 1733 TACAAAAAAAAAAAAAAAAAA 1755 structure of the aminopeptidase gene 24 BAAAAAAAAAAAAAAAAAAA 2 Query Match Matches 8888888888888888

RESULT 31 AAS20595/

AAS20595 standard; DNA; 26

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AAS20595;

(first entry) 23-APR-2002

Human zsig63 cDNA sequencing primer ZC7231.

Human; zsig63; chromosome 4q12-4q13; salivary protein; antimicrobial; ss; microbial infection; tooth decay; periodontal disease; thrush; emphysema; gastrointestinal disease; urinary tract infection; vaginal infection; skin infection; epithelial wound; chronic tissue damage; cystic fibrosis; acquired immunodeficiency syndrome; ADBS; lung infection; sarcoidosis; chronic bronchitis; gene therapy; protein therapy; primer; ZC7231.

Homo sapiens

US6331413-B1

18-DEC-2001.

17-MAR-2000; 2000US-00527345.

17-MAR-1999; 99US-0124820P.

(ZYMO ) ZYMOGENETICS INC.

Sheppard PO;

Adler DA,

WPI; 2002-096707/13

Polynucleotides encoding salivary proteins useful as anti-microbial agents.

Example 1; Col 53; 29pp; English.

The invention relates to a polynucleotide derived from the 4q12-4q13 region of human chromosome 4 and encoding a zaj653 polypeptide, a secreted aalivary protein with anti-microbial activity. Due to their microbial activity, the sequences can be used in the study of microbial infections, e.g. for recombinant production of anti-microbial proteins. The sequences can be used in the treatment of tooth decay, periodontal disease, thrush, gastrointestinal disease, uninary tract infections, vaginal infections, skin infections, epithelial wounds, chronic tissue damage, acquired immunodeficiency syndrome (AIDS), cystic fibrosis, lung infections, sarcoidosis, emphysema and chronic bronchitis. This sequence represents a sequencing primer for cDNA encoding human zsig63 

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Length 26;
Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;
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Gaps ö 1; Indels Query Match 1.2%; Score 20.6; DB 1; Best Local Similarity 91.3%; Pred. No. 1.6e+02; 1; Mismatches 1733 TACAAAAAAAAAAAAAAA 1755 21; Conservative Matches

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ABS52637 standard; DNA; 26

ABS52637;

15-NOV-2002 (first entry)

Human secreted salivary protein zsig63 PCR primer ZC7321.

Human; secreted salivary protein; zsig63; immunogen; zsig63-cytokine; antibody-cytokine; in vivo killing; pathological microbe; bacteria; fungal, viral; infection; salivary gland; anti-microbial; dental caries; tooth decay; periodontal disease; thrush; gastrointestinal disease; urinary tract infection; vaginal infection; skin infection; microflora; epithelial wound; pathogenic colonisation; invasion; pro-inflammatory; entront issue damage; vascular system; diabetes; anti-inflammatory; incompetent immune system; AIDS; acquired immunodeficiency syndrome; chemocherapy; radiation treatment; lung infection; cystic fibrosis; digestion; PCR; primer; ss.

Homo sapiens.

US2002081701-A1

27-JUN-2002.

03-AUG-2001; 2001US-00922480

17-MAR-1999; 99US-0124820P.

(ADLE/) ADLER D A. (SHEP/) SHEPPARD P O.

Adler DA, Sheppard PO; WPI; 2002-635468/68. Novel secreted salivary protein, zsig63 and polynucleotide encoding it useful for treating microbial infections, inflammatory conditions, dental caries and lung infections associated with cystic fibrosis.

Example 1; Page 29; 33pp; English.

The present invention relates to a new secreted salivary protein, zsig63.

The invention is useful for detecting in a test sample, the presence of
an antagonist or agonist of zsig63 protein activity. The invention is
also useful as an immunogen for producing an antibody to zsig63
also useful as an immunogen for producing an antibody-cytokine fusion
protein are useful for enhancing in vivo killing of target tissues.

Compresention composition comprising purified asig63 polypeptide are
useful in the treatment of conditions associated with pathological
microbes, including bacterial, fungal and viral infections. High
compression of zsig63 in salivary gland suggests that anti-microbial
comprised are useful for treatment of dental caries (tooth decay),
periodontal disease, thrush and gastrointestinal disease. Other
applications can be used in urinary tract infections, vaginal infections,
prevention of infection in skin and other epithelial wounds. The
colypeptides can be used to establish normal microflora and protect
against pathogenic colonisation and invasion. The invention is useful
when pro-inflammatory activity is desired. Applications for such pro-RESULT 32
ABS52637/C
A

inflammatory activity include the treatment of chronic tissue damage, dancticularly in areas having a limited or damaged vascular system e.g., damage in extremities associated with diabetes. Antagonists to zaig63 polypeptides may be useful as anti-inflammatory agents. The invention is useful for the treatment of patients having incompetent immune system, that have undergone chemotherapy, radiation treatment. The invention is also useful for the treatment of lung infections associated with cystic fibrosis and its agonists or antagonists are useful for adiang digestion. The present nucleic acid sequence represents a PCR primer that was used in the methods of the invention for identification of zaig63 Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other; 88888888888888888

Gaps ö 1.2%; Score 20.6; DB 1; Length 26; 91.3%; Pred. No. 1.6e+02; tive 1; Mismatches 1; Indel8 21; Conservative Local Similarity Query Match Best Loca Matches

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1733 TACAAAAAAAAAAAAAAAAA 1755 8 쉽

AAD45054/

AAD45054 standard; DNA; 26 BP.

AAD45054;

27-DEC-2002 (first entry)

2C7231 primer used in the identification of human zsig63 DNA.

Human; secreted salivary protein; zsig63 protein; host defense protein; immune modulating factor; antipathogenic; cell-cell signalling molecule; growth factor; cytokine; growth factor hormone activity; dental carries; infection; tooth decay; periodontal disease; gastrointestinal disease; thrush; urinary tract infection; vaginal infection; diabetes; obesity; anti-inflammatory; chronic tissue damage; lung dysfunction; restenois; gene therapy; salivary gland dysfunction; prostate gland dysfunction; forensic DNA profiling; chondrosarcoma; atherosclerosis; primer; ss. 

Homo sapiens.

US2002090677-A1.

11-JUL-2002.

03-AUG-2001; 2001US-00923236.

17-MAR-1999; 99US-0124820P. 17-MAR-2000; 2000US-00527345.

(ADLE/) ADLER D A. (SHEP/) SHEPPARD P O.

Adler DA, Sheppard PO;

WPI; 2002-642378/69.

Novel secreted salivary polypeptide, zsig63, useful as antimicrobial agent for treating microbial infection, dental carries, periodontal disease, thrush gastrointestinal disease, and for aiding digestion.

Example 1; Page 29; 33pp; English.

The invention relates to human secreted salivary polypeptide designated as zsig63 and nucleic acid molecules encoding such polypeptides. zsig63 can be used in detecting agonists and antagonists of its activity, and is also useful as a host defense polypeptide, immune modulating factor, antipathogenic polypeptide, cell-cell signalling molecule, growth factor, cytckine, or as secreted extracellular matrix associated proteins with growth factor hormone activity. It is useful for treating conditions

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disease, thrush and gastrointestinal disease, for treating, fungal and disease, thrush and gastrointestinal disease, for treating urinary tract infection, vaginal infection and for preventing infection in skin and other epithelial wounds. Zsig63 is useful for establishing normal and protect against pathogenic colonisation and invasion, for treating chronic tissue damage e.g. damage in extremities associated with diabetes and useful as anti-inflammatory agents. It is useful as a marker of lung dysfunction, salivary gland dysfunction, or dysfunction of prostate gland. It is also therapeutically useful for aiding disestion. Polymucleotides of the invention are used in gene therapy for increasing or inhibiting zsig63 activity, for detecting abnormalities on human chromosome 4 associated with disease or other human traits and as diagnostics in forensic DNA profiling. Sequences of the invention are useful for stimulating proliferation or differentiation of cardiac myocytes, for proliferation or differentiation of adipocytes and for inhibiting chondrosarcomas, atherosclerosis, restenosis and obesity. The present sequence is a primer used in the identification of human zsig63 DNA
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Pred. No. 1.6e+02;
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AAD55692 standard; DNA; 26 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                periodontal disease; thrush; gastrointestinal disease; epithelial wound; urinary tract infection; vaginal infection; skin infection; primer; pro-inflammatory; chronic tissue damage; vascular system; diabetes; AIDS; lung infection; cystic fibrosis; lung dysfunction; digestive; salivary gland carcinoma; Pneumocystis carinii infection; emphysema; chronic bronchitis; prostate dysfunction; prostate adenocarcinoma; cell culture media; gene therapy; human chromosome 4q12-4q13; dentinogenesis imperfecta; dentin dysplasia type II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated zsig63 polypeptide comprising at least 90% identity to an amino acid sequence which comprises domain 1 of zsig63, domain 2, domain 3, mature zsig63 and full length zsig3. Also included are the polymucleotide encoding zsig63, a zsig63 expression vector, a cultured cell comprising the vector and expressing the protein, a DNA encoding a fusion protein (comprising amino acids 1-15, 16-37, 38-126, 127-219 or 16-219 of zsig63 and an additional protein), using a matu-zsig63 antibody using zsig63 immorgenic peptides, zsig63 is useful for detecting in a test sample, the presence of antagonist of zsig63 protein activity. Zsig63 has antimicrobial activity and since exhibits high expression in salivary gland, can be used for treating dental carries, periodontal disease, thrush, and gastrointestinal disease, urinary tract infections, vaginal infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated zsig63 polypeptide, member of the adhesin family, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for treating dental carries, periodontal disease, thrush, gastrointestinal disease, urinary tract infections, vaginal infections, skin infections.
is a PCR primer used to amplify BVDV gene. (Updated on 27-OCT-2003 to standardise OS field)
                                                                                                                                       Gape
                                                                                                                                     ö
                                                                                           tch 1.2%; Score 20.6; DB 1; Length 26; al Similarity 91.3%; Pred. No. 1.6e+02; 21; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ss; PCR; zsig63; adhesin; salivary gland; dental carries;
                                                           Seguence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                              Human zsig63 PCR/sequencing primer ZC7231.
                                                                                                                                                                           1733 TACAAAAAAAAAAAAAAAAAAA 1755
                                                                                                                                                                                               Example 1; Page 29; 32pp; English.
                                                                                                                                                                                                                                                                                                              ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-AUG-2001; 2001US-00922469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0124820P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-MAR-1999; 99US-0124820P.
17-MAR-2000; 2000US-00527345.
                                                                                                                                                                                                                                                                                                            ABX93598 standard; DNA; 26
                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adler DA, Sheppard PO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SHEP/) SHEPPARD P O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-328428/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADLE/) ADLER D A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS2002173027-A1.
                                                                                                                                                                                                                                                                                                                                                                                        28-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                  ABX93598;
                                                                                                 Query Match
                                                                                                                     Local
                                                                                                                                                                                                                                                                      RESULT 35
ABX93598/c
                                                                                                                                     Matches
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                                                                                                                                                                                                             엄
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normal microfilora and protect against pathogenic colonization and invasion. Zsig63 can also be used for providing pro-inflammatory activity invasion. Zsig63 can also be used for providing pro-inflammatory activity for treating offronic, tissue damage particularly in areas having limited or damaged vascular system, e.g. in diabetes, and for treating limited or confidence and for treating limited or immunocompromised AIDS patients or in individuals that have undergone confidence and and and properties are at a section of casigas polypeptides that have undergone confidence in the trachem may indicate that such polypeptides may serve as a marker of lung dysfunction. Zsig63 is also useful in diagnosing conditions associated with salivary gland or lung dysfunction including salivary gland carcinom. Pneumocystis carinii infection, emphysema, chronic bronchitis, prostate dysfunctions such as prostate adenocarcinoma, aiding digestion, and as components of defined cell culture media and may be used to replace serum that is commonly used in culture. The DNA is useful in gene therapy applications to increase or inhibit zsig63 activity, and for detecting abnormalities on human cultume. The DNA is useful in gene therapy applications to increase or inhibit zsig63 activity, and for detecting abnormalities on human conformation dentin dysplasia type II). Zsig63 is an adhesin family member. The present sequence is a primer used to isolate and sequence nucleic acdis encoding human zsig63 other epithelial wounds. The polypeptides can be used to establish 

Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;

;; 0 Length 26; 1; Indels DB 1; 1.2%; Score 20.6; DB 1; 91.3%; Pred. No. 1.6e+02; 1; Mismatches 1733 TACAAAAAAAAAAAAAAAAA 1755 21; Conservative Best Local Similarity Query Match Matches

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Gaps

26 ВАААААААААААААААААААА 4

ACF36382 standard; DNA; 26 BP 04-DEC-2003 (first entry) ACF36382; ACF36382/
TD ACF36382/
XX ACF36382/
XX ACF3
XX Nucl
XX

Nucleotide sequence of a second back primer.

Nucleic acid manipulation; mRNA profiling; polymerase chain reaction; electrophoresis; PCR; primer; ss.

Synthetic.

WO2003064691-A2. 07-AUG-2003.

28-JAN-2003; 2003WO-IB000843.

29-JAN-2002; 2002US-0352215P

(GLOB-) GLOBAL GENOMICS AB

ducing a population of double-stranded product DNA molecules, useful mRNA profiling, comprises amplification by nested polymerase chain Linnarsson S, Ernfors P, Bauren G, Metsis A, Montelius A; WPI; 2003-618365/58. Producing a

Pihlak A;

Claim 6; Page 85; 105pp; English.

reaction.

The invention relates to producing a population of double-stranded product DNA molecules comprising amplification by a nested PCR method. The method is useful in profiling mRNA transcribed in a system under investigation. The oligonucleotides are used as size standards in

This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide sequence comprising at least a significant part of a nucleotide sequence coding for a stratum corneum chymotryptic enzyme (SCCB) or its variant, operably linked to a promoter that drives expression of heterologous sccor its variant in skin. The product of the invention is useful as a model or its variant in skin. The product of the invention is useful as a model or a study of disease with the aim of improving treatment, to relieve or ameliorate a pathogenic condition, for development or testing of a cosmetic or a pharmaceutical formulation, and for the development of a diagnostic method. It can also be used as a model for a skin disease or skin cancer. The invention is also useful for screening or identifying a compound or composition effective for the prevention or treatment of an compound or composition effective for the prevention or treatment of inflammatory skin diseases selected from diseases consisting of epidermal compound or composition effective for the prevention or treatment of inflammatory skin diseases selected from diseases consisting of epidermal compound or compositions of example inflammation, dermal inflammation, pruritus, atopic dermatitis, eczema, acce and inherited skin diseases with epidermal hyperkeratosis. The mechanisms and the testing of each of the mechanisms and the testing of each of the compound or composition of the mechanisms and the testing of the composition of the composition of the mechanisms and the testing of the composition of the composition of the mechanisms and the testing of the composition ö heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin. SCCE; murine; stratum corneum chymotryptic enzyme; kallikrein 7; serihe protease; kin cancer; hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation; prunitus; atopic dermatitis; eczema; acne; itch; KLK7; ss. ø Transgenic mammal or its embryo useful as model for human disease, has electrophoresis, and as internal controls allowing for calculation of relative amounts of material present. The present sequence represents specific example of a PCR primer used in the method of the invention Gaps ; 0 Score 20.6; DB 1; Length 26; Pred. No. 1.6e+02; 1; Mismatches 1; Indels Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other; Murine SCCE 5'-RACE oligonucleotide SEQ ID 42. 1733 TACAAAAAAAAAAAAAAAAA 1755 26 BAAAAAAAAAAAAAAAAAAAAAA 4 Example 6; Page 36; 74pp; English. ABQ76254 standard; DNA; 27 BP. 1.2%; 08-FEB-2002; 2002WO-IB001300. 09-FEB-2001; 2001CA-02332655. 09-FEB-2001; 2001DK-00000218. 08-NOV-2002 (first entry) Matches 21; Conservative Egelrud T, Hansson L; WPI; 2002-643380/69. Query Match Best Local Similarity (EGEL/) EGELRUD T. (HANS/) HANSSON L. WO200262135-A2 Mus musculus. 15-AUG-2002. ABQ76254; ABQ76254/c RESULT 37 ន្តដ្តម្ភិន ò 유 

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potential compounds and compositions for relieve of various skin diseases where itch is a component. This sequence represents a 5' RACE cDNA synthesis primer used in a method of detecting homologues to human stratum corneum chymotryptic enzyme, SCCE, gene. SCCE is a serine protease synonymous with human kallikrein 7 (KLK7) and is used in the development of the transgenic mammals described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coxeackie virus strain VD2921; diabetogenic coxeackie B virus-4; CBV-4; strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D; diabetes; diabetogenic enterovirus; beta cell loss; blindness; renal fallure; leg amputation; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymerase chain reaction and primers for detecting nucleic acids from the diabetogenic coxsackie B virus-4 strain VD2921.
                                                                                                                                           Gaps
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0
                                                                                                                                                                                                                                                                                                                                 Coxsackie B virus 4 (CBV-4) strain VD2921, PCR primer dT26V.
                                                                                                              1.2%; Score 20.6; DB 1; Length 27; 91.3%; Pred. No. 1.7e+02; ative '1; Mismatches 1; Indels
                                                                                       Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 1 Other;
                                                                                                                                                                1733 TACAAAAAAAAAAAAAAAAAA 1755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 5; Page 44; 79pp; English.
                                                                                                                                                                                  ABX12469 standard; DNA; 27 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INNO-) INNOVENTUS PROJECT AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUN-2002; 2002WO-IB003278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-JUN-2001; 2001SE-00002198
                                                                                                                                                                                                                                                                                                          10-MAY-2003 (first entry)
                                                                                                                            Best Local Similarity 91.3
Matches 21, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Frisk GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-278229/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2002103060-A2
                                                                                                                                                                                                                                                                                                                                                                                                                          Coxsackievirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tuvemo HT,
                                                                                                                                                                                                                                                                                 ABX12469;
                                                                                                                Query Match
                                                                                                                                                                                                                                RESULT 38
                                                                                                                                                                                                                                            ABX12469/
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This sequence was used to determine whether 2-5A-antisense chimeric molecules are inhibitory to cell growth. The molecules AAQ64709, AAQ64711 and AAQ64724 all lacked cytotoxicity. In the novel 2-5A-antisense oligonuclectide chimeric molecules, the antisense region targets the chimeric molecule to a particular region of RNA to be specifically clasved and the 2',5'-linked terraadenylate tail activates the 2-5A RNase. Typical applications are treatment of viral infections (esp. cleavage of an RNA virus genome), cancer; leukaemia, cardiovascular disorders (e.g. restenosis after angloplasty), genetic disorders, osteoarthritis or rheumatoid arthritis. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Specific cleavage of RNA, useful partic. for treating viral infection, cancers, etc. - by using anti-sense oligo:nucleotide coupled to activator of 2-5A dependent RNase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA
                                                                                                                                                                                                                                                                                                                                                                                                                           phosphodiester bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "the 2-5A moiety (*tag = a) and the antisense sequence (*tag = c) are linked by two 1,4-butanediol molecules linked through phosphodiester bonds"
                                                                                                                                                                                                                         틸.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "antisense region, complementary to oligo dT"
                                                                                                                                                                                                                                                    antisense; 2',5'-tetraadenylate; 2-5A dependent RNase activator; RNA cleavage; antiviral therapy; chimeric molecule; PKR; protein synthesis regulation; phosphorylation; eIF-Zalpha; eukaryotic translation initiation factor; ss
                                                                                                                                                                                                                        2',5'-linked tetraadenylate-anti(dT)18 oligonucleotide chimeric
                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a /*tag= a /*tag= a /*tag= a /*tabel= 2.,5'-linked tetraadenylate /note= "nucleotides linked through phosp at hydroxyl groups of 2' and 5' carbons"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 꿏
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lesiak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES.
(CLEV-) CLEVELAND CLINIC RES INST.
                                                                                                                  BP.
           1755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maitra R,
                                                                                                                  AAQ64724 standard; cDNA to mRNA; 22
                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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       27 BAAAAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92US-00965666.
93US-00123449.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93WO-US010103.
                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Silverman R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag=
                                                                                                                                                                           (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1994-151315/18.
                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Torrence P,
                                                                                                                                                                           25-MAR-2003
04-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9409129-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-APR-1994.
                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                AAQ64724;
                                                                                    RESULT 39
                                                                                                    AAQ6472
                                                                                                                                  ⊹∂
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Gaps

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1.2%; Score 20.6; DB 1; Length 27; 91.3%; Pred. No. 1.7e+02; tive 1; Mismatches 1; Indels

21; Conservative

Best Local Similarity

Query Match Matches /mod_base= OTHER /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine" il. .12

Location/Qualifiers

*tag=

(first entry)

(revised)

*tag= d note= "o-xyloso dimer synthon linkage" [2, .23]

/*tag= c
/label= inverted_polarity_region
/note= "see comments"

/mod_base= OTHER /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"

*tag= b

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Human interleukin-6 gene; herpes simplex; AIDS; modified; HIV; RSV; HPV; malignancy; hepatitis; inflammation; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New oligomers contg. modified bases - which form a triplex with G-C doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis, herpes malignancy and inflammation.
                                Oligomer IL6803 for forming triplex with HUMIL6 target duplex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GILE-) GILEAD SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1992-217083/26.
                                                                                                           Key
modified_base
                                                                                                                                                                                                                                           modified base
25-MAR-2003
07-DEC-1992
                                                                                                                                                               misc_feature
                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                WO9209705-A1
                                                                                                                                                                                                                                                                                                                                          25-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Froehler B,
                                                                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-1991;
                                                                                                                                                                                                                                                                                                                      11-JUN-11992
                                                                                                                                                                                                                                                                                                                                                                23-NOV-1990,
                                                                                                                                                                                                                                                                                                                                                                                                          7-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                      08-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                 17-APR-1991
                                                                                       Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNAc comprising a promoter P and an L1 cassette sequence having a core retrotransposon element, useful for random insertion of a heterologous or homologous DNA sequence into a cell genome and for correcting genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to DNA for a promoter and an L1 cassette sequence having a core retrotransposon element. The invention is useful for random insertion of a heterologous or homologous DNA sequence into a cell genome, and for correction of a genetic defect in the cell into which the insertion is made. Genetic defects which may be corrected includes cystic fibrosis, mutations in the dystrophin gene, genetic defects associated with blood clotting and other genetic defects
                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 1.2%; Score 20.4; DB 1; Length 22; 1 Similarity 95.5%; Pred. No. 1.5e+02; 21; Conservative 0; Mismatches 1; Indels
                      Length 22;
                                          1; Indels
                                                                                                                                                                                                                               Retrotransposon; genetic defect; cystic fibrosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 22 BP; 22 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Sequence 22 BP; 22 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                            Dombroski BA, Kazazian HH, Boeke JD
                    Query Match 1.2%; Score 20.4; DB 1; Best Local Similarity 95.5%; Pred. No. 1.5e+02; Matches 21; Conservative 0; Mismatches 1;
                                                                                                                                                                                                           Ll cleavage site related sequence #3.
                                                                1734 ACAAAAAAAAAAAAAAAAA 1755
                                                                                    1 AAAAAAAAAAAAAAAAAAA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 14; 87pp; English.
                                                                                                                                                                                                                                                                                                                       97US-00847844
                                                                                                                                                                                                                                                                                                                                          95US-0006831P.
96US-00749805.
                                                                                                                                                                                                                                                                                                                                                                         (UYPE-) UNIV JOHNS HOPKINS.
                                                                                                                                          AAF17413 standard; DNA; 22
                                                                                                                                                                                    09-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-060015/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                      Unidentified.
                                                                                                                                                                                                                                                                                                                      28-APR-1997;
                                                                                                                                                                                                                                                                                                                                           16-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                      15-NOV-1996;
                                                                                                                                                                                                                                                                           US6150160-A.
                                                                                                                                                                                                                                                                                                21-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                            Moran JV,
                                                                                                                                                                AAF17413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                       RESULT 40
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ph with a purine rich target sequence by coupling into the major groove of the duplex. The specific target sequence of this oligomer is the human intranslated sequence contg. a purine rich sequence concd. on one strand of the duplex. The oligomer, and others like it are useful in diagnosis and therapy of diseases characterised by specific DNA duplex targets, e.g. HPV, HER, HIV, hepatitis B. herpes, malidonal trumcurs and inflammation. The triple the subjecting the test specific DNA two assays may be carried out without subjecting the test specimen to harsh conditions. The oligomer contains an inverted polarity region formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso (mucleotides have the 3/positions of xylose sugars linked via the o-xylene ring). Two nucleotides are coupled through a xylene residue to form the dimer synthon. This additions may render the collower stable to nuclease activity. The oligomer is able to inhibit gene expression, as verified by in vitro systems. See also AAQ25452-25501 and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                              The synthetic oligomer is capable of forming a triplex at physiological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 23 BP; 2 A; 0 C; 0 G; 21 T; 0 U; 0 Other;
Claim 12; Page 71; 77pp; English.
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Gaps °;

1734 ACAAAAAAAAAAAAAAAAA 1755

Matches

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1 AAAAAAAAAAAAAAAAAA 22

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AAQ30430 standard; DNA; 23

AAQ30430/c

RESULT 41

AAQ30430;

Krawczyk S, Matteucci MD, Milligan J;

90US-00643382. 91US-00643382. 91US-00683420. 91US-00686544. 91US-00686546.

91WO-US008811

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Gaps

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The synthetic oligomer is capable of forming a triplex at physiological pH with a purine rich target sequence by coupling into the major groove of the duplex. The specific target sequence of this oligomer is the human interleukin 6 gene untranslated sequence contg. a purine rich sequence concd. on one strand of the duplex. The oligomer, and others like it are
                                                                                                                                                                                                                                         Human interleukin-6 gene; herpes simplex; AIDS; modified; HIV; RSV; HPV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New oligomers contg. modified bases - which form a triplex with G-C doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis, herpes malignancy and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= b
/mod_base= OTHER
/note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
                                                                                                                                                                                                                 Oligomer IL6804 for forming triplex with HUMIL6 target duplex.
1.2%; Score 20.4; DB 1; Length 23; 95.5%; Pred. No. 1.6e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                           11. .12
/*tag= d
/*tag= d
/*tag= 1. .xi
/*tag= 1. .xi
/*tag= 1. .xi
                                                                                                                                                                                                                                                                                                                                         /mod_base= OTHER
/note= "OTHER= N4 N4 ethanocytosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matteucci MD, Milligan J;
                                                                                                                                                                                                                                                                                                                                                                                                               *tag= c
label= inverted_polarity_region
                                                                                                                                                                                                                                                    malignancy; hepatitis; inflammation; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "see comments
                                                1733 TACAAAAAAAAAAAAAAAAA 1754
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                     23 TAAAAAAAAAAAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; Page 71; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           910S-00643382.
910S-00683420.
910S-00686544.
910S-00686546.
910S-00686546.
                                                                                                                                 BP
                                                                                                                 91WO-US008811
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                        Conservative
            Similarity
                       21;
 Query Match
Best Local
             Best Loc
Matches
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useful in diagnosis and therapy of diseases characterised by specific DNA duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant tumours and inflammation. The triple helices form under mild conditions thus assays may be carried out without subjecting the test specimen to harsh conditions. The oligomer contains an inverted polarity region formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso (nucleotides have the 3'positions of xylose sugars linked via the o-xylone tring). Two nucleotides are coupled through a xylone residue to form the dimer synthon. This additional modifications may render the oligomer stable to nuclease activity. The oligomer is able to inhibit gene expression, as verified by in vitro systems. See also AAQ25452-25501 and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           incorporated at predetermined site from a solid support involves cleaving the nucleic acid molecule at the site of unconventional nucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention is concerned with the cleavage of nucleic acids from solid supports. This is carried out by adding a non-conventional nucleotide into the nucleic acid attached to the support, so that it is recognised and cleaved by a specific DNA glycosylase and the sequence is released. This is useful in many molecular biological procedures such as sequencing, in vitro amplifications, cDNA and template preparation, DNA-based assays, mutagenesis procedures, nucleic acid purification and affinity chromatography. The present sequence is an oligonucleotide used in assays to demonstrate the methods of the invention
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detaching nucleic acid molecule comprising unconventional nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cleavage of nucleic acids from solid supports assay oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid cleavage; solid support; DNA-RNA hybrid;
affinity chromatography; sequencing; mutagenesis; DNA preparation;
nucleic acid purification; ss.
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                                                                                                                                                                                                                                                                                                 23;
                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                               1.2%; Score 20.4; DB 1; Length 95.5%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                            Seguence 23 BP; 1 A; 1 C; 0 G; 21 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         1733 TACAAAAAAAAAAAAAAAAA 1754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 16; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                            23 TAAAAAAAAAAAAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-MAR-2000; 2000WO-GB001190.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC62450 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                     21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GOLD/) GOLDSBOROUGH A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-OCT-2000.
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misc_RNA
                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                     Local
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Sequence 23 BP; 0 A; 0 C; 0 G; 22 T; 1 U; 0 Other;

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(ROBB/) ROBBINS D.
                                                                                                                                                                         LING/) LING J C.
                                                                US2001044936-A1.
                                           Homo sapiens.
                                                                                                                                22-OCT-1998;
                                                                                                          22-OCT-1999;
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                                                                                     22-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                        Detaching nucleic acid molecule comprising unconventional nucleotide incorporated at predetermined site from a solid support involves cleaving the nucleic acid molecule at the site of unconventional nucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention is concerned with the cleavage of nucleic acids from solid supports. This is carried out by adding a non-conventional nucleotide into the nucleic acid attached to the support, so that it is recognised and cleaved by a specific DNA glycosylase and the sequence is released. This is useful in many molecular biological procedures such as sequencing, in vitro amplifications, cDNA and template preparation, DNA-based assays, mutagenesis procedures, nucleic acid purification and affinity chromatography. The present sequence is an oligonucleotide used
                                                                                                                                                                                                                 Nucleic acid cleavage; solid support; affinity chromatography; sequencing; mutagenesis; DNA preparation; nucleic acid purification; se
                                                                                                                                                                                               Cleavage of nucleic acids from solid supports assay oligonucleotide #2.
                                 Gaps
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        1.2%; Score 20.4; DB 1; Length 23; 95.5%; Pred. No. 1.6e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.2%; Score 20.4; DB 1; Length 23;
95.5%; Pred. No. 1.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    affinity chromatography. The present sequence is an oin assays to demonstrate the methods of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human MSH2 (hMSH2) intronic sequence SEQ ID NO:126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23 BP; 0 A; 0 C; 0 G; 0 T; 23 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                    1734 ACAAAAAAAAAAAAAAAAA 1755
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                                                                  28-MAR-2000; 2000WO-GB001190
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Best Local Similarity 95.55.
Conservative
                                                                                                                                AAC62451 standard; RNA; 23
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                                                                                                                                                                         (first entry)
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                   Best Local Similarity 95.5
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                               (GOLD/) GOLDSBOROUGH A.
                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-664908/64
                                                                                                                                                                                                                                                                          WO200058329-A1
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                                                                                                                                                                                                                                                     Synthetic.
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                                                                                                                                                    AAC62451;
           Query Match
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ABL01773
                                                                                                          RESULT 44
AAC62451/
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The present invention describes a variant human MLH1 or MSH2 gene. Also described are: (1) a method for diagnosing or predicting susceptibility to hereditary non-polyposis colorectal cancer (HNPCC), comprising screening a DNA sample for the variant MLH1 or MSH2 gene where presence of the variant indicates presence of, or susceptibility to HNPCC; (2) a method of identifying mutants in splice donor or acceptor sites of a human MLH1 gene, comprising sequencing splice donor or acceptor sites of the genewith intronic primers for the human MLH1 gene and analysing the sequence to identify any mutants; (3) a method of identifying mutants in splice donor or acceptor sites of the gene with intronic primers for the human MSH2 gene and analysing the sequence to identify any mutants; and (4) a transgenic model system for colorectal cancer comprising cells expressing the variant MLH1 or MSH2 gene. The hMLH1 and hMSH2 variants are used to diagnose or determine a patients

OND ABL01745 and ABL01746 to ABL01831 represent hMLH1 and hMSH2 gene or the present invention mutagenic primers used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New variants of the human MLH1 and MSH2 genes for diagnosing or determining a predisposition for hereditary non-polyposis colorectal
Human, MLH1; MSH2; hMLH1; hMSH2; variant gene; diagnosis; HNPCC;
hereditary non-polyposis colorectal cancer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLYA, a competitor oligonucleotide for binding human PUR-alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 23 BP; 21 A; 0 C; 1 G; 1 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ling JC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0105180P.
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hes 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIN-GOERKE J
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The present invention describes a monoclonal antibody that specifically binds to an epitope of the PUR protein. Antibodies that bind to the PUR protein and neutralise PUR activity may be used to treat hyperproliferative diseases such as cancer. PUR antibodies may be used diagnostically to detect aberrant expression of the PUR protein and/or mutations in the PUR gene. The present sequence represents an oligonucleotide used in the cloning and sequencing of the PUR protein and its sequence element PUR repeat, in an example from the present invention
                                 This is the nucleotide sequence of an oligonucleotide used as a competitor with the PUR element in the method of the invention, involving the use of the PUR protein and its fragments, which inhibit PUR protein binding to PUR element or other proteins. Inhibitors of PUR activity may be useful for treating viral infections and hyperproliferative diseases such as cancer
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PUR element; PUR-alpha; hyperproliferative disease; cancer; human; monoclonal antibody; identification; characterisation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monoclonal antibody specific for PUR protein - useful for treating
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                                                                                                                                                                                                             Length 24;
                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide POLYA used in PUR cloning and sequencing.
                                                                                                                                                                    Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                       Score 20.4; DB 1;
Pred. No. 1.6e+02;
0; Mismatches 1;
 Example 7.1.1; Col 33; 63pp; English.
                                                                                                                                                                                                                                                                                      1734 ACAAAAAAAAAAAAAAAAA 1755
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                                                                                                                                                                                                                                                                                                                        1 AAAAAAAAAAAAAAAA 22
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                                                                                                                                                                                                         1.2%;
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95US-00470911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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Matches 21; Conservative
                                                                                                                                                                                                                           Local Similarity 95.5
les 21, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JUN-1995;
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06-JUN-1995;
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                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                     The oligonucleotides AAT99279-T99286 were used as competitor oligonucleotides for the binding of PUR prtein to DNA. The PUR sequence can be used to identify chemical or biological compounds that bind to PUR or binding fragments of PUR. Inhibitors of PUR activity may be used to treat hyperproliferative diseases such as cancer
                                                                                                                                                                                                                                                                                                                                        Assays for PUR protein ligands or modulators - using immobilised PUR protein or fragments, to treat hyper-proliferative diseases, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUR protein and its fragments - that inhibit PUR protein binding to PUR element or other proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PUR-alpha gene; inhibition; viral infection; cancer; PUR element;
hyperproliferative disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.2%; Score 20.4; DB 1; Length 24; 95.5%; Pred. No. 1.6e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide sequence of the oligonucleotide POLYA.
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                                                                                                                                                                                                                           (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
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                                                                                                                                                92US-00938189.
93US-00014943.
95US-00470911.
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93US-00014943
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Best Local Similarity 95.55,
Best Local Similarity 21,
Conservative
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                                                                                                                                                                                                                                                                  Johnson EM;
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                                                                                                                                                                                                                                                                                                    WPI; 1997-488859/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-321632/28.
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                                                                                                                                                                                                                                                                  Bergemann AD,
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Homo sapiens
                                                                                                            07-JUN-1995;
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02-FEB-1993;
                                                                                                                                                  28-AUG-1992;
                                                                                                                                                                                       36-JUN-1995;
                                                                                                                                                                      32-FEB-1993;
                                     USS672479-A
                                                                         30-SEP-1997
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RESULT 47 AAV31743 ID AAV

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1734 ACAAAAAAAAAAAAAAAAAA 1755

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25-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inserting a nucleic acid into a circular vector comprising joining their ends, melting, and reannealing ends at two different concentrations, useful for cloning small amounts of nucleic acids and forming genomic
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Pred, No. 1.6e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 24 BP; 0 A; 0 C; 0 G; 16 T; 8 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pBluescriptSK+ phagemid primer SEQ ID NO: 3.
                                                                                                                                                                                                                                                       pBluescriptSK+ phagemid primer SEQ ID NO: 9.
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                      1 AAAAAAAAAAAAAAAAA 22
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1.2%;
Best Local Similarity 95.5%;
Matches 21; Conservative
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                                                                                                                             24
                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                 Primer; cloning; ligation;
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                                                                                                                         AAA40359 standard, RNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ROMA/) ROMANTCHIKOV Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-442381/38.
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                                                                                                                                                                                                             10-NOV-2000
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                                                                                                                                                                                                                                                                                                                                           Synthetic
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                                                                                                                                                                     AAA40359;
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                                                                                                     AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAA40359/AAAA40359/AAA40359/AAAA40359/AAAA40359/AAAA40359/AAAA40359/AAAA40359/AAAA59/AAAA40359/AAAA40359/AAAA40359/AAAA40359/AAAA40359/AAAAAAAAA507
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                                                                                   RESULT
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This invention describes a novel method (M1) for inserting a nucleic acid (M1) into a circular vector (V1) comprising joining ends of N1 and V1 under a first nucleic acid concentration, melting hybridized cohesive circularization ends, and reannealing the ends at a second concentration. The methods are useful for the cloning small amounts of nucleic acids and forming genomic libraries of complex populations of DNA or cDNA. The methods allow the cloning of minute amounts of nucleic acids efficiently and avoids the size selection problems of prior art systems. Larger nucleic acid fragments are just as easily cloned, allowing highly representative libraries to be made. Vector to vector ligation is avoided using the methods. AAA40351-A40366 represents primers used to illustrate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inserting a nucleic acid into a circular vector comprising joining their ends, melting, and reannealing ends at two different concentrations, useful for cloning small amounts of nucleic acids and forming genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 66; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 AAAAAAAAAAAAAAAAA 3
Primer; cloning; ligation; ss
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                                                                                                                                                                                                                                                                               99WO-US030277.
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                                                                                                                                                                                                                                                                                                                                                                                                                 (ROMA/) ROMANTCHIKOV Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-442381/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Romantchikov Y;
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                                                                    Synthetic.
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99US-0156113P.

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The present invention relates to a method for stimulating an immune
    WPI; 2001-273485/28.
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                                                                                                                                                                                                       response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an inucleic acid. The present sequence is one such immunostimulatory nucleic acids can be pyrimidine or nucleic acids can be pyrimidine or (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects addlar unique antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. herpesviridae) acids can continuous amongolobacter, clostridium, Bscherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Thz to a Th1 immune response and to activate immune cells. Note: the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic; immunostimulatory; tumour; viral infection; bacterial infection; tungal infection; parasitic infection; cancer; asthma; infection; parasitic infection; cancer; asthma; and infections disease; allergy; immune deficiency; phosphorothioate; ss.
                                                                                                                                Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                               present invention relates to a method for stimulating an immune
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score 20.4; DB 1; Length 24;
Pred. No. 1.6e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                         present sequence may have a phosphorothicate backbone
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;
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                                                                                                                                                                     Claim 101; Page 57; 338pp; English.
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                                                                              Vollmer J;
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27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
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                                      (IOWA ) UNIV IOWA RES FOUND. (COLE-) COLEY PHARM GMBH.
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Best Local Similarity 95.5
Matches 21; Conservative
                                                                            Krieg AM, Schetter C,
                                                                                                      WPI; 2001-273485/28,
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27-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 52
 88X48XBXBXBXBXBXBXBXBXBXBXBXBBBXBBBXBBB
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The present invention relates to a method for stimulating an immune response. The method comprises administaring an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (r) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Bscherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a filt to a Thi immune response and to activate immune cells. Note: the present sequence may have a phosphorothioate backbone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anti-parasitic;
Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.
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immunostimulatory; tumour, viral infection, bacterial infection,
fungal infection; parasitic infection, cancer; asthma;
infectious disease; allergy; immune deficiency; phosphorothioate; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunostimulatory nucleic acid #873.
                                                                                                            Claim 101; Page 46; 338pp; English
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(COLE-) COLEY PHARM GMBH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 95.5
Matches 21, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-273485/28
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response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae) haemophilus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parastic antigens. The method is staphylococcus), fungal antigens and/or parastic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or
                                                                                                                                                                                                                                                                                       immune deficiency. The present sequence can also be used to redirect a Th2 to a Th1 immune response and to activate immune cells. Note: the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 1.2%; Score 20.4; DB 1; Length 24; 1 Similarity 95.5%; Pred. No. 1.6e+02; 21; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                  present sequence may have a phosphorothioate backbone
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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1734 ACAAAAAAAAAAAAAAAA 1755 | ||||||||||||||||| 1 AAAAAAAAAAAAAAAAAAA 22 ò ద

ABV14842 standard; cDNA; 24 (first entry) ABV14842; ABV14842/C

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ABV14842/C

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ABV1484

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ABV1484

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ABV1484

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ABV1484

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ABV1484

ABV14 RESULT 54

ВР

Human prostate expression marker cDNA 14833.

cytostatic; carcinogen; pharmacodyanamic marker; gene; 88. Human; prostate cancer; pharmacogenomic marker;

Homo sapiens.

WO200160860-A2.

23-AUG-2001.

20-FEB-2001; 2001WO-US005171

17-FEB-2000; 2000US-0183319P. 16-MAR-2000; 2000US-01896G2P. 25-MAY-2000; 2000US-0207454P. 09-JUN-2000; 2000US-021734P.

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

2000US-0219007P

18-JUL-2000;

13-DEC-2000; 2000US-0255281P

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Schlegel R, Endege WO, Monahan JE;

WPI; 2001-662795/76.

Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer. Claim 1; Page 2483; 11750pp; English.

The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV65213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; d) assessing the efficacy the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient;

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(f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                         Anglogenesis inhibitor; ss; anglogenesis; solid tumour growth; tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial anglogenesis; bladue neovascularisation; telangiectasia; haemophiliac joint; anglofibroma; wound granulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
                                                                                                                     Gaps
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                                                                                        ch 1.2%; Score 20.4; DB 1; Length 24; 1 Similarity 95.5%; Pred. No. 1.6e+02; 21; Conservative 0; Mismatches 1; Indels
                                                               Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                  Angiogenesis inhibitory oligonucleotide #961.
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                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                           Query Match
Best Local Si
Matches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
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ABS78477/
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Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject. WPI; 2002-566690/60.

(COLE-) COLEY PHARM GROUP INC

Bratzler RL;

14-DEC-2001; 2001WO-US048458 14-DEC-2000; 2000US-025534P.

WO200253141-A2

11-JUL-2002

Claim 2; Page 36; 276pp; English.

administering at least on antianglogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antianglogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, nubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliae, joints, angiofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic comprising The invention relates to inhibiting angiogenesis in a subject, acid of the invention

Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

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administering at least one antiangiogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted anglogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lesion, theumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
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                                                                                                                                                                                                                                                                                                                                                                                                      tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiactasia; haemophiliac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
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                                           Gaps
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    Length 24;
                                       1; Indels
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1.2%; Score 20.4; DB 1; 95.5%; Pred. No. 1.6e+02; ative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                           Angiogenesis inhibitory oligonucleotide #433.
                                                                               1734 ACAAAAAAAAAAAAAAAAAA 1755
                                                                                                                      24 AAAAAAAAAAAAAAAAA 3
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ABS77949 standard; DNA; 24
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                                         Conservative
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Query Match
Best Local Similarity
Matches 21; Conserv
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nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with soild tumour growth, tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, osler-webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         administering at least one antiangiogenic nucleic acid molecule. Also
included is a kit comprising a first container housing the antiangiogenic
                                                                                                                                                                                                         tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasis; rubeosis; osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
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                                                                                                                                                                                           Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                      Angiogenesis inhibitory oligonucleotide #962.
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                                         ABS78478 standard; DNA; 24
                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acid of the invention
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                                                                                                                  13-DEC-2002
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                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                             ABS78478;
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ABL39405/c
ID ABL3940
XX
AC ABL3940
RESULT 57
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ABL39405 standard; DNA; 24

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Gaps

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1; Indels

0; Mismatches

21; Conservative

Best Local Similarity

Query Match Matches 1734 ACAAAAAAAAAAAAAAAAAA 1755

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AAAAAAAAAAAAAAAAA 3

1.2%; Score 20.4; DB 1; Length 24; 95.5%; Pred. No. 1.6e+02;

ABL39405

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                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to methods for treating or preventing cancer, involving administering to a subject having or at risk of cancer, involving administering to a subject having or at risk of of eveloping cancer immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies. The methods are useful for treating or preventing cancer such as basal cell carcinoma, bladder cancer, bone cancer, brain and central nervous system (CNS) cancer, breast cancer, cervical cancer, colon and rectum cancer, connective tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx cancer, leukaemia, liver cancer, lung cancer, kidney cancer, larynx cancer, pancreatic cancer, prostate cancer, rabdomyosarcoma, skin cancer, stomach cancer, testicular cancer, rabdomyosarcoma, skin cancer, stomach cancer, testicular cancer, and uterine cancer. The present sequence is an immunostimulatory oligonucleotide described in the
                                                                                                                                                                                                                                                                                                                                                                   Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies to a subject having or at risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                           Antibody-induced cell lysis; cancer; immunostimulatory; CD20; anglogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
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Pred. No. 1.6e+02;
0; Mismatches 1; Indels
                                                                                                                                1. .24
/*tag= a
/mod_base= OTHER
/note= "phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A24 oligonucleotide for the creation of Pc-A24.
                                   Immunostimulatory nucleic acid SEQ ID NO: 841
                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 309; 312pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1734 ACAAAAAAAAAAAAAAAAAA 1755
                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exemplification of the invention
                                                                                                                                                                                                                                             22-JUN-2001; 2001WO-US020154
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            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21; Conservative
                                                                                                                                                                                                                                                                                                                     Weiner G, Hartmann G;
                                                                                                                                                                                                                                                                                                                                             WPI; 2002-154611/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                         developing cancer
                                                                                                                                                                                             WO200197843-A2
                                                                                                                      Key
modified_base
            16-APR-2002
                                                                                                                                                                                                                     27-DEC-2001.
                                                                                               Synthetic
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ID ABA5
XX ABAC
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DT 01-C
XX
DE A24
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The invention relates to the detection of multiple components in a medium, comprising combining the medium with at least two sensitiser reagents one reactive reagent extivated by a product generated by the sensitiser reagents when activated and differentially activated by the sensitiser reagents. The combination of sensitiser cannot be components and reactive reagents (s) allows differential detection of the components. Methods of the invention may be used for the detection of ligands, receptors and polymoclecides, and also for the detection of c ligands, receptors and polymoclecides, and also for the detection of byhaholys, phosphate esters, thiophosphates, carbamates and collyhalogenated sulfenanides) and pollutents. Methods of the invention allow the detection of multiple analytes in a single test medium. An application of the methods of the present invention would be in the field of calinical diagnostics. The current sequence represents A24 oligonucleotide for the creation of oligonucleotide coated phthalocyanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detection of multiple analytes, e.g. ligands, receptors, polynucleotides and pollutants, involves adding a combination of sensitizer reagents and reactive reagent Actuatable by a product of the sensitizer reagents.
Component detection, clinical diagnosis, cell detection, drug detection, metabolite detection, pesticide detection, ligand detection, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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/label= OTHER
/note= "modified by PO2OCH2CH2CSCH2CH2OH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                              03-MAY-2001; 2001WO-US014528.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAY-2000; 2000US-00564230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cromer R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-164078/21.
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                                                                                      Synthetic
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The present invention provides the protein and coding sequences of human phosphatidylinositol-3 (PTDINS-3) kinase 35. The sequences can be used in the treatment of cancer, haemopathy, HIV infection, development disorders, immunological diseases and inflammation. The present sequence is a PCR primer for the coding sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polymorphism detection; sequence detection; mutation detection; A24; probe; non-dissociative termolecular complex; dopTAR sensitiser particle; single nucleotide polymorphism; SNP; ss.
                                                                                                                                                                                                                  New human phosphatidylinositol-3 (PTDINS3) kinase 35 for diagnosing and treating malignant tumor, hemopathy, human immunodeficiency virus infection, immunological diseases and various inflammations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
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/note= "A is covalently linked to PO20CH2CH2CH2CH2SSCH2CH2CH2OH moiety"
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 24 BP; 3 A; 0 C; 1 G; 20 T; 0 U; 0 Other;
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                                                                                                                                     (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
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                                                                                16-MAR-2001; 2001WO-CN000328.
                                                                                                          17-MAR-2000; 2000CN-00114973
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                         WO200175014-A2
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Homo sapiens.
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This invention represents a method for detecting the presence of a polynucleotide sequence, differences in polynucleotide sequences or mutations in genomic DNA. The method involves contacting 3 oligomucleotide probes with a sample containing a polynucleotide. The first probe hybridises to a region of the polynucleotide sequence and the second and third probes can bind a second region of the polynucleotide conference of one or more nucleotides. The reaction medium is presence or difference of one or more nucleotides. The reaction medium is them subjected to conditions for forming substantially non-dissociative termolecular complexes, which can be at least one of, the polynucleotide sequence with the first and third probes. The oligomucleotide probes have labels on on-covalantly bound to allow for their detection upon binding. The mon-covalantly bound to allow for their detecting the presence of a single nucleotide polymorphism (SNP) in a fragment of genomic DNA. The method can be used for the direct detection of nucleic acid in very small can be used for the direct detection of nucleic acid in very small containties without amplification. In addition, the method may be carried out with amplification of the target and reference sequences. This sequence represents an oligomucleotide probe A24 used to create dopTAR
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                                       Detecting presence of polynucleotide, differences between polynucleotide sequences, useful for detecting single nucleotide polymorphism and alleles of polynucleotide sequence involves use of three competitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chimiluminescer sensitiser particles in the method of the invention. Binding the nucleic acid to a suspendable particle acts as a support and provides a means of segregating the bound polynucleotide target from the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.2%; Score 20.4; DB 1; Length 24; 95.5%; Pred. No. 1.6e+02; tive 0; Mismatches 1; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                                                                                            Example; Page 47; 75pp; English
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VPI; 2002-097664/13.
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WPI; 2002-188740/24

The invention relates to generating managed to providing a solution containing a nucleic acid template, comprisingly of providing a solution containing a nucleic acid template, one or more promoter-linked primers complementary to the sense conformation of the nucleic acid template, and with an RNA complementary of the nucleic acid template, and with the one of more promoter-linked primers complementary to the mucleic acid template, and with the one of more promoter-linked primers to synthesise a promoter-linked primers to synthesise a promoter-linked double-stranded nucleic acid, (d) treating the promoter-linked double-stranded nucleic acid, (d) treating the promoter-linked double-stranded nucleic acid to synthesise amplified mRNA fragments with one or more primers to synthesise managed nucleic acid to synthesise amplified mRNA fragments with one or more primers to synthesise mRNA-cDNA hybrids by reverse transcription of the amplified mRNA fragments and in vitro, for suppressing cancer-related mRNA company hybrids for transducing biological effects of interest in vitro as well as in vivo, for inhibiting gene function in studying cancer, in high throughput screening of gene functions based on microarray analysis, and as a tool in studying gene functions based on microarray analysis, and as a tool in studying gene functions in vitro, and complectules, in high throughput screening of gene functions based to screen for special gene functions. For manipulating gene expression in vitro, and for designing therapy for genetic diseases in vivo. The cDNA part of a D-RNA polymerase) enryme may provide allogue analogue in comparation to increase the stability and effectiveness of transfected proved activities. The RNA keppendent RNA polymerase) enryme may provide higher affinity of the mRNA template of a D-RNA duplexes the nucleoned of probe activities. The RNA kemplate, resulting in multiple control of the sense-RNA template, resulting in multiple squence of everse transcribe mRNA into first strand cDNA in the method of t Generating mRNA-cDNA hybrids for suppressing cancer-related genes, or treating or preventing microbe related genes, comprises thermocycling steps of promoter-linked double-stranded cDNA or RNA synthesis. invention relates to generating mRNA-cDNA hybrids, comprising (a) Seguence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other; Example 5; Page 26; 53pp; English invention ACA58802; Query Match Matches ò g

Gaрв ; 0 1.2%; Score 20.4; DB 1; Length 24; 95.5%; Pred. No. 1.6e+02; tive 0; Mismatches 1; Indels 1734 ACAAAAAAAAAAAAAAAAAA 1755 ACA58802 standard; DNA; 24 10-JUN-2003 (first entry) Local Similarity 95.5 nes 21; Conservative 

EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat; polymorphic marker prediction of ubiquitous simple sequences; POMPOUS; Rep-X; human; genetic disease; drug-treatment; Machado-Joseph; Haw River syndrome; Huntington's disease; fragile-X syndrome; Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia; spinal atrophy; bulbar atrophy; spinocerebellar ataxia. EST polymorphic DNA repeat polynucleotide #134. 99US-00475947. (TEXA ) UNIV TEXAS SYSTEM. 17-APR-2003 (first entry) US6472154-B1. 31-DEC-1999; 31-DEC-1999; 29-OCT-2002, ABX79809; . 0 Gastric ulcer; ss; immunostimulant; equine gastric ulcer syndrome; EGUS; Heliobacter pylori. Gastric ulcer treatment immunostimulatory nucleic acid #148 Synthetic.

Fondon JW;

Garner HR, Wren JD, Minna JD,

US2002198165-A1 26-DEC-2002

ulcer comprising administering a nucleic acid to a subject in need for treatment of gastric ulcer. A nucleic acid sample comprising oil gonucleotide 2006 was administered to a mouse model by an oral route or a vehicle control. Colonisation of mice by Heliobacter pylori was assessed at time points from 1 day to 1 month after treatment. The ability of the nucleic acid to reduce H. pylori colonisation was assessed. The method is useful for preventing or treating a gastric ulcer on a subject e.g. human or non-human vertebrate animal including dog, rabbit, turkey, chicken, primate, rat and mouse. The method effectively treats or prevents gastric ulcers. The present sequence represents an immunostimulatory nucleic acid for the treatment of gastric ulcers Prevention or treatment of gastric ulcer involves administering nucleic The invention relates to a method of prevention or treatment of gastric Gaps ö cch 1.2%; Score 20.4; DB 1; Length 24; al Similarity 95.5%; Pred. No. 1.6e+02; 21; Conservative 0; Mismatches 1; Indels Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other; Disclosure; Page 14; 45pp; English. 01-AUG-2001; 2001US-00920313. 01-AUG-2000; 2000US-022248P. Ğ. Bratzler RL, Petersen WPI; 2003-370798/35. BRATZLER R PETERSEN D PETE/) Local BRAT/) Matches ઠે 셤

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ABX79809 standard; cDNA; 24 BP

RESULT 64 ABX79809/

for

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repeat within a coding sequence (expressed sequence tag, EST), which comprises detecting tandem repeats in a target coding sequence, scoring the repeats for polymorphic probability and generating a dataset correlating the repeats with polymorphic probability to identify a candidate polymorphic repeat. The computational methods (polymorphic marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are useful for identifying and detecting candidate polymorphic repeats in human genes, which can be used to understand, treat or eliminate genetic diseases, predispositions or adverse drug-treatment reactions. Examples of diseases linked to nucleotide repeats are Machado-Joseph, Haw River syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis, myotonic dystrophy, hyperandrogenesmia, spinal and bulbar atrophy and spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are the polymorphic repeats identified for a search of human ESTS
                                                                                                                                                                  The invention discloses a method for identifying a candidate polymorphic
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                                    Identifying a candidate polymorphic repeat within a coding sequence, funderstanding or treating genetic disease, comprises detecting tandem repeats in a target coding sequence and scoring the repeats for polymorphic probability.
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(COLE-) COLEY PHARM GMBH.
(IOWA ) UNIV IOWA RES FOUND.
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03-JUL-2002; 2002US-0393952P.
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nes 21; Conservative
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The present invention describes immunostimulatory nucleic acids of 14-100 nucleotides in length comprising the formula 5' XIDCGHX2 3' (I) where XI or XZ = independently any sequence 0-10 nucleotides D = nucleotide other than C; C = Cytosine; G = guanine; H = nucleotide other than G; The immunostimulatory nucleic acid further comprises a sequence consisting of pand N positioned immediately 5' to X1 or 3' to X2 and N is a B cell neutralising sequence, where N begins with a CGC trinucleotide and is at least 10 nucleotides long and P is GC-rich palindrome containing sequence at least 10 nucleotides long Also described: (I) a pharmaceutical composition comprising the immunostimulatory nucleic acid and a carrier; and (2) treating an alergic condition. (I) has antiallergic activity and CC can be used in gene therapy. (I) can be used for preparing a composition of a variety of immune related disorders such as cancer, infectious diseases and allergic disorders. (I) also stimulates the contraining activation of instural killer cells and the production of type interventing and activation of type interventing a composition of type interventing and allergic disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Improved polymerase thermocycling reaction for nucleic acid amplification, by thermal cycling of promoter-linked nucleic acid template synthesis and in vitro transcriptional amplification of nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                 interferon (\mbox{IFN}). The present sequence represents an immunostimulatory oligonucleotide, which is used in an example from the present invention
                                      New immunostimulatory nucleic acid, useful for preparing a composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an improved polymerase thermocycling reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ss; PCR; RT-PCR; primer; reverse transcriptase PCR; antisense therapy; mRNA expression profile; promoter containing primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.2%; Score 20.4; DB 1; Length 24; 95.5%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1734 ACAAAAAAAAAAAAAAAAAA 1755
                                                           for treating an allergic condition.
                                                                                                   Example 1; Page 44; 115pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 AAAAAAAAAAAAAAAAAAA 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 7; Page 14; 28pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACA62284 standard; DNA; 24 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligo (dT)24 RT-PCR primer.
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WPI; 2003-268241/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-479488/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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us10008789-3.rng

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containing the annual of nucleic acid sequences, involves denaturing a number of nucleic acid templates [1], combining the annual of nucleic acid templates [1], combining the containing brimer [P2], a primer [P2], a number of deoxynucleotide triphosphates and ribonucleotide triphosphates and ribonucleotide triphosphates and ribonucleotide triphosphates and reverse transcription enzyme, a DNA-dependent DNA polymerase and RNA polymerase, contacting PU with [1] to generate a number of promoter-containing templates; contacting PU with [1] to generate a number of promoter-containing double-stranded nucleic acid templates to form a number of containing double-stranded nucleic acid templates to form a number of containing double-stranded DNA templates to form a number of containing double-stranded DNA templates, and thus for producting the method is useful for flugroved polymerase thermocycling reaction for limprove profile of a cell by M1 to generate multiple copies of the mRNA, millial a diseased state, by generating an expression profile of the cells in both normal and diseased state, and the cells in both normal and diseased state, and the cells in both normal and diseased state, and the cells in mRNA sequences of cell(s) in the containing the differer from mRNA in the substant protein production of the solated mRNA, and contained by aberrant protein prod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           production of cell in a diseased state by the above method, amplifying the aberrant protein by M1 and using recombinant techniques to determine the effect of proposed drug on the aberrant protein. M1 is also useful for differential screening of tissue-specific gene expression at a cellular level, for preparing labeled RNA/DNA probes for a gene chip technology, and for determining the efficacy of a drug regiment against gene or its cDNAs. The present sequence is an Oligo (dT)24 RT-(reverse transcriptase) PCR primer used to produce first strand cDNA in the method
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Length 24; 1; Indels Seguence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other; Score 20.4; DB 1; Pred. No. 1.6e+02; 0; Mismatches 1.2%; Best Local Similarity 95.5 Matches 21; Conservative Query Match ò

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Immunostimulatory nucleic acid #415. ACD99729 standard; DNA; 24 25-SEP-2003 (first entry) ACD99729; RESULT 67 ACD99729/ 

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Immunostimulatory; antiinflammatory; dermatological; antipsoriatic; antiulcer; gene therapy; vaccine; non-allergic inflammatory disease; psoriasis; eczema; allergic contact dermatitis; latex dermatitis; inflammatory bowel disease; ulcerative colitis; crohn's disease; se.

Synthetic

The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic contect dermatitis, latex dermatitis or inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease. This sequence represents an immunostimulatory nucleic acid Treating non-allergic inflammatory diseases, such as psoriasis, ecz allergic contact dermatitis, latex dermatitis or inflammatory bowel disease by administering an immunostimulatory nucleic acid. ch 1.2%; Score 20.4; DB 1; Length 24; ll Similarity 95.5%; Pred. No. 1.6e+02; 21; Conservative 0; Mismatches 1; Indels Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other; 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755 Disclosure; Page 20; 229pp; English 24 AAAAAAAAAAAAAAAAAA 3 29-MAR-2002; 2002US-00112653. 29-MAR-2001; 2001US-0279642P WPI; 2003-521815/49 Krieg AM, Berg DJ; (KRIE/) KRIEG A M. (BERG/) BERG D J. US2003050268-A1 13-MAR-2003. Query Match Local Matches 6

Immunostimulatory; antiinflammatory; dermatological; antipsoriatic; antiulcer; gene therapy; vaccine; non-allergic inflammatory disease; psoriasis; eczema; allergic contact dermatitis; latex dermatitis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss. Immunostimulatory nucleic acid #920. ACH03285 standard; DNA; 24 BP. 25-SEP-2003 (first entry) ACH03285; RESULT 68 ACH03285

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0; Gaps

29-MAR-2002; 2002US-00112653. US2003050268-A1. 13-MAR-2003. Synthetic. 

WPI; 2003-521815/49. Krieg AM, Berg DJ;

29-MAR-2001; 2001US-0279642P.

(KRIE/) KRIEG A M. BERG D J.

BERG/)

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Indels

Score 20.4; DB 1; Pred. No. 1.6e+02; 0; Mismatches 1;

24 AAAAAAAAAAAAAAAAA 3

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(first entry)

Length 24;

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The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases, such as psortasts, eczema, allergic contect dermatisis, latex dermatitis or inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease. This sequence represents an immunostimulatory nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease by administering an immunostimulatory nucleic acid.
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ss; nucleic acid amplification; multiple step elimination; varying reaction condition elimination; poly A tract.
                          Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;
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                                                                                    Query Match
Best Local Similarity 95.5%;
Matches 21; Conservative
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                                                                                                                                                                                                             The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases, such as psortasis, eczema, allergic context dermattis, latex dermatitis or inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease. This sequence represents an immunostimulatory nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunostimulatory; antiinflammatory; dermatological; antipsoriatic; antiulocr; gene therapy; vaccine; non-allergic inflammatory disease; psoriasis; eczema; allergic contactitis dermatitis; latex dermatitis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
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allergic contact dermatitis, latex dermatitis or inflammatory bowel
                              Treating non-allergic inflammatory diseases, such as psoriasis, ecz allergic contact dermatitis, latex dermatitis or inflammatory bowel disease by administering an immunostimulatory nucleic acid.
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Pred. No. 1.6e+02;
0; Mismatches 1; Indels
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                                                                                                                                                    Disclosure; Page 34; 229pp; English
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Best Local Similarity 95.5°
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2003050268-A1.
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/*tag= a /note= "Binds to nucleotides 42-19 of the 1st strand CDNA

synthesis primer"

Ryder TB;

Location/Qualifiers

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The invention relates to a method of amplification of nucleic acid which comprises primer extension by reverse transcriptase and hybridising an oligomorelectide to the single stranded DNA, where the oligomorelectide is blocked from extension at the 3' and. The method is useful for amplification of nucleic acids. In the new method, a promoter is protected from degradation throughout the method. The promoter is constructed so that it does not serve as a primer for extension of a sequence that is complementary to the target sequence, i.e. it is blocked. The method can be combined with other processes to eliminate the need for multiple steps and varying reaction conditions and their associated problems. At least three otherwise separate enzymatic reactions can occur consecutively in one phase (i.e., without organic extraction and precipitation), more preferably in the same reaction vessel. Preferably, cDNA synthesis according to the new method may occur in a modified low salt buffer. The present sequence represents the poly A tract of a mRNA used to illustrate the method of the invention.
                                                                                                      Amplification of nucleic acids, where the promoter is blocked from extension at the 3' end, useful for eliminating multiple step reactions.
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                                                                                                                                                                                                                                                                                 Disclosure, Fig 2, 9pp; English
WPI; 2003-656427/62.
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Best Local Similarity
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The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G nucleic acid in an aerosol formulation. The methods and compositions of the present invention are useful for disgnosing and/or treating asthma and allergy especially in a hypo-responsive subject. The present sequence represents an immunostimulatory nucleic acid of the invention.
                                                                                                                                                                                                                                                 Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ds; allergy; asthma; poly-G nucleic acid; aerosol formulation; hypo-responsive subject; immunostimulatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                1.2%; Score 20.4; DB 1; Length 24; 95.5%; Pred. No. 1.6e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;
                                                                                                                                                                                               Fouron Y;
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                                                                                                                                                                                                                                                                                      Disclosure; Page 11; 221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunostimulatory nucleic acid #873.
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                                                                                                                    03-FEB-2000; 2000US-0179991P.
                                                                                          02-FEB-2001; 2001US-00776479.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-PEB-2000; 2000US-0179991P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB37259 standard; DNA; 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Conservative
                                                                                                                                                                                              Bratzler RL, Petersen
                                                                                                                                            (BRAT/) BRATZLER R L.
(PETE/) PETERSEN D M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BRAT/) BRATZLER R L.
(PETE/) PETERSEN D M.
(FOUR/) FOURON Y.
                                                                                                                                                                                                                      WPI; 2003-657977/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-657977/62
                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                      (FOUR/) FOURON Y.
                                        US2003087848-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2003087848-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-DEC-2003
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                                                                  08-MAY-2003
                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G nucleic acid in an ascrosol formulation. The methods and compositions of the present invention are useful for diagnosing and/or treating asthma and allergy especially in a hypo-responsive subject. The present sequence represents an immunostimulatory nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.
  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                      ds; allergy; asthma; poly-G nucleic acid; aerosol formulation; hypo-responsive subject; immunostimulatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ds; allergy; asthma; poly-G nucleic acid; aerosol formulation; hypo-responsive subject; immunostimulatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 24;
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 20.4; DB 1;
Pred. No. 1.6e+02;
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             Bratzler RL, Petersen DM, Fouron Y;
                           1734 ACAAAAAAAAAAAAAAAAA 1755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1734 ACAAAAAAAAAAAAAAAAAA 1755
                                                                                                                                                                                              Immunostimulatory nucleic acid #872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 18; 221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunostimulatory nucleic acid #420
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                                                                                                                  BP.
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                                                                                                                  ADB37258 standard; DNA; 24
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ADB36806 standard; DNA; 24
                                                                                                                                                                   (first entry)
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21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          BRATZLER R L.
PETERSEN D M.
FOURON Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-657977/62
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                                                                                                                                                                                                                                                                                    US2003087848-A1.
                                                                                                                                                                   04-DEC-2003
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                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                           ADB37258;
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(PETE/) I
(FOUR/) I
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 Matches
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Gaps

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recombination products between two mucleotide sequences. The method comprises combining an initial set of oligonucleotides corresponding to a first nucleotide sequence with a subsequent set of oligonucleotides corresponding to a distinct nucleotide sequence and further combining the initial and subsequent set of combination oligonucleotides having a sequence region corresponding to the initial nucleotide sequence and sequence region corresponding to the sinitial nucleotide sequence and sequence region corresponding to the sicond oligonucleotide sequence. Also described is a method of creating a collection of recombination products between two genes. The methods and compositions of the present invention are useful in the field of synthetic gene technology, and more specifically, to generating a collection of recombination between distinct nucleotide sequences. They can also be used in assembling a library, or a population or a collection of polypeptide
                                                                                                     The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G nucleic acid in an aerosol formulation. The methods and compositions of the present invention are useful for diagnosing and/or treating asthma and allergy especially in a hypo-responsive subject. The present sequence represents an immunostimulatory nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Butterfly biliverdin binding protein BBP-BIX oligonucleotide SEQ ID:106.
Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a method for creating a collection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Creating recombination products between two distinct nucleotide sequences, useful in the field of synthetic gene technology, and in assembling a library, or a population or a collection of polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    recombination product; synthetic gene technology; butterfly; biliverdin binding protein; ss.
                                                                                                                                                                                                                                                                                             1.2%; Score 20.4; DB 1; Length 24; 95.5%; Pred. No. 1.68+02; ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                        Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; SEQ ID NO 106; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                 1734 ACAAAAAAAAAAAAAAAAAA 1755
                                                               Disclosure; Page 18; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                        1 AAAAAAAAAAAAAAAA 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (EGEA-) EGEA BIOSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADD31867 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                 Local Similarity es 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADD31867;
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                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADD31867/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 74
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The invention is directed to novel methods of amplifying and detecting DNA using colling circle amplification (RCA). The invention relates to detecting a target sequence (I), which involves using a capture probe (CP) that is complementary to an open circle probe and includes a cleavage site. The method comprises: attaching a capture probe (CP) to a substrate, at both ends, where the CP includes one domain complementary to an OCP (open circle probe) and a second domain that contains a cleavage site (CS), to form a device; treating CP with (I) and OCP for form, a hybridisation complex (HC); treating CP with (I) and OCP for stroularised, forming a second complex (HC2); treating CP with a ligase so that OCP is circularised, forming a second complex (HC2); treating CP with a cleavage agent, to cut at CS, and adding an extension enzyme (EB) and nucleotide triphosphates (NTPs) to form an extended CP, which is detected. The method is used for detecting (I) that comprises two target domains. The method is used for detecting, genotyping and/or quantification of target sequences, for research, clinical use, quality control or field
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting nucleic acid targets, useful e.g. for diagnosing single nucleotide polymorphisms, by extension of capture probe complementary to
                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        Rolling circle amplification related probe control oigo POS1/2.
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variants that correspond to single or multiple polynucleotide recombination products. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RCA; rolling circle amplification; genotyping; single-nucleotide polymorphism; single base extension; SBE; immuno-hybridisation; probe; ss.
                                                                                                         1.2%; Score 20.4; DB 1; Length 24; 95.5%; Pred. No. 1.6e+02;
                                                                                                                                                 1; Indels
                                                                         Seguence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;
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                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                          24 AAAAAAAAAAAAAAAAAA 3
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/mod_base= OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3xample 1, Fig 5, 66pp, English.
                                                                                                                                                                                                                                                                                                              BP
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                                                                                                                                                                                                                                                                                                          ADE25524 standard; DNA; 24
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                                                                                                                                               21; Conservative
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                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             open circle probe.
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modified_base
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                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                           ADE25524/c
                                                                                                                                                 Matches
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                             method permits a high level of multiplexing, and since it provides localized product detection, with linear kinetics, is sensitive enough for direct detection and quantitation of unmodified targets. The present sequence is that of a single base extension (SBE) probe used in SNP genotyping with RCA signal amplification to demonstrate the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotides AAQ95959-82 are examples of oligonucleotides used in a novel method of immobilising oligonucleotides to a solid support by incubating in the presence of a salt or cationic detergent e.g. NaCl (50-250 mW, pH 6.0-8.0) or 1-ethyl-3-(3'-dimethyl amino propyl)-1.3 carbodiimide hydrochloride (ECD). The oligonucleotides can be capture probes for detection of specific nucleic acids by hybridisation or can be primers for template-dependent extension from the immobilised primers on nucleic acid from a target organism. The method can be used in hybridisation assays, sequencing and analysis of genetic polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immobilising synthetic nucleic acid on solid support - by incubation in presence of salt or cationic detergent, for use in hybridisation assays, sequencing and analysis of polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide biotin-T25 for novel nucleic acid immobilisation method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immobilisation; solid support; salt; cationic detergent; capture probe; hybridisation; primer; template-dependent extension; target organism; sequencing; genetic polymorphism; ss.
   testing, particularly detection of single-nucleotide polymorphisms. The
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                      Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                 Score 20.4; DB 1;
Pred. No. 1.6e+02;
0; Mismatches 1;
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"biotinylated"
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                                                                                                                                                                                                                                                                                                                     1.2%;
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AAQ95960 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOLE-) MOLECULAR TOOL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                21; Conservative
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/note=
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                                                                                                                                                                                                                                                                                                                     Query Match
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AAQ95960/

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Seguence 25 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein inhibiting apoptosis, useful in the diagnosis and treatment of Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a PCR primer used to isolate DNA encoding the human Nck associated protein 1 (Napl) of the invention. Napl inhibits apoptosis. The protein can be used in the investigation, diagnosis and treatment (e.g. by gene therapy) of Alzheimer's disease
                                                                                                                                                                                                                                        Nck associated protein 1; Napl; human; apoptosis; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rapid detection; probe; target nucleic acid; enzymatic amplification;
                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                               PCR primer for human Nck associated protein 1 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.2%; Score 20.4; DB 1; Length 25; 95.5%; Pred. No. 1.7e+02;
  Length 25;
                         1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 25 BP; 0 A; 1 C; 0 G; 24 T; 0 U; 0 Other;
1.2%; Score 20.4; DB 1;
95.5%; Pred. No. 1.7e+02;
iive 0; Mismatches 1;
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                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                 (KYOW ) KYOWA HAKKO KOGYO KK. (SAKA/) SAKAKI Y.
                                                                                                                                                                                                                                                                                                                                                                  98WO-JP005646.
                                                                                                                                        AAX84260 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA39306/c
ID AAA39306 standard; RNA; 25
                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
              Similarity 95.5
21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         isolation, detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                      therapy; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-395181/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                  WO9931239-A1
                                                                                                                                                                                                                                                                                                                                                                 14-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1997;
                                                                                                                                                                                        08-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
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                           21;
                                                                                                                                                                                                                                                                                                                                         24-JUN-1999
                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sakaki Y;
                                                                                                                                                                 AAX84260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA39306;
  Query Match
              Best Local
Matches 2
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                                                                                                                            AAX84260/
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The present invention describes a rapid pairing reagent (1) for the isolation or detection of a polymuclectide (PN) analyte molecule having a selected target base sequence, in a sample containing the analyte molecule and non-target polymuclectide, comprising a capture component (A) and a target-specific probe (B) linked to a solid substrate. The isolated sequences are useful for enzymatic amplification. (I) is capable of rapidly binding nucleic acids in the sample and pacing them in close proximity to target probes on the reagent, thus enabling binding under low stringency. Combination of rapid capture and concentration of polymuclectides with selective targeting of analyte molecules, greatly enhances the isolation process. Non-ionic morpholino oligomers used as probes are not extended by polymerases and therefore do not interfere with amplification of target molecule. AAA39306 to AAA39316 represent oligomuclectides used in the exemplification of the present invention
                                                                                                                                                                                                                                                                     Reagent for rapidly detecting or isolating target nucleic acid sequences in polynucleotide-containing sample, comprises capture component and target-specific probe linked to solid substrate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.2%; Score 20.4; DB 1; Length 25; 95.5%; Pred. No. 1.7e+02; ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    c-myc fusion; non-nucleoside spacer; capture probe;
nucleic acid-protein fusion; ribosome display particle; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Capture probe CP125 specific for c-myc fusion targets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 25 BP; 0 A; 0 C; 0 G; 0 T; 25 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1734 ACAAAAAAAAAAAAAAAAAAAA 1755
                                                                                                                                                                                                        Wages JM, Summerton JE, Weller DD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 AAAAAAAAAAAAAAAAAAAAA 4
                                                                                                                                                                                                                                                                                                                                    Example 3; Col 17; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ30267 standard; DNA; 25 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0080686P
                                                                                                             97US-00969B13
                                                                                                                                           96US-0030963P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-FEB-2000 (first entry)
                                                                                                                                                                        (AVIB-) AVI BIOPHARMA INC
                                                                                                                                                                                                                                         WPI; 2000-364413/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PHYL-) PHYLOS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-APR-1998;
                                                                                                                                           15-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-1999;
                                                                                                             13-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9951773-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-0CT-1999
                                              US6060246-A
                                                                             09-MAY-2000
              Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ30267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          c-myc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 79
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Gaps ö

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The present sequence represents a capture probe specific for a c-myc fusion target. It is used in the method of the invention. The specification describes the use of non-nucleoside spacers to immobilise an array of capture probes on a solid support. The solid support carries an array of capture probes, each consisting of non-nucleoside spacers plus an oligonucleotide to which a nucleic acid-protein fusion or a ribosome display particle is bound. Non-nucleoside spacers prevent interaction of proteins with the support surface, ensuring efficient hybridisation between capture probes and bound nucleic acid/protein display partice. The arrays of capture probes are used to screen for interactions between proteins and compounds (e.g. other proteins, ligands or nucleic acids), particularly to identify potential therapeutic agents, anzyme substrates or unknown proteins that interact with drugs, but also for diagnosis (detecting disease-associated proteins) and for quantifying target molecules in a sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNPE, genotyping, agammadlobulinaemia, diabetes insipidus, cancer, Lesch-Nyhan syndrome, muscular dystrophy, familial hypercholesterolaemia, polycystic kidney disease, osteogenesis imperfecta, autoimmune disease, acute intermittent porphyrla, rheumatoid arthritis, multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single nucleotide polymorphism; SNP; single nucleotide primer extension;
                                                                                          Attaching capture probes to solid phases through non-nucleic spacers, producing arrays for detecting interactions of proteins with other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammation; forensic investigation; paternity analysis; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.2%; Score 20.4; DB 1; Length 25; Best Local Similarity 95.5%; Pred. No. 1.7e+02; Matches 21; Conservative 0; Mismatches 1; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP specific SNPE primer SEQ ID 1311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1734 ACAAAAAAAAAAAAAAAAAAA 1755
                                                                                                                producing arrays for detecting inte
compounds, e.g. for drug screening.
                                                                                                                                                                      Example 8; Page 29; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 AAAAAAAAAAAAAAAAAAAAA 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH38515 standard; DNA; 25 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-OCT-2000; 2000WO-US028436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-AUG-2001 (first entry)
                  Wagner R;
                                                      WPI; 2000-013048/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200129262-A2.
    Kuimelis RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH38515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH38515,
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New genotyping oligonucleotide, useful for detecting the presence,

(ORCH-) ORCHID BIOSCIENCES INC.

Picoult-Newburg L, Pohl M;

WPI; 2001-290930/30

15-OCT-1999; 99US-0160096P.

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Preparation of controlled pore glass-polytetrafluoroethylene resin chromatography membrane by heating, calendering and sintering mixture of controlled pore glass and aqueous dispersion of polytetrafluoroethylene.
                                                                                                                                                                                                            Sequence 25 BP; 1 A; 1 C; 0 G; 23 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                     1734 ACAAAAAAAAAAAAAAAAA 1755
                     Claim 1; Page 56; 83pp; English.
                                                                                                                                                                                                                                                                  25 AAAAAAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                     ВР
                                                                                                                                                                                                                                                                                                                                                                                                                        99US-00305219
                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-00604440
                                                                                                                                                                                                                                                                                                     ABK49986 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                               15-JUL-2002 (first entry)
                                                                                                                                                                                                                                       21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-534961/59.
                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CPGC-) CPG INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                     21-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                        04-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                            US6261497-B1
       acid sample.
                                                                                                                                                                                                                                                                                                                                                                                                         17-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                  ABK49986;
                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wong YN,
                                                                                                                                                                                               sednence
                                                                                                                                                                                                                                        Matches
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The invention relates to a method of preparing a controlled pore glass-polytetrafluoroethylene (PTE) resin chromatography membrane, comprising controlled pore glass and an aqueous dispersion of PTFE to form a paste-like mass, heating the paste-like mass at 50-70 plus oC, calendering to form a foldable sheet, and sintering the sheet to produce a rigid, porous sheet. The method prepares a controlled pore glass-PTFE resin chromatography membrane for use in various biotechnical procedures. The membrane is useful in place of controlled pore glass as a support the synthesis, isolation, and purification of nucleic acids and for the isolation and purification of proteins. The method produces a membrane that may be used in lieu of controlled pore glass. The present sequence represents an oligonucleotide prepared on the membrane in an example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe carrier manufacturing method for inkjet system, involves scanning liquid discharge head in direction orthogonal to scanning direction, at angle satisfying predetermined relation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel probe carrier and the method for manufacturing the carrier. The invention enables stable discharge of solution, and removes liquid droplets adhering to discharge nozzle. I present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 1.2%; Score 20.4; DB 1; Length 25; 1 Similarity 95.5%; Pred. No. 1.7e+02; 21; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 1.2%; Score 20.4; DB 1; Length 25; Local Similarity 95.5%; Pred. No. 1.7e+02; les 21; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 25 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide of the invention SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; SEQ ID NO 4; 17pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1734 ACAAAAAAAAAAAAAAAAA 1755
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                             Example 12; Col 8; 6pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВЪ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ss; probe carrier; discharge.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-MAR-2002; 2002JP-00093023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-MAR-2001; 2001JP-00094400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADC54009 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CANO ) CANON KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JP2003035711-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADC54009;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADC54009/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 82
  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequences AAH17205 - AAH40944 represent PCR primers, single nucleotide
primer extension (SNPE) primers, and the sequences of regions flanking
stees of single nucleotide polymorphisms SNPs. The present invantion
includes kits for determining the presence or absence of a SNP, using the
includes kits for determining the presence or absence of a SNP, using the
oligonucleotides are useful for genotyping a nucleic acid sample by
performing a single-nucleotide primer extension reaction. The
oligonucleotides are useful for determining the presence, absence or
cleantity of a SNP and for genotyping nucleic acid samples, for e.g. to
assess by association analysis the genotypic crait suspected of being
caused by one or more SNPs. Phenotypic trait suspected of being
caused by one or more SNPs. Phenotypic traits include disease e.g.
agammaglobulinaemia, diabetes insipidua, Lesch-Nyhan syndrome, muscular
dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
craits also include symptoms of or susceptibility to multifactorial
cliesase of which a component is or may be genetic such as autoimmune
diseases, including, rheumatoid arthritis, multiple sclerosis,
microorganism. The method is also useful in forensic investigations and
pathen. The present sequence represents a single nucleotide
paternity analysis. The present sequence represents a single nucleotide
paternity analysis. The present sequence represents a single nucleotide
paternity analysis. The present sequence represents a single nucleotide
paternity analysis. The present sequence represents a single tone.
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absence or identity of single polynucleotide polymorphism in a nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example oligonucleotide #2 prepared on glass-synthetic resin membrane.
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0
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Gaps

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1734 ACAAAAAAAAAAAAAAAAAAAA 1755

Matches

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Gaps

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NAZ are noncomplementary nucleic acid sequences, ---S--- = a scissile linkage; n= 1 or 1,000, which is used for the detection of specific DNA or RNA sequences in a test soln. The scissile link probes may be PL (Permanent Linkage to Solid support) or HL (Hydrolyaable Linkage to Solid Support). The differential liability of DNA and RNA may be exploited in a heterogenous system when the scissile linkage is an RNA molecule in the examples, counter probe molecules 9 through 16 were used to determine suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The patent claims a new molecule of formula (NA1----S----NA2)n. NA1 and NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile linkage; n = 1 or 1,000, which is used for the detection of specific DNA or RNA sequences in a test soln. The scissile link probes may be PL (Permanent Linkage to Solid Support) or HL (Hydrolygable Linkage to Solid
                                                                                                                                                                                            patent claims a new molecule of formula (NA1----S----NA2)n. NA1 and
                                                                                                           Synthetic nucleic acid probes - comprising two nucleic acid sequences linked by a scissile linkage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic nucleic acid probes - comprising two nucleic acid sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                       1.2%; Score 20.4; DB 1; Length 26; 95.5%; Pred. No. 1.7e+02; tive 0; Mismatches 1; Indel8
                                                                                                                                                                                                                                                                                                                                                                            Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence of scissile link probe MRC059 (HL).
                                              Robertson JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Robertson JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1734 ACAAAAAAAAAAAAAAAA 1755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 AAAAAAAAAAAAAAAA S
                                            Bender R, Crosby W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bender R, Crosby W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86EP-00116906.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linked by a scissile linkage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85US-00805279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example; p29; 46pp; English.
                                                                                                                                                           Example; p29; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAN70275 standard; DNA; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                             21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hybridisation; probe; ss
               (MEIO-) MEIOGENICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MEIO-) MEIOGENICS INC.
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                                                                            4PI; 1987-186567/27
                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-DEC-1986;
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26-MAY-1991
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                                                                                                                                                                                                                                                                                                                                             os field.)
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                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                              Duck P,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe carrier manufacturing method for inkjet system, involves scanning liquid discharge head in direction orthogonal to scanning direction, at angle satisfying predetermined relation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel probe carrier and the method for manufacturing the carrier. The invention enables stable discharge of solution, and removes liquid droplets adhering to discharge nozzle. present sequence is used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.2%; Score 20.4; DB 1; Length 25; larity 95.5%; Pred. No. 1.7e+02; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 25 BP; 25 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                            Oligonucleotide of the invention SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence of scissile link probe MRC060 (HL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; SEQ ID NO 3; 17pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1734 ACAAAAAAAAAAAAAAAA 1755
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 AAAAAAAAAAAAAAAAAAA
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                                                                                                                                                                                                                                                                                                                                             28-MAR-2002; 2002JP-00093023
                                                                                                                                                                                                                                                                                                                                                                             28-MAR-2001; 2001JP-00094400
                                                                                                                                                                                                             вв; probe carrier; discharge
                                                                            ADC54008 standard; DNA; 25
                                                                                                                                             18-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-535999/51
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Matches 21; Conserv
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                                                                                                                                                                                                                                                                                                            37-FEB-2003
                                                                                                                                                                                                                                               Synthetic.
                                                                                                             ADC54008;
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(Updated on 25-MAR-2003 to correct PR field.)

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Support). The differential liability of DNA and RNA may be exploited in a heterogenous system when the scissile linkage is an RNA molecule. In the examples, counter probe molecules 9 through 16 were used to determine suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting target nucleic acid molecules - using excess complementary
nucleic acid probes and nicking to complete a cycling sequence.
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                                                                                                                  1.2%; Score 20.4; DB 1; Length 26; 95.5%; Pred. No. 1.7e+02; tive 0; Mismatches 1; Indels
                                                                                        Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;
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*tag= a
note= "deoxyribonucleotides."
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/note= "deoxyribonucleotides."
                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe MRCO59; solid support; ribonuclease
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*tag= b
'note= "ribonucleotides."
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(revised)
(first entry)
                                                                                                                                                  21; Conservative
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/*tag= c
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                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bender R;
                                                                                                                                                                                                                                                                                                                                                                                                        SS probe MRC059,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-APR-1988;
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31-OCT-2002
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                                                          os field.)
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                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting target nucleic acid molecules - using excess complementary nucleic acid probes and nicking to complete a cycling sequence.
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                      1.2%; Score 20.4; DB 1; Length 26; 95.5%; Pred. No. 1.7e+02; tive 0; Mismatches 1; Indels
Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                   '*tag= a
'note= "deoxyribonucleotides."
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/note= "deoxyribonucleotides."
                                                                                                                                                                                                                                                                                                                   Probe MRCO60; solid support; ribonuclease.
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/note= "ribonucleotides.
17. .26
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                                                                                               26 AAAAAAAAAAAAAAAAA S
                                                                                                                                                                              BP
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AAN92242 standard; DNA; 26
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(revised)
(first entry)
                                        Local Similarity 95.5
nes 21; Conservative
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                                                                                                                                                                                                                                                                                        SS probe MRCO60.
                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
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25-APR-1990
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                         Query Match
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Primer #4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a method of producing full-length cDNA libraries from single cells, designated single-cell cDNA library amplification (SCLA). The method is useful in gene chip technology, differential screening, pathological diagnosis, physiological prognosis and genetic identification. No further information about this sequence is given in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Generating a complete full-length cDNA library from single cells for use in gene chip technology, involves reverse transcribing intracellular mRNAs, adding polynucleotide tail and amplifying formed cDNAs.
                                                                                                                                                                                                                                                                               cDNA library production; SCLA; gene chip technology;
differential screening; pathological diagnosis; genetic identification;
single-cell cDNA library amplification; ds.
                                              Gaps
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                 1.2%; Score 20.4; DB 1; Length 26; 95.5%; Pred. No. 1.7e+02; ative 0; Mismatches 1; Indels
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AAF77536;
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AAF77536;
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AAF77536;
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CDNA library production metho
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CDNA library production; SCLA
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Mingle-cell cDNA library ampl
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CDNA library production; SCLA
Mingle-cell cDNA library ampl
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Synthetic.
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VS Synthetic.
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CHOV.1998; 98US-00197951.
XX
CHOV.1998; 98US-00197951.
XX
A (LINS) LIN S.
PA (CHUON) CHUONG C.
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XX
A (LINS) LIN S.
PA (CHUON) CHUONG C.
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MPI; 2001-243448/25.
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A (YING) YING S.
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A (MAKA, adding polymucleotide
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C Generating a complete full-le
YI in gene chip technology, invo
PT mRNAs, adding polymucleotide
XX
C The present invention describ
C amplification (SCLA). The met
CC amd genetic identification. N
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Sequence 26 BP; 0 A; 0 C; 0 C
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Sequence 26 BP; 0 A; 0 C; 0 C
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Query Match
Best Local Similarity
Local 21; Conservative
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Matches 21, Conservative
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The present invention relates to generating amplified messenger RNAs with polymerase reaction activity, comprising cycling steps of reverse transcription, denaturation, double-stranded cDNA synthesis and in vitro transcription. The invention is used for generating amplified mRNAs from limited mRNAs from single cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Generating amplified messenger RNA sequences from single cells, involves cycling steps of reverse transcription, denaturation, double-stranded DNA sequences and in vitro transcription.
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1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 1.7e+02;
Matches 21; Conservative 0; Mismatches 1; Indels
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Primer; mRNA; amplification; 88.
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                                                                                                                                                                                                                          99WO-US012461
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ID AAI73048 standard; DNA; 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ying S, Chuong
                                                                                                                                                                                                                                                                                                                                (LINS/) LIN S.
(YING/) YING S.
(CHUO/) CHUONG C.
(WIDE/) WIDELITZ R B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-061734/07
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                                                                                                              40200075356-A1
                                                                                                                                                                                                                          04-JUN-1999;
                                                    Unidentified
                                                                                                                                                                                                                                                                               04-JUN-1999;
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This sequence represents a molecular scaffold which may be used in a composition of matter comprising multiple fluorophores. The fluorophores are bound to the molecular scaffold at separate predetermined positions, to permit fluorescence energy transfer between two fluorophores. The fluorophores are characterized by maximum emission wavelength of one being greater than the minimum excitation wavelength of the other. The composition is useful for determining whether a preselected nucleotide residue is present at a predetermining whether a preselected nucleotide analysis, and identifying multiple single nucleotide presence of a number of given nucleotide residues is determined
                                                          Composition of matter useful for multi-component analyses, comprises multiple fluorophores bound to molecular scaffold at preset positions to permit fluorescence energy transfer between two fluorophores.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New zalphall ligand polypeptides and polynucleotides, useful for stimulating proliferation, activation, differentiation and/or induction of inhibition of specialized cell function, or for stimulating an
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytokine; zalphall Ligand; zalphall receptor; NK cell progenitor; natural Killer cell proliferation; T-cell proliferation; B-cell proliferation; anti-tumour response; immune system; immunostimulant; cytostatic; human; sequencing primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                      1.2%; Score 20.4; DB 1; Length 26; 95.5%; Pred. No. 1.7e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Foster DC, Holly
Dillon SR, Hammond
                                                                                                                                                                                                                                                                                                                                        simultaneously by the composition of the invention
                                                                                                                                                                                                                                                                                                                                                                        Sequence 26 BP; 0 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human zalphall Ligand sequencing primer ZC7764b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sprecher CA,
Nelson AJ, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1734 ACAAAAAAAAAAAAAAAAAA 1755
                                                                                                                            Disclosure; Page 43; 113pp; English.
 Russo JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0123547P.
99US-0123904P.
99US-0142013P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS20672 standard; DNA; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-APR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 95.5
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ZYMO ) ZYMOGENETICS INC.
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Johnston JV,
 Tong A,
                               WPI; 2002-575158/61.
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Li Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US6307024-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-MAR-1999;
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01-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novak JE,
Gross JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS20672;
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
 Ju J,
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The present invention relates to the isolation of a novel cytokine, zalphall Ligand and the polynucleotide encoding it. The invention also gives the sequence for the zalphall receptor and the polynucleotide encoding it. The zalphall Ligand polypeptide stimulates proliferation of encoding it. The zalphall Ligand polypeptide stimulates proliferation of natural killer (KK) cells or NK cell progenitors, the activation of NK cells, proliferation of B-cells stimulated with anti-CD40 antibodies, stimulates an antigenic response in a mammal, and anti-CD40 antibodies, stimulates an antigenic response in a mammal, and calphall Ligand polypeptide is also useful in preparing antibodies. The zalphall Ligand polypoptide is also useful in preparing antibodies that bind to zalphall Ligand epitopes. The zalphall Ligand gene, be used as probes or primers to clone regions of a zalphall Ligand gene, and in gene therapy. Zalphall Ligand may also be used to identify inhibitors of its activity, to enhance the generation of anti-tumour responses with or without the infusion of donor lymphocytes, and to activate or stimulate the immune system. The present sequence represents a sequencing primer used to sequence CDNA clones in the isolation of human zalphall Ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method for obtaining a single stranded polynucleotide tag from a biological sample by cleaving one of the complementary strands of a double stranded polynucleotide with a cleavage agent capable of recognising a double stranded polynucleotide comprising complementary strands and cleaving only one of the strands of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Obtaining single stranded polynucleotide tags from a biological sample, for analyzing gene expression or diagnosing clinical conditions, comprises employing nicking endonucleases that cleave complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Single stranded polynucleotide tag; cleavage agent; gene expression; primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.2%; Score 20.4; DB 1; Length 26; 95.5%; Pred. No. 1.7e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer #2 used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 26 BP; 0 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1734 ACAAAAAAAAAAAAAAAAA 1755
Example 7; Col 139; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example; Page 294; 302pp; English.
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12-FEB-2001; 2001US-0267704P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD43853 standard; DNA; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 95.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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1734 ACAAAAAAAAAAAAAAAAAAAA 1755

25 AAAAAAAAAAAAAAAAAAAA

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polynucleotide in the process of generating a single stranded polynucleotide tag. The method is useful for separating, analysing, quantifying or obtaining single stranded polynucleotides comprising tags originating partly, and preferably wholly from a source of DNA and/or RNA in a sample comprising biological cells. The method is particularly for analysing gene expression (expression profiling or differential gene expression (expression profiling or differential gene expression), or in diagnosing clinical conditions. The present sequence is a primer used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes a purified polypeptide or its fragment derived from the LS147 gene capable of selectively hybridising to the nucleic acid of the gene and has at least 50% identity with the polymucleotide. The LS147 polypeptide is useful for preparing a composition for treating cancer, e.g. lung cancer using gene therapy. This sequence represents a universal primer used to sequence LS147 expressed sequence tag (EST)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New LS147 polypeptide, useful for preparing a composition for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LS147; cancer; lung cancer; gene therapy; cytostatic; ss; sequencing; primer; EST clone; expressed sequence tag clone.
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LS147-specific polynucleotide sequencing related universal primer #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klass MR
                                                                                                                                                                          Score 20.4; DB 1; Length 26;
Pred. No. 1.7e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Colpitts TL, Friedman PN,
                                                                                                                                               Sequence 26 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 26 BP; 0 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
                                                                                                                                                                                                                                             1734 ACAAAAAAAAAAAAAAAAAA 1755
                                                                                                                                                                                                                                                                           26 AAAAAAAAAAAAAAAAA S
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                                                                                                                                                                                                                                                                                                                                                             BP.
                                                                                                                                                                               1.2%;
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                                                                                                                                                                                                                                                                                                                                                           ABX93461 standard; DNA; 26
                                                                                                                                                                          Query Match
Best Local Similarity 95.5'
Matches 21, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAY-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COLPITTS T L. FRIEDMAN P N.
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RUSSELL J C.
STROUPE S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BILLINGEL P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-341045/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e.g., lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2002188114-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COHEN M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Billingel P,
Russell JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                           ABX93461;
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(COHE/)
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(KLAS/)
(RUSS/)
(STRO/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clones
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Score 20.4; DB 1; Length 26; Pred. No. 1.7e+02;

1.2%;

Query Match Best Local Similarity

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                                                                                                                                                     Immunostimulant; oligodeoxynucleic acid; ODN; vaccine; DNA-RNA hybrid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New oligodeoxynucleic acid molecules useful for the preparation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Pred. No. 1.7e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 26 BP; 0 A; 0 C; 0 G; 1 T; 25 U; 0 Other;
                                                                                                                                                                                                                                                                                                 /note= "thiophosphate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INTE-) INTERCELL BIOMEDIZINISCHE FORSCHUNGS.
(CIST-) CISTEM BIOTECHNOLOGIES GMBH.
                                                                                                                         24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schmidt W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1734 ACAAAAAAAAAAAAAAAA 1755
                                                                                                                        Oligodeoxynucleic acid molecule ODN
                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 8; Page 32; 57pp; English.
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/mod_base= OTHER
                           BP
                                                                                                                                                                                                                                                                                                                                                                                          17-MAY-2002; 2002WO-EP005448
                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAY-2001; 2001AT-00000805
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                           56
                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lingnau K, Schellack C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21; Conservative
                           ABZ24784 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VPI; 2003-183880/18.
                                                                                                                                                                                                                                                                                                                              WO200295027-A2
                                                                                                                                                                                                                                 Key
modified_base
                                                                                         07-APR-2003
                                                                                                                                                                                                  Synthetic.
                                                            ABZ24784;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   accine
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              ABZ24784/
RESULT
                                             a
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ACA62282 standard; DNA; 26
            12-AUG-2003 (first entry)
                Oligo (dT) primer #1
                              US2003022318-A1
                                                  Lin S, Ying S;
                                  30-JAN-2003.
                          Synthetic.
        ACA62282;
RESULT 95
ACA62282/c
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The invention relates to an improved polymerase thermocycling reaction (MI) for linear amplification of nucleic acid sequences, involves denaturing a number of nucleic acid templates (I), combining the denaturing a number of nucleic acid templates (I), combining the containing primer (P2), a number of denaturing templates of promoter-containing primer (P2), a reverse transcription enzyme, a DNA-dependent DNA polymerase and RNA contacting PN with (I) to generate a number of promoter-containing templates, contacting PV with the denaturing the promoter-containing templates, contacting PV with the denatured promoter-containing templates, contacting PV with the denatured promoter-containing templates, contacting PV with the denatured promoter-containing double-stranded nucleic acid templates to form a number of generate a number of promoter-containing double-stranded DNA templates, contacting the primer region of the promoter-containing double-stranded DNA templates, contacting the primer region of the promoter-containing double-stranded DNA templates, contacting the primer region of the promoter-containing double-stranded DNA templates, contacting the primer region of the promoter-containing double-stranded DNA templates, contacting the primer region of the promoter-containing double-stranded DNA templates, contacting the primer region of the promoter-containing double-stranded DNA templates, contacting the amplified RNA sequences, and denaturing the DNA-RNA hybrid templates. The method is useful for improved bolymerase thermocycling reaction for linear and incleased so incleased acid sequences, and thus for producing mRNA expression profile of a cell by MI to generate multiple copies of the above method, of cells in both normal and diseased states, and determining the differences in mRNA composition of the call(s) in new diseased state, and diseased state, and diseased state, and diseased state, and determining aberrant protein synthesising an antisense cell in a diseased state, determining aberrant proteins, synt Improved polymerase thermocycling reaction for nucleic acid amplification, by thermal cycling of promoter-linked nucleic acid template synthesis and in vitro transcriptional amplification of nucleic acid sequences. ss; PCR; primer; antisense therapy; mRNA expression profile; promoter containing primer. Example 4; Page 14; 28pp; English. 07-SEP-2001; 2001US-00949305 25-JAN-2000; 2000US-00494212 (EPIC-) EPICLONE INC WPI; 2003-479488/45.

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Gaps

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Query Match 1.2%; Score 20.4; DB 1; Length 27; Best Local Similarity 95.5%; Pred. No. 1.8e+02; Matches 1; Conservative 0; Mismatches 1; Indels

Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 2 U; 0 Other;

OS field.)

ö carrier. M1 is also useful for predicting the efficacy of a proposed drug targeted against an aberrant protein, by determining aberrant protein production of cell in a diseased state by the above method, amplifying the aberrant protein by M1 and using recombinant techniques to determine the effect of proposed drug on the aberrant protein. M1 is also useful for differential screening of tissue-specific gene expression at a cellular level, for preparing labeled RNA/DNA probes for a gene chip technology, and for determining the efficacy of a drug regiment against a gene or its cDNAs. The present sequence is an Oligo (dT) primer used to produce second strand cDNA in the method of the invention The patent claims a new molecule of formula (NA1----S----NA2)n. NA1 and NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile linkage; n= 1 or 1,000, which is used for the detection of specific DNA or RNA sequences in a test soin. The scissile link probes may be Pt (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid Support). The differential liability of DNA and RNA may be exploited in a heterogenous system when the scissile linkage is an RNA molecule. In the examples, counter probe molecules 9 through 16 were used to determine suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing Synthetic nucleic acid probes - comprising two nucleic acid sequences linked by a scissile linkage. Gaps ö Query Match 1.2%; Score 20.4; DB 1; Length 26; Best Local Similarity 95.5%; Pred. No. 1.7e+02; Matches 21; Conservative 0; Mismatches 1; Indels Sequence 26 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 0 Other; Sequence of scissile link probe MRC071 (HL). Duck P, Bender R, Crosby W, Robertson JG; 1734 ACAAAAAAAAAAAAAAAAAA 1755 26 AAAAAAAAAAAAAAAAA 5 AAN70281 standard; DNA; 27 BP 86EP-00116906. 85US-00805279 Example; p29; 46pp; English. (first entry) Hybridisation; probe; 88 (MEIO-) MEIOGENICS INC. (revised) WPI; 1987-186567/27 04-DEC-1986; 03-OCT-2002 26-MAY-1991 05-DEC-1985; 08-JUL-1987. EP227976-A. Synthetic. AAN70281; RESULT 96 AAN70281/ 888888888888888 ò a 

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Probe MRCO46 is bound by a permanent linkage to a solid support at its 3' end. It is used by reacting excess probe with a target nucleic acid; nicking hybridised probe at least once within a predetermined sequence to form 2 or more probe fragments hybridised to the target sequence, which identifying probe fragments becoming hybridised to another probe; and identifying probe fragments, so detecting the target sequence. The probe can react with target sequence to complete a cycling sequence. Using this system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can be obtd. The probe is cleavable at the ribonucleotides by a ds RNase, eg (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting target nucleic acid molecules - using excess complementary nucleic acid probes and nicking to complete a cycling sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 1.2%; Score 20.4; DB 1; Length 27; 1 Similarity 95.5%; Pred. No. 1.8e+02; 21; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 27 BP; 0 A; 0 C; 0 G; 21 T; 6 U; 0 Other;
                                                                                                              *tag= a
note= "deoxyribonucleotides."
                                                                                                                                                                                                                     /*tag= c
/note= "deoxyribonucleotides."
     Probe MRCO46; solid support; ribonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probe MRCO71; solid support; ribonuclease.
                                                                                                                                                            /*tag= b
note= "ribonucleotides
17. .27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1734 ACAAAAAAAAAAAAAAAA 1755
                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 24; 34pp; English
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AAN92247 standard; DNA; 27
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                                                                                                                                           91. .
                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                 (MEIO-) MEIOGENICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NPI; 1989-339977/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bender R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SS probe MRC071
                                                                         Key
misc_feature
                                                                                                                                                                                                                                                                                                                                             29-APR-1988;
                                                                                                                                               misc_feature
                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                              29-APR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-OCT-2002
25-APR-1990
                                                                                                                                                                                                                                                                       VO8910415-A
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                                                                                                                                                                                                                                                                                                          02-NOV-1989
                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAN92247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Duck P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAN92247,
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAZ are noncomplementary nucleic acid sequences; ---S--- a scissification of specific DNA inkage; n= 1 or 1,000, which is used for the detection of specific DNA or RNA sequences in a test soln. The scissile link probes may be PL (Permanent Linkage to Solid Support) or HL (Hydrolyaable Linkage to Solid Support). The differential liability of DNA and RNA may be exploited in a fleterogenous system when the scissile linkage is an RNA molecule. In the examples, counter probe molecules 9 through 16 were used to determine guitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The patent claims a new molecule of formula (NAI----S----NA2)n. NAI and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic nucleic acid probes - comprising two nucleic acid sequences linked by a scissile linkage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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1.2%; Score 20.4; DB 1; Length 27;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 27 BP; 0 A; 0 C; 0 G; 21 T; 6 U; 0 Other;
                                                                                                                                                                                                                                                 Sequence of scissile link probe MRC046 (PL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Robertson JG
 1734 ACAAAAAAAAAAAAAAAAA 1755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1734 ACAAAAAAAAAAAAAAAAA 1755
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                           AAAAAAAAAAAAAAAAAAAAA
                                                                                                                         AAN70274 standard; DNA; 27 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                               86EP-00116906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                85US-00805279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example; p29; 46pp; English.
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AAN92240 standard; DNA; 27
                                                                                                                                                                                           (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MEIO-) MEIOGENICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised) (revised)
                                                                                                                                                                                                                                                                                    Hybridisation; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1987-186567/27.
                                                                                                                                                                                                                                                                                                                                                                                                                               04-DEC-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35-DEC-1985;
                                                                                                                                                                                           03-OCT-2002
26-MAY-1991
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25-APR-1990
                                                                                                                                                                                                                                                                                                                                                                                            08-JUL-1987
                                                                                                                                                                                                                                                                                                                                                        EP227976-A.
                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                            AAN70274;
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Duck P,

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Gaps

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Synthetic

SS probe MRCO46

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Gaps

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1; Indels

27;

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The sequence is given in the disclosure to illustrate the invention
                                                                Replication of DNA - useful in genetic engineering and medical
                                                                                                                                                             1.2%; Score 20.4; DB 1; Length 95.5%; Pred. No. 1.8e+02; ive 0; Mismatches 1; Indels
                                                                                                                                         Sequence 27 BP; 27 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                         1734 ACAAAAAAAAAAAAAAAA 1755
                                                                                                Disclosure; Page 20; 20pp; Japanese.
                                                                                                                                                                                                                        26-AUG-1991; 91JP-00240525.
                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                    21; Conservative
                    (UYAR-) UNIV ARIZONA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weindel K, Brand J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-055287/05.
                                          WPI; 1993-171830/21.
                                                                                                                                                                          Local Similarity
                                                                           applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-JUN-1998;
                                                                                                                                                                                                                                                                                                                                10-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                           08-DEC-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                    EP962536-A1
                                                                                                                                                                                                                                                                                                        AAZ43904;
                                                                                                                                                                Query Match
                                                                                                                                                                            Best Loca
Matches
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AAZ43904/c
SXCXBXFFXBXBXBXBXBX
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                                                                                                                                                                                                                                                                                                                                        3 end. It is used by reacting excess probe with a target nucleic acid; nicking hybridised probe at least once within a predetermined sequence to form 2 or more probe fragments hybridised to the target sequence, which results in the probe fragments becoming hybridised to another probe; and identifying probe fragments, so detecting the target sequence. The probe can react with target sequence to complete a cycling sequence. Using this system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can be obtd. The probe is cleavable at the ribonucleotides by a ds RNase, eg RNase H or ExoIII. (Updated on 31-0CT-2002 to add missing OS field.)
                                                                                                                                                                                                                                                                                                                               Probe MRCO71 is bound by a hydrolysable linkage to a solid support at its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                         Detecting target nucleic acid molecules - using excess complementary nucleic acid probes and nicking to complete a cycling sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 1.2%; Score 20.4; DB 1; Length 27; Local Similarity 95.5%; Pred. No. 1.8e+02; nes 21; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 2 U; 0 Other;
                    /*tag= a
/note= "deoxyribonucleotides."
                                                                                      /*tag= c
/note= "deoxyribonucleotides."
                                                                                                                                                                                                                                                                                                                                                                                                                                          (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA sequence used in DNA replication method.
                                              /*tag= b
/note= "ribonucleotides."
18. .27
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1734 ACAAAAAAAAAAAAAAAAAA 1755
ocation/Qualifiers
                                                                                                                                                                                                                                                                                                          Disclosure; Page 24; 34pp; English
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                                                                                                                                                                88US-00187814
                                                                                                                                                                                   29-APR-1988; 88US-00187814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ40854 standard; DNA; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                          .17
                                                                                                                                                                                                          (MEIO-) MEIOGENICS INC
                                                                                                                                                                                                                                                    WPI; 1989-339977/46
                                                                                                                                                                                                                                Bender R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-AUG-1991;
                                                                                                                                                                29-APR-1988;
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         misc_feature
                                          misc_feature
                                                                           misc_feature
                                                                                                                    WO8910415-A
                                                                                                                                          02-NOV-1989.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ40854;
                                                                                                                                                                                                                               Duck P,
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Matches
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This invention describes a novel method for the selective detection of nucleic acids which comprises amplification of the nucleic acid with the help of labeled primers and detection with a trap probe. The methods and reagents are used for the detection of a marker primer and at least 2 immobilized (or immobilizable) trap probes with the corresponding nucleic acid sequence of interest for mutation analysis. The method can be used to detect a specific sequence in a sample of one or more nucleic acids by using several sets of primers and trap probes (i.e. in an array). The methods are useful in molecular biology and diagnostic applications, especially for simultaneous detection of multi-pathogens, typing of organisms, analyzing genetic diversity and sequencing of genes or primer sequence represents a primer used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                RNA polymerase; rpo-beta; detection; diagnostic; trap probe; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amplification with labeled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 27 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Selective detection of nucleic acids by primers and detection with a trap probe.
                                                                                                                                                                                                                                                                                                  M. tuberculosis rpo-beta primer 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1c; Page 19; 27pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HOFF ) ROCHE DIAGNOSTICS GMBH
AAZ43904 standard; DNA; 27 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98DE-01024900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99EP-00110458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis
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Anglogenesis inhibitor; se; anglogenesis; solid tumour growth; tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial anglogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; anglocibroma; wound granulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.

Angiogenesis inhibitory oligonucleotide #911.

(first entry)

13-DEC-2002

ABS78427;

BP

ABS78427 standard; DNA; 27

us10008789-3.rng

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RESULT: 103
                              ABS78427/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immunostimulatory. The present sequence is one such immunostimulatory nucleic acids can be pyrimidine or nucleic acids. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is slab useful for preventing cancer, asthma, infectious disease, alleryy or immune deficiency. The present sequence can also be used to redirect a Th2 to a Th1 immune response and to activate immune cells. Note: the
                                                                                                                                                                                                                                         Vaccine, cytostatic, virucidal, bactericidal, fungicidal, anti-parasitic, immunostimulatory, tumour; viral infection; bacterial infection; fungal infection; cancer, asthma; infection; and infection; infections disease; allergy, immune deficiency; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a method for stimulating an immune
                              ö
1.2%; Score 20.4; DB 1; Length 27;
llarity 95.5%; Pred. No. 1.8e+02;
Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 95.5%; Pred. No. 1.8e+02;
21; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present sequence may have a phosphorothicate backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 27 BP; 0 A; 0 C; 0 G; 27 T; 0 U; 0 Other;
                                                   Immunostimulatory nucleic acid #822.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 101; Page 56; 338pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Krieg AM, Schetter C, Vollmer J;
                                                                          27 ARAAAAAAAAAAAAAAA 6
                                                                                                                                                                                                                                                                                                                                                                                                         25-SEP-1999; 99US-0156113P.
27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
                                                                                                                                                                                                                                                                                                                                                                                  25-SEP-2000; 2000WO-US026383
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IOWA ) UNIV IOWA RES FOUND. (COLE-) COLEY PHARM GMBH.
                                                                                                                                    AAF99706 standard; DNA; 27
                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-273485/28.
              Similarity
                                                                                                                                                                                                                                                                                                                                 VO200122972-A2
Query Match
Best Local Simi
Matches 21;
                                                                                                                                                                                          12-JUN-2001
                                                                                                                                                                                                                                                                                                                                                         05-APR-2001
                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                 AAF99706;
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Best Local (
                                                                                                                           AAF99706,
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14-DEC-2000; 2000US-025534P. 14-DEC-2001; 2001WO-US048458.

40200253141-A2

Synthetic.

11-JUL-2002.

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                                                                                                                                                                                                     Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . Match 1.2%; Score 20.4; DB 1; Length 27; Local Similarity 95.5%; Pred. No. 1.8e+02; es 21; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 27 BP; 0 A; 0 C; 0 G; 27 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                             Claim 2; Page 35; 276pp; English.
(COLE-) COLEY PHARM GROUP INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABL39406 standard; DNA; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acid of the invention
                                                                                                                                     WPI; 2002-566690/60
                                                                    Bratzler RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL39406;
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Matches
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Gaps

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1734 ACAAAAAAAAAAAAAAAA 1755

21;

Matches

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27 AAAAAAAAAAAAAAAAAAA 6

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androgen receptor; AR; cancer; liver tumour; cytostatic; PCR; 5'RACE
                                                                                                                                                                                                                                                  cancer
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ABS54324/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to methods for treating or preventing cancer, involving administering to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies. The methods are useful for treating or preventing cancer such as basal cell carcinoma, bladder cancer, bone cancer, cervical cancer, colon and rectum cancer, connective breast cancer, cervical cancer, colon and rectum cancer, connective cancer, leukaemia, liver cancer, iung cancer, Hodgkin's lymphoma, non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin cancer, sequence is an immunostimular cancer, and uterine cancer. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                           Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies to a subject having or at risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human androgen receptor complex-associated protein 5'RACE PCR primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; androgen receptor complex-associated protein; ARCAP; primer; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                           Antibody-induced cell lysis; cancer; immunostimulatory; CD20; angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.2%; Score 20.4; DB 1; Length 27; 95.5%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                            1. 27
/*tag= a
/mod_base= OTHER
/note= "phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 27 BP; 0 A; 0 C; 0 G; 27 T; 0 U; 0 Other;
                      Immunostimulatory nucleic acid SEQ ID NO: 842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 310; 312pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1734 ACAAAAAAAAAAAAAAAAAA 1755
                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JUN-2001; 2001WO-US020154
                                                                                                                                                                                                                                    22-JUN-2000; 2000US-0213346P.
                                                                                                                                                                                                                                                          (IOWA ) UNIV IOWA RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABS53863 standard; DNA; 27
16-APR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-NOV-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21; Conservative
                                                                                                                                                                                                                                                                                 Hartmann G;
                                                                                                                                                                                                                                                                                                     WPI; 2002-154611/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                             cancer
                                                                                                                                                                    WO200197843-A2
                                                                                                  Key
modified_base
                                                                                                                                                                                         27-DEC-2001
                                                                                                                                                                                                                                                                                                                                                            developing
                                                                                                                                                                                                                                                                                 Weiner G,
                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; androgen receptor complex-coupled protein; ARCAP; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel substantially pure androgen receptor (AR) complex-associated protein which binds to AR and increases ability of AR to transactivate androgen-responsive gene, useful as drug target for treating liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 1.2%; Score 20.4; DB 1; Length 27; Il Similarity 95.5%; Pred. No. 1.8e+02; 21; Conservative 0; Mismatches 1; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human ARCAP associated 5'RACE PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1734 ACAAAAAAAAAAAAAAAAA 1755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                  (VETE-) VETERANS GEN HOSPITAL
                                                                                                                                                                                                                                                             17-JAN-2001; 2001US-0262312P.
12-FEB-2001; 2001US-00781693.
                                                                                                                                                                                               16-JAN-2002; 2002EP-00250305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2001; 2001JP-00055192.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-676576/73.
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Homo sapiens.
                                                              EP1227150-A2
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                                                                                                                                31-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Tai-Jay
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disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic contact dermatitis, latex dermatitis or inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease. This sequence represents an immunostimulatory nucleic acid

Sequence 27 BP; 0 A; 0 C; 0 G; 27 T; 0 U; 0 Other;

1734 ACAAAAAAAAAAAAAAAAAA 1755

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Gaps

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Query Match 1.2%; Score 20.4; DB 1; Length 27; Best Local Similarity 95.5%; Pred. No. 1.8e+02; Matches 21; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                       The present invention relates to the isolation of human androgen receptor complex-coupled protein (ARCAP), and the polynucleotide sequence encoding it. The ARCAP Polypeptide complexes with an androgen receptor to increase the activity of the androgen receptor, transactivating the androgen responsing gene. The invention also describes a vector containing the ARCAP Polynucleotide sequence, and a host cell containing the ARCAP polynucleotide sequence. The ARCAP polypeptide can be used as a treating agent. The present sequence represents a PCR primer used in the example of the present invention
                                                                      Novel substantially pure androgen receptor (AR) complex-associated protein which binds to AR and increases ability of AR to transactivate androgen-responsive gene, useful as drug target for treating liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes a method of treating non-allergic inflammatory
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunostimulatory; antiinflammatory; dermatological; antipsoriatic; antiulcer; gene therapy; vaccine; non-allergic inflammatory disease; psoriasis; eczema; allergic contact dermatitis; latex dermatitis; inflammatory bowel disease; ulcerative colitis; crohn's disease; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treating non-allergic inflammatory diseases, such as psoriasis, allergic contact dermatitis, latex dermatitis or inflammatory bo disease by administering an immunostimulatory nucleic acid.
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                                                                                                                                                                                                                                                                                                        Score 20.4; DB 1; Length 27;
Pred. No. 1.8e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                 Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                          1734 ACAAAAAAAAAAAAAAAAA 1755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunostimulatory nucleic acid #880.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page 32, 229pp, English
                                                                                                                                                                                                                                                                                                                                                                                  25 AAAAAAAAAAAAAAAAAAAAAA 4
                                                                                                                                    Example; Page 15; 18pp; Japanese.
 HOSPITAL
                                                                                                                                                                                                                                                                                                          1.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAR-2002; 2002US-00112653
                                                                                                                                                                                                                                                                                                                                                                                                                                              ACH03245 standard; DNA; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-SEP-2003 (first entry)
                                                                                                                                                                                                                                                                                                                     Local Similarity 95.5
hes 21; Conservative
(VETE-) VETERANS GEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-521815/49.
                                                WPI; 2002-676576/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Krieg AM, Berg DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (KRIE/) KRIEG A M. (BERG/) BERG D J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2003050268-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-MAR-2003
                         Tai-Jay C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACH03245
                                                                                                            cancer
                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 107
ACH03245/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                    nucleic acid; aerosol formulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 20.4; DB 1; Length 27; Pred. No. 1.8e+02;
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                                                                                                                                                                                                                                                                                                                    ds; allergy; asthma; poly-G nucleic acid; a
hypo-responsive subject; immunostimulatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fouron Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 17; 221pp; English.
                                                                                                                                                                                                                                                                      Immunostimulatory nucleic acid #822.
9
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AAAAAAAAAAAAAAAAAAAA
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                                                                                                                     ADB37208 standard; DNA; 27
                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BETE/) BEATZLER R
(PETE/) PETERSEN D
(FOUR/) FOURON Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              JS2003087848-A1
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                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
27
                                                                                                                                                                        ADB37208;
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                                                                       RESULT 108
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                                                                                                ADB37208,
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Takashi M;

Teh BT,

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29-MAR-2002; 2002WO-US009576.
                                                                                              29-MAR-2001; 2001US-0279411P.
                                                                                                                    (VAND-) VAN ANDEL INST
                                                                                                                                        Haab B, Rhodes D,
                               WO200279411-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified_base
                                                    10-OCT-2002
           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 111
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                                                                                                                                                                                                                                                                                                                       Producing a molecular array with a plurality of molecules immobilized to a solid substrate, useful in genetic analysis, gene expression studies or the detection or typing of single nucleotide polymorphisms in a sample of
                                                                                                                                                                                                                                                                                                                                                                                              The invention comprises a method for producing a molecular array, the method involves immobilising molecules to a solid phase at a density which allows individual immobilised molecules to be individually resolved. The molecular array produced by the method of the invention is useful for identifying one or more target molecules in a sample. The molecular array is also useful in genetic analysis, gene expression studies, identifying molecules which interact with a target molecule, detection/typing of single nucleotide polymorphisms, haplotyping and sequencing. The present DNA sequence represents a PCR primer that was used in an example of the invention
                                                                                                        ss; target molecule identification; genetic analysis; SNP detection; haplotyping; sequencing; PCR; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          differential expression profile, aggressive CC-RCC tumour type, non-aggressive CC-RCC tumour type, clear cell renal carcinoma; gene expression profiling; tumour tissue; oligo-dT; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 20.2; DB 1; Length 22;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                  Molecular array production method-related PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Microarray; solid surface; immobilised probe; CC-RCC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligo-dT primer used in human CC-RCC invention.
                                                                                                                                                                                                                                                        (UYCH-) UNIV CHANCELLOR MASTER & SCHOLARS OXF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
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                                                                                                                                                                                                                         16-MAR-2001; 2001GB-00006635.
                   AAL50570 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABX74887 standard; DNA; 22
                                                             12-DEC-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                   WPI; 2002-732872/79.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                  gene expression;
                                                                                                        Molecular array;
                                                                                                                                                           WO200274988-A2.
                                                                                                                                                                                                                                                                                                                                                        nucleic acids
                                                                                                                                      Unidentified
                                                                                                                                                                                 26-SEP-2002.
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                                         AAL50570;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                               Mir K;
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The present invention relates to a microarray comprising a matrix of at least one CDNA probe from a set of probes immobilised to a solid surface in a predetermined order, where a row of pixels corresponds to replicates of one distinct probe from the set. The probes are complementary to nucleic acid sequences that are expressed differentially in aggressive as compared to non-aggressive types of clear cell renal carcinoma (CC-RCC) and that hybridise to the probes under high stringency conditions. The microarray is useful for the propossis of patients with CC-RCC, wherein aggressive and non-aggressive CC-RCC tumour types are characterised by differential expression profiles of genes that hybridise with one or more probes immobilised on the microarray. The arrays are useful for gene expression profiling of tumour and normal tissues. The present sequence represents an oligo-dT primer used in the examples of the present
                                                             New microarray, comprising a matrix of cDNA probe from a set of probes immobilized to a solid surface in predetermined order, useful in the prognosis of patients with clear cell renal carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.2%; Score 20.2; DB 1; Length 22; 95.2%; Pred. No. 1.6e+02; ive 1; Mismatches 0; Indels
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/mod_base= OTHER
/note= "OTHER= locked nucleic acid"
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/mod_base= um
/note= "2'-0-methyluridine"
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                                                                                                                                                                                                           Example 2; Page 30; 179pp; English
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ID ACC48484 standard; DNA; 22
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*tag≂
WPI; 2003-040679/03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention
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Best Local 8
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The present sequence is that of pyrene-anchored locked nucleic acid (LNA) oligo(dT) primer ON14, which was used in first-strand cDNA synthesis from eukaryotic mRNA. It includes compound '17d' at its 3' end, which is based on an LNA-type 2'-O,4'-C-methylene-beta-D-ribofuranosyl moiety. It is one of a set of such primers (see also ACC48482-85) that were used in an example from the invention to demonstrate improved reverse transcription of mRNA using pyrene-LNA anchored oligo(T) primers. The following results
                                                                                                                                                                                                                                                                                                                                                                                                                                        Wengel J, Kauppinen S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oxazole/imidazole.
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were observed: efficient priming on mRNAs with short poly(A) tails; efficient anchoring of the oligo(T) primer by pyrene-LNA and LNA-C/G/T units resulting in an improved T20-VN anchor primer and thus avoiding reverse transcription of long poly(A) tracts; and improved reverse transcription of eukaryotic poly(A) +RNA directly from total RNA extracts due to increased specificity. The invention relates to modified LNA units that comprise unique base groups. Desirable nucleobase and nucleosidic base substitutions can mediate universal hybridisation when incorporated into nucleic acid strands. The novel LNA compounds can be used e.g. as PCR primers, in sequencing, the synthesis of antisense oligonucleotides, and in diagnostics
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                                                                                                                                                                                                                                        1.2%; Score 20.2; DB 1; Length 22; 95.2%; Pred. No. 1.6e+02; tive 1; Mismatches 0; Indel8
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/mod_base= OTHER
/note= "OTHER= locked
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/mod_base= OTHER
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ACC48485 standard; DNA; 22
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                                                                                                                                                                                                                                                                            Conservative
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nes 20; Conserva
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Matches
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                        /mod_base= OTHER
/note= "OTHER= locked nucleic acid"
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|mod_base= OTHER
|note= "OTHER= locked nucleic acid"
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'note= "OTHER= locked nucleic acid"
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/mod_base= OTHER
/note= "OTHER= locked nucleic
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/mod_base= OTHER
/note= "OTHER= Compound 17d"
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mod_base= OTHER
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22-SEP-2001; 2001US-0323967P
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nucleic acid"

The present sequence is that of pyrene-anchored locked nucleic acid (LNA) oligo(dT) primer ON15, which was used in first-strand cDNA synthesis from eukaryotic mRNA. It includes compound '17d' at its 3' end, which is based on an LNA-type 2'-0,4'-C-methylene- beta-D-ribofuranosyl moiety. It is

Example 24a; Page 90; 119pp; English.

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one of a set of such primers (see also ACC48482-84) that were used in an example from the invention to demonstrate improved reverse transcription of mRNA using pyrene-LNA anchored oligo(T) primers. The following results were observed: efficient priming on mRNAs with short poly(A) tails; efficient anchoring of the oligo(T) primer by pyrene-LNA and LNA-C/G/T units resulting in an improved T20-VN anchor primer and thus avoiding reverse transcription of long poly(A) tracts; and improved reverse transcription of long poly(A) tracts; and improved reverse the comprise unique base groups. Desirable nucleobase and nucleosidic base substitutions can mediate universal hybridisation when incorporated into nucleic acid strands. The novel LNA compounds can be used e.g. as PCR primers, in sequencing, the synthesis of antisense oligonucleotides, and in diagnostics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 20.2; DB 1; Length 22; Pred. No. 1.6e+02;
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/mod_base= OTHER
/note= "OTHER= locked nucleic acid"
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/note= "OTHER= locked nucleic acid"
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/mod_base= OTHER
/note= "OTHER= locked nucleic acid"
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/mod_base= OTHER
/note= "OTHER= locked nucleic acid"
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/note= "OTHER= locked nucleic acid"
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/note= "OTHER= locked nucleic acid"
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/note= "OTHER= locked nucleic acid"
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/note= "OTHER= Compound 17d"
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The present sequence is that of pyrene-anchored locked nucleic acid (LNA) coligo(dT) primer ONI3, which was used in first-strand cDNA synthesis from eukaryotic mRNA. It includes compound '17d' at its 3' end, which is based on an LNA-type 2'.0,4'-C-methylene-beta-D-ribofuranosyl moiety. It is one of a set of such primers (see also ACC48482-85) that were used in an example from the invention to demonstrate improved reverse transcription of mRNA using pyrene-LNA anchored oligo(T) primers. The following results efficient anchoring of the oligo(T) primer by pyrene-LNA and LNA-C/G/T units resulting in an improved T20-VN anchor primer and thus avoiding transcription of long poly(A) tracts; and improved reverse transcription of long poly(A) tracts; and improved reverse transcription of eukaryotic poly(A)+RNA directly from total RNA extracts due to increased specificity. The invention relates to modified LNA units that comprise unique base groups. Desirable mucleobase and nucleosidic base substitutions can mediate universal hybridisation when incorporated into nucleic acid strands. The novel LNA compounds can be used e.g. as the condition of the computer of the open condition of a condition of the object of the computer of the condition                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laminitis, viral disease; vaccine; bacterial disease; primer; epistaxis; gastritis; gastric ulcer; respiratory ailment; fracture; joint disease; musculoskeletal damage; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acid comprising a locked nucleic acid unit having a modified base that comprises an optionally substituted carbocyclic aryl moiety, or modified nucleobase or nucleosidic base other than oxazole/imidazole.
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                                                                                                                                                                            04-SEP-2001; 2001US-0317034P. 22-SEP-2001; 2001US-0323967P.
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                                                                                                                                                                                                                                                                                                              Wengel J, Kauppinen S;
                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-363021/34.
                                                                                                                                                                                                                                                          (EXIQ-) EXIQON AS
                        WO2003020739-A2.
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Local S.
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                                                                           13-MAR-2003
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14-NOV-2002.

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The present invention relates to a method for providing a profile of mRNA molecules present in a sample. The method comprises generating two independent patterns characteristic of the population of mRNA molecules expressed in the sample and analysing the patterns using a combinatorial algorithm, comparing gene expression by different or same cell types under different conditions, and identifying genes having a role in various cellular processes. The method is useful for the analysis and identification of transcribed genes, and fingerprinting. The method can be used to identify genes which play a role in determining various cellular processes, including susceptibility to external factors, development, and disease. The present sequence for a PCR primer is used in the methods of the present invention
                                                                                                      Providing mRNA profile, by generating two independent patterns characteristic of sample mRNA population, analyzing patterns, comparing gene expression by cell types under varied conditions, and identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.2%; Score 20.2; DB 1; Length 23; 95.2%; Pred. No. 1.7e+02; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GESL ) FORSCHUNGSZENTRUM KARLSRUHE GMBH
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                                                                                                                                                                                                                                     Example 2; Page 45; 67pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABX94936 standard; DNA; 26
     Linnarsson S, Ernfors P,
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Best Local Similarity
                                                      WPI; 2002-217065/27.
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                                                                                                                                                                                       genes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method for assessing a condition of a performance animal. The method involves determining in sample abundance of expressed target nucleic acid; transmitting in sample abundance of expressed target nucleic acid; transmitting digital sample signal to remote diagnostic server; processing digital sample signal to remote diagnostic server; processing digital sample signal at remotely corrected database to correlate digital signal with digital information and returning report of particular condition of a mimal. The method is useful cor camel. The condition can be an athletic ability and a condition that enhances, hinders, impedes or does not change an expected ability of the performance animal; and also normal, pre-clinical, overt progress and/or stage of disease, undiagnosed of unclassified conditions, presence of drugs, response to environmental conditions. Diseases assessed by the invention include laminitis, lameless, viral or bacterial disease, interpressing quastritis, gastric ulcers, respiratory allments, fractures, episteaxis, musculoskeletal damage or disorders and joint diseases. The present
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                                                                                                                                                                                                                                                                                Assessing condition e.g. athletic ability, stage of disease, presence of drugs, response to exercise, response to vaccines, therapies, nutritional states, of performance animal involves analyzing nucleic acid expression.
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                                                                                                                            (GENO-) GENOMICS RES PARTNERS PTY LTD.
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21-JUL-2000; 2000US-0219925P.
                                                04-MAY-2001; 2001AU-00004809
29-JUN-2001; 2001US-00896941
03-MAY-2002; 2002WO-AU000553
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                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 46; 87pp;
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A genetically modified glucocorticoid receptor which is transactivation deficient is used to identify cofactors which will be useful to provide inflammation-inhibiting and immunosuppressive treatment.
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                                                                                                      Luciferase, ubiquitin promoter; glucocorticoid receptor; PCR; primer; transrepression protein-protein reciprocal effect; immunosuppressive; transactivation deficient inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soettlicher M, Heilbock C, Herrlich P, Litfin M, Schneider
Renilla luciferase associated PCR primer N-Termrev.
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WPI; 1992-201578/25.

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construct comprising at least a nucleic acid encoding the glucocorticoid receptor, operably linked with regulatory sequences of a reporter gene, preferably a DNA-binding domain for a reporter gene, (2) identifying, a gene encoding a cofactor involved in glucocorticoid receptor modulation of at least another transcription factor comprising; (a) using the above construct with an expression bank of a eukaryotic cell expressed in a cyeast two hybrid system; (b) detecting a specific protein-protein complex or the receptor and a cofactor through growth in a selective medium for the receptor and a cofactor through growth in a selective medium for the receptor and a cofactor through growth in a selective medium for the receptor and (c) isolating and characterising the nucleic acid encoding the cofactor in the CDNA clone; (3) a cofactor with construction specific for the glucocorticoid receptor which in a downstream segment the N-terminal AR-1 and the DNA-binding domain of the receptors are bound; (4) identifying an agent which affects the cettors and/or cofactors, whereby the receptor with a petential agent and modulation of the interaction of the protein complex binding; (5) an agent for modulating interaction of the glucocorticoid receptor with a cofactor which binds either at the cofactor protein-protein complex binding; (5) an agent for modulating interaction of the glucocorticoid receptor with a cofactor which binds either at the coffect comprising the above agent. The genetically modified and inflammation-inhibiting or immunosuppressive from transment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to produce an inflammation-inhibiting or immunosuppressive treatment. This sequence represents a PCR primer NTermrev used to amplify a Renilla reniformis luciferase gene which is then cloned into a reporter construct
is transactivation deficient. The invention also describes (1) a gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.2%; Score 20.2; DB 1; Length 26; 88.0%; Pred. No. 1.8e+02; Live 0; Mismatches 3; Indels
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/note= "3-amino modified"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    behind a ubiquitin promoter
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modified_base
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02-DEC-1992
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AAQ25565/
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                                New dye-coupled modified nucleosides, nucleotides and oligo:nucleotides useful for synthesis of antisense DNA and RNA strands in presence of template, also for in-vivo and in-vitro detection of genetic material.
                                                                                                                                           The sequence is an example of a dye coupled 3'-amino modified oligonucleotide, it can be used in the synthesis of DNA and RNA nucleosides, nucleotides and oligonucleotides and for the synthesis of opposite strands in the presence of a template strand and in fluorescence microscopic and macroscopic detection in vivo and in vitro of genetic material. It is labelled with a fluorescent dye. See also AAQ25566 and AAQ25567. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polymorphic bovine DNA markers - used in genetic identification, gene
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                            1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                          Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Microsatellite sequence from clone AGLA247.
                                                                                                                                                                                                                                                                                                                                                                                                       1736 AAAAAAAAAAAAAAAAA 1755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Table 7; Page 150; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mapping, and selective breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                             20 AAAAAAAAAAAAAAAA
                                                                                                          Example; Page 9; 17pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ33554 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92WO-US000340.
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                                                                                                                                                                                                                                                                                                                                                                  20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9213102-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JAN-1992;
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02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ33554;
                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 118
                                                                                                                                                                                                                                                                                                                                                                    Matches
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us10008789-3.rng

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Alpha-anomeric oligonucleotide ligand 1803 for oestradiol hapten.
                                              (first entry)
                                   (revised)
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                                                                                                                                                                                             modified_base
                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                              .0-JUN-1994;
                                                                                                                                                                                                                                                                                                                    11-JUN-1993;
                                                                                                                                                                                                                                                     WO9429723-A1
                                   25-MAR-2003
                                             24-AUG-1995
                                                                                                                                                                                                                                                                         22-DEC-1994.
                                                                                                                      Synthetic
             4AQ94205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                        (CROS/)
(KURF/)
                                                                                                                                                                                                                                                                                                                                                                                              Cros P,
                                                                                                                                                                                                                                                                                                                                                                         (PIGA/)
                                                                                                                                                                                                                                                                                                                                                                BATT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The inventors claim a method of transporting a nucleic acid deriv. accros a membrane which comprises using a receptor that uses salt bridgin, aromatic stacking, H bonding and chelation to recognise the nucleic acid deriv. AAQ56305, AAQ56577-86 are nucleic acid derivs used in the
used to identify individuals, for parentage testing, and in the genetic mapping of economic traits loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transport of nucleic acid derivs. across membranes - using new receptors which use salt bridging, aromatic stacking, hydrogen bonding and
                                                                                                                                                                                                                                                                                   Sequence of synthetic RNA oligo which is a target nucleotide for a novel
                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                            ö
                                                                                   Query Match
1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.1%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            examples. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                   Novel receptor; nucleic acid; transport; oligo; ss
                                                                Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example; Table 1, page 38; 103pp; English.
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                                                                                                                               1736 AAAAAAAAAAAAAAAAA 1755
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                                                                                                                                                   20 AAAAAAAAAAAAAAAA 1
                                                                                                                                                                                                         AAQS8578 standard; RNA; 20 BP
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                                                                                                                                                                                                                                                   (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rebek J,
                                                                                                                                                                                                                                                                                                                                                                                                                             14-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                         13-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                              VO9404194-A1
                                                                                                                                                                                                                                                  25-MAR-2003
21-AUG-1994
                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chelation
                                                                                                                                                                                                                              AAQ58578;
                                                                                                                                                                                                                                                                                              receptor.
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AAQ94205 standard; DNA; 20 BP

RESULT 120 AAQ94205/

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Assay device for hapten or its specific antibodies - comprises support having competitive reagent immobilised via nucleic acid ligand to improve orientation and accessibility.
                                                                                                                                                                                                        /*tag= b
/note= "the glycosidic bonds between nucleotides are all
                                                                                                                                                                                                                                                                                                                                                       /mod_base= OTHER
/note= "carries a group derived ffrom aminopropanediol"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Oligonucleotide ligand; steroid hormone; hapten; immobilisation; immunodetection; estradiol; alpha-anomer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                        in the alpha-anomer form"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Piga N;
                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1736 AAAAAAAAAAAAAAAAAA 1755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 10; 39pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Battail N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAAAAAAAAAAAAAAAA
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                                                                                                                                                                                                     *tag=
                                                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kurfurst R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CROS P.
KURFURST R.
BATTAIL N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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AAQ75568/C
ID AAQ755
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                                                                                                                                                                                                                                          A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
                                                                                                                                                                                                 gene expression - by amplification of mRNA followed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  self-addressable electronic device; SAED; hybridisation;
                                                                                                                                                                                                                                                                                                                                                              Gaps
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"3' aminolink2 Thymine; allows binding to any
                                            Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
                                                                                                                                                                                                                                                                                                                                                               ö
                          Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                                                                                                                                                                                                                        1.1%; Score 20; DB 1; Length 20;
100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T2 (synthetic DNA probe with 5' amino terminal #4).
                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
                                                                                                                                                             (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
                                                                                                                                                                                                          by digestion with restriction enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                           Disclosure; Page 5; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                               1733 TACAAAAAAAAAAAAAA 1752
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                                                                                                                                           93JP-00112515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
         04-AUG-1995 (first entry)
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amine"
                                                                                                                                                                                                 Analysis of cDNA and
                                                                                                                                                                               WPI; 1995-018287/03
                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rz; HLA; dQa;
                                                                                       JP06303997-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-OCT-1994;
                                                                                                                         16-APR-1993;
                                                                                                                                           16-APR-1993;
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                                                                                                       01-NOV-1994.
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                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-HTLV-1 anti-sense oligo:nucleotide - is complementary to region of tax gene from human T-cell lymphotropic virus type 1 and inhibits viral antigen expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotides having a partial sequence consisting of at least 15 bases of AAT61641 (an antisense oligo complementary to a region of the tax gene which can inhibit human T-cell lymphotropic virus type 1 (HTLV-
                                                                                                                                                                                                                                                       New self-addressable electronic devices - used for multi-step and multiplex reactions such as DNA hybridisation(s), clinical diagnostics and bio:polymer synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antisense; complementary; tax gene; inhibit; HTLV-1;
human T-cell lymphotropic virus type 1; viral antigen expression; ss.
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100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ř
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                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 41; 86pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 AAAAAAAAAAAAAAAAAA
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93US-00146504.
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                                                                                                                                                                                          WPI; 1995-185870/24.
                                                         (NANO-) NANOGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                             콛
01-NOV-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUN-1997
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                                                                                                                             Heller MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT63649;
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AAT63649/c
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Length 20;

Query Match

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Gaps

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1) viral antigen expression) are claimed. In an example, six antisense oligos were designed, T1-T6 (AAT63650-55) and were compared to six oligos derived from other regions of HTLV-1, i.e. SJ1 (Splice junction), P1 (p21), R1 (rex), RR1 (rex response element), E1 (env) and G1 (gag), four reference oligonuclectides T1S (tax-sense), HC (dC20), HT (dT20) (AAT63647-49) and a random 20mer (RAN) in a HTLV-1 virus antigen expression inhibiting test. Oligonuclectide T1 gave the best results
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium vaccae polypeptides - used to develop products for use in detection, therapy and prevention of mycobacteria infections or as immune response enhancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This oligonucleotide is used in the DNA cloning strategies of the Mycobacterium vaccae antigens. The invention provides M. vaccae polypeptides that comprise an immunogenic portion of a soluble M. vaccae antigen, or a variant, where the antigen induces an immune response in patients previously exposed to a mycobacterium. Such M. vaccae polypeptides can be used in methods for enhancing non-specific immune response. The methods and products can be used for the detection, treatment and prevention of infectious diseases caused by mycobacteria such as M. vaccae, M. avium or M. tuberculosis. The products also have the ability to induce cell proliferation and cytokine products also have interferon-gamma and interleukin-12 production) in T cells, NK cells, and the macrophages. They can be used for enhancing immune responses for use in vaccines or immunotherapy of infectious diseases and cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium vaccae, antigen, therapy, prevention, cytokine production, M. avium; M. tuberculosis, immune response enhancer; cell proliferation; mycobacteria infection; vaccine, cancer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hiyama J, Visser E, Skinner MA, Scott LM, Prestidge RL;
                                                                                                                                                                                                            Query Match
1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M. vaccae antigenic sequence hybridising oligo AD12.
                                                                                                                                                                     Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 8; Page 99; 153pp; English.
                                                                                                                                                                                                                                                                                                 1736 AAAAAAAAAAAAAAAA 1755
                                                                                                                                                                                                                                                                                                                                        20 AAAAAAAAAAAAAAAAA 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV34591 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-00873970.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-NZ000105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium vaccae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-216926/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV34591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ran P,
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 124
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process using capillary affinity gel electrophoresis. The invention process using capillary affinity gel electrophoresis. The invention crelates to selective separation of electrically charget molecules in an analytical mixture. It comprises capillary affinity gel electrophoresis using a capillary tube which is at least partly filled with a polymer. An electric field of at least 50 volts/cm is applied. The capillary tube is charged with the analytical mixture. In a first separation stage, the target molecules are eluted, optionally while creeptors and the remaining components are eluted, optionally while plitting open. In a second stage, the elution conditions are changed, optionally in stages, so that the affinity of the target molecules for the receptor is aliminated and the target molecules are eluted and detected, optionally whilet splitting open. The process is useful for selective separation and/or determination of charged organic compounds, such as oligonucleotides, peptides or carbohydrates. It may be used, e.g. for isolation of specific proteins and DNA molecules, purification of antibiodies, analysis of antibense compounds or screening for anzyme inhibitors. The process achieves higher resolution and selectivity than inhibitors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prior art processes, especially in the case of complex biological analytical mixtures. It has high sensitivity, even with small amounts of samples. The derivatised polymers may be synthesised specifically using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Separation of electrically charged target molecules - by capillary affinity gel electrophoresis using polymer-gel to which receptors for
                                               Gaps
                                                                                                                                                                                                                                                                                                                         Oligonucleotide separated by capillary affinity gel electrophoresis.
                                                                                                                                                                                                                                                                                                                                                           Capillary afinity gel electrophoresis; separation; polymer-gel; polyacrylamide; ss.
                                               ö
                                               0; Indels
           Score 20; DB 1; Le
1.1%; Sco...
100.0%; Pred. No. ...
0; Mismatches
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                                                                                 1736 AAAAAAAAAAAAAAAA 1755
                                                                                                                     1 ААААААААААААААААА 20
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                                                                                                                                                                                                                ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96CH-00001320.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                target molecules are bound.
                                                                                                                                                                                                               AAT86606 standard; DNA; 20
                                                                                                                                                                                                                                                                                     (first entry)
                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muscate A, Paulus A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-041763/04.
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                              1 Similarity
20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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                                Local
                              Best Loca
Matches
                                                                                                                                                                          RESULT 125
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Gape

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1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels

Conservative

20;

Matches

Best Local Similarity

Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match

Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Mycobacterium vaccae protein; antigen; T cell activation; cytokine; dendritic cell maturation; infectious disease; immune disorder; cancer; respiratory system; mycobacterial infection; allergy; tuberculosis; leprosy; sarcoidosis; lung cancer asthma; skin disorder; psoriasis; dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma; squamous cell carcinoma; melanoma; PCR primer; ss.

Mycobacterial 16S rRNA specific oligo AD12.

(first entry)

25-OCT-1999

AAZ11326;

AAZ11326 standard; DNA; 20 BP

RESULT 127

AAZ1132(

89

Page

us10008789-3.rng

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2-Silyloxymethyl ribonucleosides and their phosphonate derivatives - have high purity, use in machine synthesis of ribonucleic acids, enable longer oligonucleotide chain construction, and larger amounts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Silyloxymethyl; phosphonate; silyloxymethyl halide; diagnosis; ss; cyanoethyl phosphoramidate coupling; isomerisation; steric hindrance.
                                                                                                                                                                                                                                                                                                                                                                                             Synthetic RNA sequence produced by the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 20; DB 1; Lengtn 22,
Pred. No. 1 68+02;
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v 100.0%; Pred. No. ...
o; Mismatches
   1736 AAAAAAAAAAAAAAAAA 1755
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                                                           20 AAAAAAAAAAAAAAAA 1
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                                                                                                                                                                                                              AAX27533 standard, RNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-EP005215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97CH-00001931
                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PITS/) PITSCH S.
(WEIS/) WEISS P.A.
(JENN/) JENNY L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-AUG-1998;
                                                                                                                                                                                                                                                                                                                                  27-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                         AAX27533;
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                                                                                                                                            RESULT 126
AAX27533/c
AX27533/c
AX27533/c
AX27533/c
AX27533/c
AX27533/c
AX27533/c
DY 27-MAY.
XX SHIPloi
XX SHIPLOI
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Watson J, Visser ES, Skinner MA, Prestidge RL;

(GENE-) GENESIS RES & DEV CORP LTD.

98US-00205426

04-DEC-1998;

97US-00997080. 98US-00095855.

3-DEC-1997;

23-DEC-1997 1-JUN-1998 .7-SEP-1998

98WO-NZ000189

23-DEC-1998;

01-JUL-1999

Mycobacterium vaccae.

Synthetic.

WO9932634-A2

Enhancing immune response to an antigen. Example 15; Page 177; 243pp; English.

WPI; 1999-430163/36.

Tan P,

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The invention relates to silyloxymethyl protected D- or L-ribonucleosides and their phosphonates (I), and silyloxymethyl halides (II). (I) are intermediates for synthesis of RNA-oligonucleotides with predetermined nucleotide sequence, particularly by machine synthesis. The groups of examothyl phosphoramidate coupling. Uses of the oligoribonucleotide products in diagnosis, therapy, and as research tools, are well known, and are not dealt with in detail. (II) is an intermediate for (I). The products in diagnosis, therapy, and as research tools, are well known, and are not dealt with in detail. (II) is an intermediate for (I). The silyloxymethyl halide reagent is easy to prepare, and yields are high. Introduction of the silyloxymethyl group into the ribonucleoside is simple and rapid, and the acetal bond formed does not migrate, almple and rapid, and the acetal bond formed does not migrate. The methylenedioxy group spacer between the silyl group and nucleoside ring results in lass steric hindrance than bulky direct silyloxy invages, enabling first, a range of choices for the silyl substituents, to provide, e.g., acid or base stability; and second, higher yields in coupling. Purer products are therefore obtained than in prior art, enabling larger quantities and longer chains of oligoribonucleotides to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 be synthesised successfully, and in shorter times
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M. vaccae proteins. The M. vaccae proteins may be employed to activate T cells and natural killer cells, to stimulate the production of cytokines, to enhance the expression of co-stimulatory molecules on dendritic cells and monocytes, and to enhance dendritic cell maturation and function. The proteins can be expressed by standard recombinant methodology. Pharmaceutical compositions comprising the proteins or nucleic acid sequences encoding the proteins can be used for the treatment, prevention, and detection of disorders including infectious diseases, immune disorders and cancer. In particular, the compounds and methods are used for treatment of diseases of the respiratory system, such as mycobacterial infections, asthma, allergies, tuberculosis, leprosy, sarcoidosis and lung cancers, and disorders of the skin such as alopecia areata, and skin cancers such as basal carcinoma, squamous cell carcinoma and melanoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention provides heat-killed Mycobacterium vaccae, or recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
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1736 AAAAAAAAAAAAAAAAA 1755

Conservative

Best Local Similarity

20;

Matches

20 AAAAAAAAAAAAAAAAAAA 1

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This invention describes a novel method for quantitatively analysing a biochemical compound (1) which comprises contacting (1) with double biochemical compound (1) which comprises contacting (1) with double translated by the surface of an electrode at their terminals in which electrochemically active threading intercalators are intercalated, in an aqueous medium under application of electric potential to the electrode in the presence of an oxidase which oxidizes the biochemical compound and becomes reduced, and detecting electric current flowing between the electrode and a second electrode in the aqueous medium. The method is useful for detection of biochemical compounds such as glucose, cholesterol, urea nitrogen, bilitubin, uric acid, haemoglobin and lactic acid in body fluids such as whole blood, plasma, serum, urine, and lymph cor diagnosis of various diseases. The method allows detection of biochemical compounds quickly and easily with a high sensitivity using a simple compound equal that a processor is simple apparatus. This sequence represents DNA fragment used as a target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quantitative analysis of a biochemical compound such as glucose, in body a body fluid such as blood, comprising detecting enhanced electron transfer between an oxidase and a DNA-immobilized electrode, useful for diagnosis of disease.
                                                                                                                                                                      Electrochemical detection; glucose; cholesterol; urea nitrogen;
bilirubin; uric acid; haemoglobin; lactic acid; body fluid; blood;
plasma; serum; urine; lymph diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02;
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                                                                                                                                     Electochemical detection method sample DNA target.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Electochemical detection method fixed probe DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Prec. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 8; 14pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              (FUJF ) FUJI PHOTO FILM CO LID
                     AAA40449 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA40448 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                     99JP-00001111.
99JP-00143599.
                                                                                                                                                                                                                                                                                                                                                                 07-JAN-2000; 2000EP-00100126.
                                                                                               13-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Takenaka S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-444372/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 simple apparatus
sample in the men
                                                                                                                                                                                                                                                                                                                                                                                                       06-JAN-1999;
24-MAY-1999;
                                                                                                                                                                                                                                                                                        EP1018646-A2
                                                                                                                                                                                                                                                                                                                             12-JUL-2000
                                                                                                                                                                                                                                                    Synthetic.
                                                           AAA40449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ogawa M,
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AAA40448/C
ID AAA404
XX
AC AAA404
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DT 13-NOV
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This invention describes a novel method for quantitatively analysing a biochemical compound (I) which comprises contacting (I) with double stranded DNA fixed to the surface of an electrode at their terminals in which electrochemically active threading intercalators are intercalated, in an aqueous medium under application of electric potential to the electrode in the presence of an oxidase which oxidizes the biochemical compound and becomes reduced, and detecting electric current flowing between the electrode and a second electrode in the aqueous medium. The method is useful for detection of biochemical compounds such as glucose, cholesterol, urea nitrogen, blitubin, uric acid, haemoglobin and lactic acid in body fluids such as whole blood, plasma, serum, urine, and lymph con diagnosis of various diseases. The method allows detection of biochemical compounds quickly and easily with a high sensitivity using a simple apparatus. This sequence represents DNA fragment used as fixed
                                                                                                                                                                                                                                                                                                                                                                                            Quantitative analysis of a biochemical compound such as glucose, in body a body fluid such as blood, comprising detecting enhanced electron transfer between an oxidase and a DNA-immobilized electrode, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Abietane derivative; labelling; diagnostic test; biotin substitute; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
              Electrochemical detection; glucose; cholesterol; urea nitrogen; bilirubin; uric acid; haemoglobin; lactic acid; body fluid; blood; plasma; serum; urine; lymph diagnosis; probe; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide #5 for conjugation to abietane derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 20; DB 1; Length 20;
; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probe DNA in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1736 AAAAAAAAAAAAAAAAAA 1755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 7; 14pp; English
                                                                                                                                                                                                                                                                                                                      Takagi M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 AAAAAAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                  (FUJF ) FUJI PHOTO FILM CO LTD.
                                                                                                                                                                                                                                99JP-00001111.
99JP-00143599.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ91117 standard; DNA; 20 BP
                                                                                                                                                                                            07-JAN-2000; 2000EP-00100126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20; Conservative
                                                                                                                                                                                                                                                                                                                      Ogawa M, Takenaka S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis of disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-444372/39.
                                                                                                                       EP1018646-A2.
                                                                                                                                                                                                                              06-JAN-1999;
24-MAY-1999;
                                                                                                                                                         12-JUL-2000.
                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ91117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ91117,
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Gaps

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04-FEB-2000

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11-FEB-2000; 2000WO-US003543
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                                                                                                                                                                                AAA50193 standard; DNA; 20
                                                                                                                                                                                                07-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                               Maier MA;
                                                                                                                                                                                                                                                                                       (ISIS-) ISIS PHARM INC
                            Charles MH, Piga N,
                                    WPI; 2000-239603/21
                                                                                                                                                                                                                                                                                                       WPI; 2000-558188/51.
                    (INMR ) BIO MERIEUX
                                                                                                                                                                                                                                                      WO200047593-A1
                                                                                                                                                                                                                                     modified_base
   31-JUL-1998;
                                                                                                                                                                                                                                                                                               Manoharan M,
            31-JUL-1998;
                                                                                                                                                                                                                                                                              12-FEB-1999;
                                                                                                                                                                                                                                                              17-AUG-2000
                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                        AAA50193;
                                                                                                                                    Query Match
                                                                                                                                                                        RESULT 131
                                                                                                                                            Matches
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The present sequence is that of a phosphodiester oligonucleotide containing 20 T nucleobases, 19 having a 2'-methoxyethoxy group on its 5' cribosyl sugar moiety. It is an example of an oligomeric compound produced according to the methods of the invention. The invention provides a compounds having phosphodiester internucleoside linkages in addition to phosphorothicate and/or phosphoramidate internucleoside linkages in circanucleoside linkages. The methods also include incorporation of boranophosphate internucleoside linkages. The methods untilse H-phosphonate intermediates that are coupled together forming contiguous regions of 1 or more H-phosphonate internucleoside linkages. Each contiguous region is subsequently oxidized to phosphotosphotosphoromidate or boranophosphate internucleoside linkages prior to further elongation. Mixed backbone oligomeric compounds are prepared in this manner by oxidizing adjacent regions with different reagents. Oligomeric compounds of the invention are prepared using novel oxidation steps that oxidize a region of 1 or more H-phosphonate internucleoside inhance or steps that oxidize a region of 1 or more H-phosphonate internucleoside inhance or steps that oxidize a region of 1 or more H-phosphonate internucleoside conjudence or steps that oxidize a region of 1 or more H-phosphonate internucleoside conjudence or steps in the order diagnostic tests on e.g. conjudence in the invention are prepared using novel oxidation or probes, linkers, gene fragments and for other diagnostic tests on e.g. contribled in the order or and service or articles of the order or are research reagents, and as
           Preparation of mixed backbone oligomeric compounds useful as e.g. primers for diagnostic tests, involves oxidation of H-phosphonate internucleoside linkages to phosphodiester internucleoside linkages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunostimulatory oligodeoxynucleotide; immunostimulatory ODN; immunostimulatory DNA-binding protein; nucleolin; hnRNP D; AUF1; hnRNP A; lugus La protein; functional modifier identification; agonist; antagonist; minic, inhibitor; drug screening; cellular target identification; oligonucleotide optimisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phosphorothioate poly I oligonucleotide, SEQ ID NO:17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
                                                                                                                                 Example 12; Page 34; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1736 AAAAAAAAAAAAAAAAA 1755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC87238 standard; DNA; 20 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
ses 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunotherapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiviral agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200067023-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC87238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC87238/
8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                         Saturated and unsaturated derivatives of abietic acid and their conjugated derivatives with natural and synthetic polymers, having use in diagnostics, chemical reactions and analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to novel saturated and unsaturated abjetane derivatives. The new compounds may be used directly or indirectly in the development of new disgnostic tests, to follow infections, especially viral infections, to follow and/or measure chemical products, especially potential pollutants. In diagnostic tests they may be used as markers, or to form a universal solid phase after immobilization on a solid support, to produce monochonal antibodies or polyclonal antibodies having diagnostic uses. The oligonucleotides AB21113.291117 represent examples of sequences that can be labeled with the new abjetane derivatives. The new derivatives may be used to substitute for biotin in diagnostic tests,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              but because they are not found naturally in humans the risk of potential interactions with biological molecules is eliminated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                   Veron L, Delair T, Mandrand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphodiester oligonucleotide; H-phosphonate chemistry; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "2'-methoxyethoxy modified thymidine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.1%; Score 20; DB 1; Length 20; 00.0%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match
Local Similarity 100.0%; Pred. NO. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2'-Methoxyethoxy-modified oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1736 AAAAAAAAAAAAAAAAA 1755
                                                                                                                                                                                   Battail PN,
                                                                                                                                                                                                                                                                                                                                                                                                   Example 5; Page 20; 39pp; French
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                         98FR-00010084.
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Gaps

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(CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.

(IOWA ) UNIV IOWA RES FOUND

99US-0131830P

29-APR-1999;

03-MAR-2000; 2000US-0186845P

Krieg AM;

Schetter C,

Noll BO,

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The invention relates to the use of an immunostimulatory single-stranded DNA-binding protein in screening assays to identify compounds which bind to tand thereby act as functional modifiers of immunostimulatory oligodeoxynucleotide (ODN) activity. Such modifiers of ODN activity consist of immunostimulatory DNA binding inhibitors, immunostimulatory DNA binding inhibitors, immunostimulatory DNA agoniets and antagoniets. Immunostimulatory DNA binding competitors, and to DNA minics, and immunostimulatory DNA binding competitors, and to methods to identify immunostimulatory DNA binding competitors, and to optimize an immunostimulatory DNA binding protein bound to an immunostimulatory DNA binding protein bound to an immunostimulatory DNA binding protein bound to an immunostimulatory DNA competitulatory DNA additionally be used to screen a panel of candidate target molecules to identify the cellular target molecules of the immunostimulatory DNA. The immunostimulatory DNA-binding proteins used in the methods of the invention are the RNA-binding proteins cused in the methods of the invention are the RNA-binding proteins mucleolin, hnRNP D, AUPI, hnRNP Al and lupus La protein. The screening methods are useful for identifying a compound that inhibits interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between immunostimulatory DNA and an immunostimulatory DNA-binding protein and for identifying agonists useful in immunotherapy. The complex is useful in screening for immunostimulatory DNA cellular target molecules. The candidate immunostimulatory ODN competitors allow the investigation of structure/activity relationships of immunostimulatory DNA-binding proteins and immunostimulatory ODNs. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        represents an oligonucleotide used in an exemplification of the invention
                                                              Immunostimulatory DNA binding proteins to identify immunostimulatory DNA functional modifiers, immunostimulatory DNA binding competitors and to optimize immunostimulatory oligodeoxynucleotides for stimulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunostimulatory oligodeoxynucleotide; immunostimulatory ODN;
immunostimulatory DNA-binding protein; nucleolin; hnRNP D; AUF1;
hnRNP A1; lupus La protein; functional modifier identification; agonist;
antagonist; mimic; inhibitor; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antagonist; mimic; inhibitor; drug screening;
cellular target identification; oligonucleotide optimisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.1%; Score 20; DB 1; Length 20;
100.0%; Pred. No. 1.6e+02;
rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Digoxigenin-labelled poly T oligonucleotide, SEQ ID NO:9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1736 AAAAAAAAAAAAAAAAA 1755
                                                                                                                                                               Example 1; Page 45; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 AAAAAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC87230 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-APR-2000; 2000WO-US011697.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-MAR-2000; 2000US-0186845P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20; Conservative
                     WPI; 2001-016002/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunotherapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200067023-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-NOV-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Gaps . 0

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The invention relates to the use of an immunostimulatory single-stranded DNA-binding protein in screening assays to identify compounds which bind to the ind thereby act as functional modifiers of immunostimulatory or clisqueoxynucleotide (ODN) activity. Such modifiers of ODN activity consist of immunostimulatory DNA binding inhibitors, immunostimulatory DNA binding inhibitors, immunostimulatory DNA agonists and antagonists. Immunostimulatory DNA agonists and antagonists. Immunostimulatory DNA binding competitors, and to optimize an immunostimulatory DNA binding competitors, and to optimize an immunostimulatory DNA binding protein bound to an immunostimulatory DNA binding protein bound to an immunostimulatory DNA binding protein bound to an immunostimulatory DNA binding protein a panel of candidate target molecules to identify the cellular target molecules of the immunostimulatory DNA binding proteins used in the methods of the invention are the RNA-binding proteins nucleolin, hurny D, AUFI, hurny A and lupus La protein. The screening methods are useful for identifying a compound that inhibite interaction control of the immunostimulatory DNA binding proteins are the control of the invention and that inhibite interaction control of the immunostimulatory DNA binding proteins are the control of the invention and that inhibite interaction control of the immunostimulatory DNA but and lupus La protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between immunostimulatory DNA and an immunostimulatory DNA-binding protein and for identifying agonists useful in immunotherapy. The complex is useful in screening for immunostimulatory DNA cellular target molecules. The candidate immunostimulatory ODN competitors allow the investigation of structure/activity relationships of immunostimulatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA-binding proteins and immunostimulatory ODNS. The present sequence represents an oligonucleotide used in an exemplification of the invention
                                                                                                                                      Immunostimulatory DNA binding proteins to identify immunostimulatory DNA functional modifiers, immunostimulatory DNA binding competitors and to optimize immunostimulatory oligodeoxynucleotides for stimulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunostimulatory oligodeoxynucleotide; immunostimulatory ODN; immunostimulatory DNA-binding protein; nucleolin; hnRNP D; AUFL; hnRNP AI, lugus La protein; functional modifier identification; agonist; antagonist; minic; inhibitor; drug screening; cellular target identification; oligonucleotide optimisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.1%; Scor.
100.0%; Pred. No. 1...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Poly T oligonucleotide, SEQ ID NO:20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1736 AAAAAAAAAAAAAAAAA 1755
                                                                                                                                                                                                                                     Example 1; Page 45; 95pp; English.
                                              Krieg AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 AAAAAAAAAAAAAAAAA 1
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(IOWA ) UNIV IOWA RES FOUND.
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                                              Schetter C,
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                                                                                            WPI; 2001-016002/02
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                                              Noll BO,
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99US-0131830P.

29-APR-1999;

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98US-00173936
                                                                                                                                               AAS10402 standard; DNA; 20
                                                                                                                                                          24-OCT-2001 (first entry)
             Noll BO, Schetter C,
                   WPI; 2001-016002/02
                                                                                                                                                                                           16-OCT-1998;
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                                                                                                                                                                                      29-MAY-2001
                                                                                                                                                                           Synthetic.
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                                                                                                                                          RESULT 135
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(HUAN/) HUANG Z. (SZOS/) SZOSTAK J W. RESULT 136 AAD16997, ò 셤 The invention relates to the use of an immunostimulatory single-stranded DNA-binding protein in screening assays to identify compounds which bind to to it and thereby act as functional modifiers of immunostimulatory coligodeoxynucleotide (DDN activity. Such modifiers of ODN activity consist of immunostimulatory DNA binding inhibitors, immunostimulatory DNA agonists and antagonists.

CC DNA minds, and immunostimulatory DNA binding competitors, and to methods to identify immunostimulatory DNA binding competitors, and to optimize an immunostimulatory DNA-binding protein bound to an complexes of an immunostimulatory DNA-binding protein bound to an immunostimulatory DNA-binding protein bound to an immunostimulatory DNA-binding protein bound to an immunostimulatory DNA-binding proteins of the immunostimulatory DNA-binding proteins to identify the cellular target molecules of the immunostimulatory DNA-binding proteins used in the methods of the invention are the RNA-binding proteins to use the methods of the invention are the RNA-binding proteins of the invention are the RNA-binding proteins to between immunostimulatory DNA and an immunostimulatory DNA-binding protein concein and for identifying agonists useful in immunostimulatory DNA-binding for immunostimulatory DNA-binding in useful in screening in useful in screening the screening and some protein and for identifying agonists useful in immunotherapy. The complex is useful in screening the screening t ö molecules. The candidate immunostimulatory ODN competitors allow the investigation of structure/activity relationships of immunostimulatory DNA-binding proteins and immunostimulatory DNNs. The present sequence represents an oligonucleotide used in an exemplification of the invention DNA Immunostimulatory DNA binding proteins to identify immunostimulatory DN functional modifiers, immunostimulatory DNA binding competitors and to optimize immunostimulatory oligodeoxynucleotides for stimulation. Gaps ; 0 1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other; (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH. (IOWA ) UNIV IOWA RES FOUND. Example 1; Page 45; 95pp; English. Krieg AM; 03-MAR-2000; 2000US-0186845P

Ouery Match Best Local Similarity 100.0 Matches 20, Conservative

DNA template for 3' end labeling of an RNA molecule, #14.

BP

3' RNA end labeling; DNA template; Okazaki fragment; 5' overhang; ss

97US-0063757P

Fibronectin scaffold protein array for obtaining a protein/compound which binds to a compound/protein, comprises a fibronectin type III domain having a randomized loop, a randomized beta-sheet or their combination.

WPI; 2001-557782/62.

Disclosure; Page 41; 67pp; English

(CHEN/) CHEN G

ö The sequence represents a synthetic DNA template molecule used to demonstrate the method of the invention. The invention relates to a method of modifying (e.g. 3' end labelling with 32P dATP) the 3' terminus of an RNA molecule by providing a DNA oligonucleotide, complimentary to the 3' end of the RNA molecule, with an overhang at the 5' end which allows incorporation of the labeling nucleotide into the RNA molecule. The method, based on the synthesis of Okazaki fragments, is useful for labeling and modifying the 3'-termini of other nucleic acids such as DNA fragments. The method is a simple and efficient way of labeling or modifying RNA 3'-termini using DNA polymerase and a synthetic template Modifying a 3' terminus of a pre-selected DNA sequence, useful for labeling and modifying 3'-termini of other nucleic acids, comprises using a synthetic nucleotide template with a defined overhang nucleotide. Gaps ö Scaffold protein; antibody mimic; fibronectin type III domain; randomised loop; randomised beta-sheet; diagnostic purpose; protein designing; probe; tenth module of human Fn3; 10Fn3; fibronectin module of type III; Fn3; ss. 1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.66+02; tive 0; Mismatches 0; Indels Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other; Kuimelis RG; 1736 AAAAAAAAAAAAAAAAAA 1755 with defined overhang nucleotides Example 5; Col 13; 22pp; English 20 AAAAAAAAAAAAAAAAAAA 1 BP. 28-FEB-2001; 2001WO-US006414. 29-FEB-2000; 2000US-00515260. AAD16997 standard; DNA; 20 29-NOV-2001 (first entry) Query Match
Best Local Similarity 100.
Matches 20, Conservative Lipovsek D, Wagner RW, Szostak JW; WPI; 2001-366470/38. (PHYL-) PHYLOS INC. Capture probe CP5' WO200164942-A1 Unidentified 07-SEP-2001. AAD16997; Huang Z, 

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The present invention relates to an array of proteins (antibody mimics) comprising a fibronectin type III domain having a randomised loop, a randomised beta-abeet, or their combination, and has the capacity to bind to a compound that is not bound by a corresponding naturally-occurring fibronectin, immobilised onto a solid support. The antibody mimics is sample. It is also useful to detecting a compound preferably a protein, in a biological sample. It is also useful to detect one or more different analytes simultaneously in a sample. Hence is useful for diagnostic purposes. It is also useful for the purpose of designing proteins capable of binding to virtually any compound of interest. The present sequence is a capture probe used to self-assemble and anchor the tenth module of human fibronectin module of type III (Fn3) (10Fn3) which is used in an exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
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1.1%; Score 20; DB 1; Length 20;
100.0%; Pred. No. 1.6e+02;
ative 0; Mismatches 0; Indels
                                                                     1736 AAAAAAAAAAAAAAA 1755
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                   Best Local Similarity 100.
Matches 20; Conservative
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Query Match

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Conjugate forming oligonucleotide ON5 SEQ ID 5. AAF60896 standard; DNA; 20 BP 15-MAY-2001 (first entry) AAF60896; AAF60896 

Transport, membrane, cytostatic; virucide, vasotropic; dermatological; antipsoriatic; antiasthmatic; gene therapy; tumor cell; antisense; tumor therapy; drug; phosphodiester linkage; ss.

Unidentified

DE19935302-A1

08-FEB-2001.

99DE-01035302 28-JUL-1999; 99DE-01035302 28-JUL-1999; (AVET ) AVENTIS PHARMA DEUT GMBH.

Schwerdel Gothe G, Unger E, Greiner B, Uhlmann E,

WPI; 2001-203679/21.

New substituted aryl conjugates of parent molecules, especially oligonuclectides, having improved transmembrane and intracellular transport properties, useful as medicaments or diagnostic agents.

Disclosure; Page 9; 28pp; German.

This invention describes a novel conjugate (I) which consists of (A) a molecule to be transported and (B) at least one aryl residue of formula Ar-(X-C(Y)-R_1) in (II). Ar = group containing at least one aromatic ring; X = 0 or N (Bic); Y = 0, S or NH-R 2 (Bic); R 1 = optionally substituted 1-23C alkyl (optionally containing double and/or triple bonds); R 2 = optionally substituted 1-18C alkyl (optionally containing double and/or triple bonds); n = integer of 1 or more. (A) is bonded to (B) directly or via a chemical group, provided that the chemical group is other than CH2 sif the bond is via a phosphodiester linkage of (A). The invention also describes (i) the preparation of a conjugate (I') of (A') a molecule to be transported and (B') at least one aryl residue (not restricted to (II)), by preparing (A') containing a reactive function at the position

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at which (B') is to be bonded, preparing (B') and reacting (A') and (B');

and (ii) the use of aryl groups (II) (optionally bonded via a chemical

group) for transporting (A) across biological membranes. The products of

the invention have cytostatic, virucide, vasotropic, dermatological,

antipsoriatic and antiasthmatic activity and can be used for gene

cherapy. Conjugation of (A) with (B) is useful for transporting (A)

across biological membranes or into eukaryotic or prokaryotic cells

corporationally bacterial, yeast or mammalian cells, including human cells,

containing (I) are also claimed. Typically (I) are antisense

containing (I) are also claimed. Typically (I) are antisense

containing (I) are also claimed. Typically (I) are antisense

containing (I) are succeeded for tumor therapy; oligonucleotide drugs for

treating viral infections or diseases associated with integrins or cell-

cell interactions (c.g. restenosis, vitiligo, psoriasis or asthma); or

cell interactions (Conjugation with (B) markedly improves the cellular uptake

of (A), e.g. in tumor cells. (B) include fluorescein derivative residues,

cn which case the conjugates (I) are fluorescently labeled, allowing

microscopic monitoring of cellular uptake etc. The cellular uptake of

is superior to that obbtained using other conjugated groups related to

confirm of that obtained using other conjugated groups related to

confirm of the cope of (B)) have superior uptake to corresponding fluorescein
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Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Gaps ö Score 20; DB 1; Length 20; Pred. No. 1.6e+02; 0; Indels 1.1%; Scor. 100.0%; Pred. No. 1... 0; Mismatches Local Similarity 100. nes 20; Conservative Query Match Matches

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AAS63428 standard; DNA; 20 AAS63428; RESULT 138 AAS63428

BP

(first entry) 29-JAN-2002

Oligonucleotide-nanoparticle probe; diagnostic; forensic analysis; nucleic acid detection; nanostructure; biochip; biofilter; drug delivery; Oligonucleotide-nanoparticle probe #52.

Synthetic.

WO200173123-A2.

04-OCT-2001.

26-APR-2000; 2000US-0200161P. 26-UN-2000; 2000US-0213906P. 08-DEC-2000; 2000US-0213906P. 11-DEC-2000; 2000US-0254392P. 12-JAN-2001; 2001US-00760500. 28-MAR-2001; 2001WO-US010071. 28-MAR-2000; 2000US-0192699P. 

(NANO-) NANOSPHERE INC.

28-MAR-2001; 2001US-00820279

Elghanian R; Storhoff JJ, Mucic RC, Letsinger RL, Park S, Li Z; Park S, Mirkin CA, raton TA,

WPI; 2001-656926/75

Detecting and separating nucleic acid, useful e.g. for diagnosis,

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having at least 2 portions, comprising treatment with nanoparticles that carry oligonucleotides complementary to at least 2 parts of [1], where detectable change caused by hybridisation of the oligonucleotide to [1], e.g. for diagnosing a wide variety of diseases, sequencing, in forensic analysis etc., and generally to detect analytes other than (1). The cliponucleotide-derivatised nanoparticles are also useful for preparing nanostructures useful, for example, as blochips, biofilters, mechanical devices, separation membranes, chemical sensors, in computers, and for drug delivery. Very stable nanoparticle-oligonucleotide conjugates can be produced, allowing their direct use (as probes) in polymerase chain reaction, i.e. they survive multiple heating/cooling cycles so do not change, without the need for special equipment, making possible rapid field testing for e.g. pathogens. AAS633448 represent
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comprises reaction with nanoparticles that carry oligonucleotides complementary to parts of the target.
                                                                            The invention relates to a method for detection of nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.1%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 20; Conservative 0; Mismatches 0; Indels
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                                               Example 18; Page 158; 404pp; English
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                                                                                                                                                                                                                                                                                                                                              method of the invention
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STORHOFF J J.
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Detecting nucleic acid, useful for e.g. diagnosis of diseases, forensics

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                                                                                                                     for detecting
                                                                                                               The present sequence is an oligonucleotide used in a method for detecting a nucleic acid having at least 2 portions. The method comprises hybridising the nucleic acid with oligonucleotides, such as the present sequence, attached to a substrate and/or particle and detecting a change in colour, conductivity or optical density. The method is useful for the diagnosis and/or monitoring of diseases, in forensics, in DNA sequencing, for paternity testing, for cell line authentication and for monitoring gene therapy. Detecting nucleic acids based upon observing a colour change is cheap, fast, simple, and does not require specialised or expensive equipment. The nanoparticle oligonucleotide conjugates remain stable for at least 6 months. A single base mismatch and as little as 2 of femtomoles (fM) of target can be detected using the conjugates
and DNA sequencing, comprises observing detectable change brought about by hybridization of nucleic acid with substrate or particle bound oligonuclectides.
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100.0%; Pred. No. 1.6e+02;
iive 0; Mismatches 0; Indels
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                                                                                  Disclosure; Page 199; 205pp; English
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26-APR-2000; 2000US-02001G.IP.
26-UJN-2000; 2000US-00603830.
12-JAN-2001; 2001US-00760500.
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Matches 20; Conserv
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                                                                                                     The sequence represents a cyclic disulphide linked oligonucleotide which may be coupled with colloidal gold particles (nanoparticles) and used to demonstrate the method of the invention. The invention relates to isolating or detecting a nucleic acid of interest, in a mixture of have a nanoparticle standard to their 5' ends. The nanoparticles (e.g. colloidal gold) artached to their 5' ends. The nanoparticles (e.g. colloidal gold) are used to both isolate and detect (e.g. by linking the particle to a fluorescent probe) the resultant complex. The methods are useful for detecting nucleic acids, natural or synthetic, and modified or unmodified. The methods may also be applied in the diagnosis of genetic, bacterial and viral diseases, in forensics, in DNA sequencing, for cell line authentication, and for monitoring gene therapy. The methods are further useful in research and analytical laboratories in DNA sequencing, in the field to detect the presence of specific pathogens, for quick identification of an infection to assist in cry preserviption, and in homes and health centres for inexpensive first-line screening. The methods, which are hased on observing colour change with the naked eye, are cheap, fast, simple, robust (reagents are stable).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.
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100.0%; Pred. No. 1.6e+02;
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                                                       Example 24; Fig 44; 323pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     no instrumentation is required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF99427 standard; DNA; 20 BP
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27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-273485/28
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                                       The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Thi immune response and to activate immune cells. Note: the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccine, cytostatic, virucidal, bactericidal, fungicidal, anti-parasitic, immunostimulatory, tumour, viral infection, bacterial infection; fungal infection, parasitic infection, cancer, asthma, infections disease; allergy, immune deficiency; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                              present sequence may have a phosphorothioate backbone
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunostimulatory nucleic acid #215.
Claim 101; Page 49; 338pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 101; Page 42; 338pp; English.
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27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
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(COLE-) COLEY PHARM GMBH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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Best Local &
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Gaps

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Phosphorothioate; anti-viral therapy; stereochemical pathway; ss.
                                                            Score 20; DB 1; Length 20;
Pred. No. 1.6e+02;
                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note = "All bases are phosphorothioate"
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/mod_base= OTHER
/note= "Modified with 2'-0-methyl"
                     Seguence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
                                                 1.1%; Sco...
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                               1736 AAAAAAAAAAAAAAAAA 1755
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                                                                                                                                                                                      1 AAAAAAAAAAAAAAA 20
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                                                                                                                                                                                                                                                                                           AAH46465 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JAN-2000; 2000US-00481486.
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                                                              Query Match
Best Local Similarity 100.
Matches 20; Conservative
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*tag=
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Best Local Similarity
Matches 20; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide #13.
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modified_base
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                                                                                                                                                                                                                                                                                                                                                                             14-SEP-2001
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                                                                                                                                                                                                                                                                                                                                    AAH46465;
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against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxophasma, haemophilus, campylobacter, clostridium, Bscherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence an also be used to redirect a Th2 to a Th1 immune response and to activate immune cells. Note: the present sequence may have a phosphorothioate backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vaccine, cytostatic, virucidal, bactericidal, fungicidal, anti-parasitic, immunostimulatory, tumour; viral infection, bacterial infection; fungal infection; parasitic infection, cancer, asthma, infections disease, allergy, immune deficiency; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.
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                                                                                                                                                                                                                           Query Match 1.1%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                        Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunostimulatory nucleic acid #547.
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27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
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AAF99431
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Preparing sulfurized 2' substituted phosphorothioate oligonucleotides useful in biological research, comprises phosphitylating the 5'-hydroxyl of a nucleic acid having a nucleoside with a 2' modification.
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The present sequence was used to demonstrate the ability of deoxynuclaic S-Methythiourea (DNRT) compounds to form triplexes with DNA oligomers. An increase in the C content of the oligos resulted in a large decrease in binding. This experiment was performed as an example of a method for preparing oligonucleotides comprising a backbone of alkyl or alkoxy thiourea linkages. The method is useful for preparing oligonucleotides comprising a backbone of alkyl or alkoxy thiourea linkages. The method is useful for preparing oligonucleotides for use in antisense or antigene herapy, to inhibit production of proteins associated with genetic diseases, cardiovacular, inflammatory and neurocellular diseases, and for antiviral therapy, e.g. to treat human immunodeficiency virus, human-cytomegalovirus, influenza and herpes infections. The compounds are also useful as diagnostic reagents to detect the presence or absence of the target DNA or RNA sequences to which they specifically bind and by antagonising the normal biological activity of a target protein, they can be used in the manipulation of tissue e.g. tissue differentiation, both in vivo and in ex vivo tissue cultures. The method provides an efficient and rapid solid-phase method contents and S-methylthiourea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Preparing novel deoxymucleic alkyl thiourea oligonucleotide for use in antisense therapy, by synthesizing oligonucleotides comprising backbone of alkyl or alkoxy thiourea linkages in solution or on solid phase.
                                        Deoxynucleic S-Methythiourea; DNmt; antisense therapy; cardiovascular disease; inflammatory disease; neurocellular disease; antiviral therapy; human immunodeficiency virus; human-cytomegalovirus; influenza; herpes; infection; ss.
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    DNA oligomer #1.
                                                                                                                                                                                 US6169176-B1
                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                               28-SEP-1999;
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                                                                                                                                                                                                                                                                                                       02-JUL-1998;
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  The specification describes a method for identifying a nucleic acid in a pool of interest. The method comprises pooling individually identifiable nucleic acids into at least two pools of one nucleic acid each; expressing nucleic acid pools to obtain protein expression product pools; assaying protein expression product pools for products having interaction with target molecule; selecting nucleic acid pools corresponding to identified protein expression product pools; and identifying individual nucleic acid (e.g. cDNA) in a pool of interest and for identifying a nucleic acid (e.g. cDNA) in a pool of interest and for identifying a nucleic acid (e.g. cDNA) in a pool of interest and for identifying several nucleic acids of interest and for for screening genomic DNA libraries or other source of individual cDNAs, mRNAs, synthetic libraries of nucleic acids e.g. combinatorial libraries. The present sequence was used in the course of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Screening nucleic acids (NA) in pool of interest comprises pooling, expressing NA to form expression product pool and identifying NA in NA pool corresponding to expression product pool having interaction with
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                                                                                                                                                                                                                                                                                                   Nucleic acid identification; DNA library screening; ss.
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                                                                                                                                                                                                                                                               Nucleotide sequence of a cDNA sequence.
1736 AAAAAAAAAAAAAAAAA 1755
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                                        20 AAAAAAAAAAAAAAAAAA 1
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                                                                                                                                      AAH78547 standard; cDNA; 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    target moiety.
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                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                            AAH78547;
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                                                                                                 RESULT 145
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98US-0111800P. 99US-00347443.

Bruice TC;

99US-00407675. 98US-0091481P.

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tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
diabetic retinopathy; retinopathy of prematurity; macular degeneration;
                                                                  Gaps
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                              1.1%; Score 20; DB 1; Length 20; 00.0%; Pred. No. 1.6e+02;
                                                                  0; Indels
Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                 Angiogenesis inhibitory oligonucleotide #226.
                         Query Match
Best Local Similarity 100.0%; Pred. No. 1.6
                                                                                                     1736 AAAAAAAAAAAAAAAAA 1755
                                                                                                                         1 AAAAAAAAAAAAAAAA 20
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ABS77742 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                 13-DEC-2002
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                                                                                                                                                                                             RESULT 147
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ID ABS7
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1736 AAAAAAAAAAAAAAAA 1755

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Conservative

Best Local Similarity Matches 20; Conserv

AAF28351 standard; DNA; 20

AAF28351;

AAF28351 ID AAF; XX AC AAF; XX DT 02-4

02-APR-2001 (first entry)

us10008789-3.rng

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The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antiangiogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metaetasis, precancerous lession, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, obler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and hyperirophic scars. The present sequence is an antiangiogenic nucleic
                                                                                                                                                                                                                                                                                                                                                          Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
             rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
plaque neovascularisation; telangiectasia; haemophiliac joint;
angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
scleroderma; hypertrophic scar.
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100.0%; Pred. No. ...
... 0; Mismatches
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                                                                                                                                                                                                                                                                                             Bratzler RL;
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         Score 20; DB 1; Length 20, Pred. No. 1.66+02; Indels
Seguence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
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ABS78076 standard; DNA; 20 BP

ABS7807

(first entry)

13-DEC-2002

ABS78076;

Anglogenesis inhibitor; ss; anglogenesis; solid tumour growth; tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial anglogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; anglofibroma; wound granulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.

Synthetic

14-DEC-2001; 2001WO-US048458.

WO200253141-A2

11-JUL-2002

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                                                                                                                                                                                                                                                                                   Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
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100.0%; Pred. No. 1.6e+02;
trive 0; Mismatches 0;
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                 WO200253141-A2
                                                                                                                                                                                                           Bratzler RL;
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Matches
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Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth; tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection, neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis; Angiogenesis inhibitory oligonucleotide #560. scleroderma; hypertrophic scar. Synthetic 

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                                                                                                                                                                                                     The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antiangiogenic nucleic acid molecule. Also finculed is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lession, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosts, obler Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and hypericophic scars. The present sequence is an antiangiogenic nucleic
                                                                                                                           Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
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100.0%; Pred. No. 1.6e+02;
ative 0; Mismatches 0; Indels
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                              (COLE-) COLEY PHARM GROUP INC
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14-DEC-2000; 2000US-025534P.
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1es 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                          acid of the invention
                                                                                              WPI; 2002-566690/60.
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modified_base
                                                                Bratzler RL;
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                                                                                                                                       The present invention relates to methods for treating or preventing cancer, involving administering to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies. The methods are useful for treating or preventing cancer such as basal cell carcinoma, bladder cancer, brain and central nervous system (CNS) cancer, breast cancer, cervical cancer, colon and rectum cancer, connective tissue cancer, cervical cancer, elon and rectum cancer, connective tissue cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian cancer, pancreatic cancer, testicular cancer, rhabdowyosarcoma, skin cancer, stomach cancer, testicular cancer, and uterine cancer. The present sequence is an immunostimulatory oligonucleotide described in the
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               Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies to a subject having or at risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies to a subject having or at risk of
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Pred. No. 1.6e+02;
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100.0%; Pred. No. 1...
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                                                                                                         Disclosure; Page 309; 312pp; English
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20; Conservative
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                                                                        developing cancer.
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The present invention relates to methods for treating or preventing cancer, involving administering to a subject having or at risk of developing cancer immunostianulatory nucleic acids that induce expression of cell surface antigens and antibodies. The methods are useful for treating or preventing cancer such as basal cell carcinoma, bladder cancer, brain and central nervous system (CNS) cancer, brain and central nervous system (CNS) cancer, brain and central nervous system (CNS) cancer, connective tissue cancer, cervical cancer, clon and rectum cancer, connective tissue cancer, levasemia, liver cancer, lung cancer, Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian cancer, spancreatic cancer, prostate cancer, rhabdomyosarcoma, skin cancer, spancreatic cancer, prostate cancer, rhabdomyosarcoma, skin cancer, stomach cancer, resticular cancer, and uterine cancer. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of the invention
of cell surface antigens and antibodies. The methods are useful for treating or preventing cancer such as basal cell carcinoma, bladder cancer, bone cancer, brain and central nervous system (CNS) cancer, breast cancer, cervical cancer, colon and rectum cancer, connective tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin cancer, stomach cancer, testicular cancer, rhabdomyosarcoma, skin present sequence is an immunostimulatory oligonucleotide described in the
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Best Local Similarity 100.0
Matches 20, Conservative
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                                                                                                                                                                                                                                                                                                            CD14; receptor; SNP;
                                    1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; tive 0; Mismatches 0; Indels
           Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                      single-nucleotide polymorphism; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                           enzyme; ACE;
                                                                                                                                                                                                                                                                               CD14 receptor PCR primer SEQ ID NO 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 10; 10pp; Japanese
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                                                                                                                                                                                               ABL54775 standard; DNA; 20
                                                                                                                                                                                                                                                     (first entry)
                                                    Local Similarity 100.
hes 20; Conservative
                                                                                                                                                                                                                                                                                                            converting
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                                                                                                                                                                                                                                                                                                            Angiotensin-I
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                                       Query Match
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Matches
                                                                    Matches
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Mon Aug 16 16:46:36 2004

(first entry)

02-JUL-2002

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The invention relates to a method of detecting a nucleic acid (NA) having
                                      Nanoparticle-oligonucleotide; nanofabrication; nucleic acid detection;
                                                                                                                                                                                                                                                                     Detecting nucleic acid, useful for diagnosis of genetic, viral or bacterial disease, comprises hybridizing nanoparticles with attached oligonucleotides to nucleic acid and detecting change brought about h
                                                                                                                                                                                                                       Mirkin CA, Letsinger RL, Mucic RC, St
Taton TA, Garimella V, Li Z, Park S;
                                                                                                                                                                                                                                                                                                                      Example 18; Page 410; 412pp; English.
                   Nanoparticle-oligonucleotide #55.
                                                                                                                                                    08-DEC-2000; 2000US-0254392P.
11-DEC-2000; 2000US-025535P.
12-JAN-2001; 2001US-00760500.
28-MAR-2001; 2001US-00820279.
                                                                                                                         10-AUG-2001; 2001WO-US025237.
                                                                                                                                            2000US-0224631P.
(first entry)
                                                                                                                                                                                                     (NANO-) NANOSPHERE INC
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                                                                                    WO200218643-A2
                                                                                                                                                                                                                                                                                                   hybridization.
                                                                                                                                           11-AUG-2000;
02-JUL-2002
                                                                                                     07-MAR-2002
                                                                 Synthetic.
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Storhoff JJ, Elghanian R;

at least 2 portions comprising; (a) producing annoparticles (NP) with attached oligonucleotides (GGN), where OGN has a sequence complementary to the sequence of NA; (b) contacting NA and NP under conditions effective to allow hybridisation of GGN with NA, and (c) observing a detectable change brought about by hybridisation of GGN with NA. The method is useful for detecting a nucleic acid, separating a selected nucleic acid from others and methods of nanofabrication. Detecting analytes such as nucleic acids and proteins are useful for the diagnosis of genetic, bacterial and viral diseases. The CGN-NP conjugates that use cyclic disulphide linkers improve the sensitivity of diagnostic assays. In particular assays using CGN-NP conjugates prepared using linkers comprising a steroid residue attached to a cyclic disulphide have been found to be approximately 10 times more sensitive than assays employing conjugates prepared using alkanethiols or acyclic disulphides as the linker. The CGN-NP conjugates are stable allowing them to be used directly in PCR solutions. Therefore conjugates added as probes to a DNA target to be PCR amplified can be carried through the 30 or 40 heating conling cycles of the PCR and are still able to detect the amplicons without opening the tubes and causing contamination. ABK64981-ABK65055 ö Gaps ö y Match 1.1%; Score 20; DB 1; Length 20; Local Similarity 100.0%; Pred. No. 1.6e+02; nes 20; Conservative 0; Mismatches 0; Indels represent nanoparticle-oligonucleotides of the invention Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other; Query Match Matches

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1736 AAAAAAAAAAAAAAAAAA 1755
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ABK65050 standard; DNA; 20 BP RESULT 155
ABK65050
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AC ABK650

ABK65050;

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The invention relates to a method of detecting a nucleic acid (NA) having at least 2 portions comprising: (a) providing nanoparticles (NP) with tracked oligonucleotides (GOM), where GOM has a sequence complementary to the sequence of NA; (b) contacting NA and NP under conditions detectable change brought about by hybridisation of OGN with NA. The method is useful for detecting a nucleic acid from others and methods of nanofabrication. Detecting nucleic acid from others and methods of nanofabrication. Detecting analytes such as nucleic acids and proteins are useful for the diagnosis of genetic, bacterial and viral diseases. The OGN-WP conjugates that use cyclic disulphide linkers improve the sensitivity of diagnostic assays. In particular assays using OGN-NP conjugates prepared using linkers comprising a steroid residue attached to a cyclic disulphides have been found to be approximately 10 times more sensitive than assays employing conjugates prepared using alkanethiols or acyclic disulphides as the linker. The OGN-NP conjugates are stable allowing them to be used directly in PCR solutions. Therefore conjugates added as probes to a DNA target to be PCR amplified can be carried through the 30 or 40 heating coling cycles of the pCR and are still able to detect the amplicant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting nucleic acid, useful for diagnosis of genetic, viral or
bacterial disease, comprises hybridizing nanoparticles with attached
oligonucleotides to nucleic acid and detecting change brought about by
                                                                                              Nanoparticle-oligonucleotide; nanofabrication; nucleic acid detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contamination. ABK64981-ABK65055
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Li Z, Park S;
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Best Local Similarity 100.0%; Pred. No. 1.v
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                                                       Nanoparticle-oligonucleotide #70.
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08-DEC-2000; 2000US-0254392P.

11-C2001; 2000US-025359.

11-JAN-2001; 2001US-00760500.

28-MAR-2001; 2001US-00820279.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hybridization.
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                                                                                                                                                       Synthetic.
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AAL45122/c
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(NANO-) NANOSPHERE INC
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11-DEC-2000;
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                                                                                                                                      23-DEC-1997;
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                       11-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                              Oligonucleotide synthesis; polynucleotide array; protecting group; oxidation; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
                                                                                                           Oligonucleotide synthesis method related DNA #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JUL-2000; 2000US-00627249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dellinger DJ, Perbost MGM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis
                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-APR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL36232 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-156732/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the invention
                                                                                                                                                                                                                                                                                                          EP1176151-A1
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                                                  24-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           composition.
                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2002.
                                                                                                                                                                                                                                                    Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid detection method, nanoparticle-oligonucleotide conjugate, nanoparticle, viral RNA detection, bacterial DNA detection, fungal DNA detection; nanoprobe conjugate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                         Inhibiting skin inflammation associated with skin disorder e.g. psoriasis, by administering composition comprising delipidated and deglycolipidated Mycobacterium vaccae cells or Mycobacterium vaccae culture filtrate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 5; Col 99-100; 116pp; English
                                                                                                                                               (GENE-) GENESIS RES & DEV CORP LTD
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                                                                                                                                                                                                                     Prestidge R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AAAAAAAAAAAAAAAAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABS64673 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 JAN-2001; 2001US-00760500.
28 WAR-2001; 2001US-00820279.
09-APR-2001; 2001US-0282640P.
10-AUG-2001; 2001US-00927777.
99US-00324542
                                                                     97US-00997080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0254418P,
2000US-0255235P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0255236P
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                                                                                                                                                                                                                         Watson JD, Tan PLJ,
                                                                                                                                                                                                                                                                                           WPI; 2002-138361/18
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83

Storhoff JJ, Elghanian R;

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The invention describes a method of detecting (M1) a nucleic acid having
                                                         Detecting nucleic acid having two portions, by providing nanoparticles having oligonucleotides attached to it, contacting nucleic acid and nanoparticles to allow hybridization, and observing detectable change.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid detection method; nanoparticle-oligonuclectide conjugate; nanoparticle; viral RNA detection; bacterial DNA detection; fungal DNA detection; nanoprobe conjugate; 88.
                                                                                                                                                                                                                                                                                                 polyvalent analyte) in a sample. This sequence represents a polynucleotide used to demonstrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid detection method associated polynucleotide #70.
                                                                                                                                                                                                                                                                                                                                                  1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. No.
         , Mucic RC, SI
Li Z, Park S;
                                                                                                    Example 18; Page 437; 442pp; English.
                                                                                                                                                                                                                                                                                                                                                                                          1736 AAAAAAAAAAAAAAAAAA 1755
                                                                                                                                                                                                                                                                                                                                                                                                      1 AAAAAAAAAAAAAAAAA 20
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2000US-025535P
2001US-0076030P
2001US-00820279
2001US-00820279
2001US-0082640P
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABS64688 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-DEC-2001; 2001WO-US046418.
         Letsinger RL,
Garimella V, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-NOV-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
nes 20; Conservative
                                       WPI; 2002-608256/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200246472-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-MAR-2001; 2
09-APR-2001; 2
10-AUG-2001; 2
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         Mirkin CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                    Taton TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABS64688;
                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                     Matches
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Gaps

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The invention describes a method of detecting (M1) a nucleic acid having two portions, involving providing nanoparticles having oligonucleotides attached to it, which has a sequence complementary to sequence of two portions of nucleic acid, contacting nucleic acid and nanoparticles, to allow hybridisation of oligonucleotides with two or more portions of nucleic acid, and observing a detectable change brought about by hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide conjugates (II) and the aggregate probe are useful for detecting two or more nucleic acids (from a biological source) having at least two portions, such as viral RNA, bacterial or fungal DNA, a gene associated with a disease, synthetic, or structurally-modified natural or synthetic RNA or a product of a polymerase chain reaction amplification.

(II) is useful for preparing a nanoprobe conjugate for detecting an analyte, and for detecting a nanoprobe conjugate for detecting a selected curled acid having two portions from other nucleic acids. (I), (II) and the aggregate probe are useful for detecting an analyte (sepecially conjugate) in a sample. This sequence represents a sequence represents a part of the aggregate probe are useful for the sequence represents and problems.
                                                                                                                                           Detecting nucleic acid having two portions, by providing nanoparticles having oligonucleotides attached to it, contacting nucleic acid and nanoparticles to allow hybridization, and observing detectable change.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein scaffold; antibody; binding protein; immunoglobulin;
tumour necrosis factor alpha; TNF-alpha; protein framework; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polyvalent analyte) in a sample. This sequence represents a polynucleotide used to demonstrate the method of the invention
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                                                 Storhoff JJ, Elghanian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 20; DB 1; Length 20; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.1%; Scor.
100.0%; Pred. No. 1...
0; Mismatches
                                                   Letsinger RL, Mucic RC, Si
Garimella V, Li Z, Park S;
                                                                                                                                                                                                                   Example 24; Fig 44; 442pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Capture probe CP5' SEQ ID NO:23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABN87103 standard; DNA; 20 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20; Conservative
             (NANO-) NANOSPHERE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                        WPI; 2002-608256/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUL-2002
                                                 Mirkin CA,
                                                                      raton TA,
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Lipovsek D, Wagner RW, Kuimelis RG;

(PHYL-) PHYLOS INC

WPI; 2002-444238/47

16-OCT-2001; 2001WO-US032233. 16-OCT-2000; 2000US-00688566

WO200232925-A2

Synthetic.

25-APR-2002.

us10008789-3.rng

New non-antibody proteins having an immunoglobulin fold, useful in research, therapeutic or diagnostic fields, particularly as scaffolds for designing proteins with specific properties, e.g. for binding any antigen

Disclosure; Page 58; 94pp; English.

The present invention describes a non-antibody protein, comprising a domain having an immunoglobulin-like fold, derived from a reference protein having a mutated amino acid sequence, where the non-antibody protein brinds with a Kd at least as tight as 10 mM to a compound that is not bound as tightly by the reference protein. The non-antibody protein is useful as exaffolds for selecting or designing a protein framework with specific and favourable properties, e.g. for binding any antigen of interest, or for destroying or inactivating antibody molecules. The non-antibody protein is also useful in all areas where antibodies are used, e.g. research, therapeutic or diagnostic fields, and for screening novel binding proteins useful in the above-mentioned fields. The present proteins and can be evolved rapidly in vitro. The present proteins or antibodies, and can be evolved rapidly in vitro. The present proteins or antibody mimics exhibit improved biophysical properties, such as stablish improved biophysical properties, such as stablish in prokaryotic systems (e.g. Escherichia coli), in eukaryotic systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit reticulocyte lysate system). Furthermore, these proteins are extremely amenable to affinity maturation techniques involving multiple cycles of selection, e.g. in vitro selection using RNA-protein fusion technology, the avannité and in the present sequence is used in the avannité and in the present sequence is used in the exemplification of the present invention

Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Gaps ., 1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels Query Match Best Local Similarity 100. Matches 20, Conservative

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ABZ88267 standard; DNA; 20

ABZ88267;

BP

17-OCT-2003 (first entry)

Human oligonucleotide sequence.

antiinflammatory steroid, ubiquinone, antiinflammatory; antiallergic, antiantergrent antiantergrent antiantergrent antiantergrent entranse gene therapy; respiratory; lung, adenosine sensitivity; adenosine receptor; bronchodiation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds. Human; antisense; lung dysfunction; nasal airway dysfunction; RESULT 161
ABZ88267
XX
AC ABZ8827
XX
DT 17-0CTXX
M Human,
XX
M antian;
XW A

Homo sapiens.

WO200285308-A2

31-OCT-2002.

23-APR-2002; 2002WO-US013135

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC

Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D; Nyce JW,

Shahabuddin S; Tang L, Miller S,

WPI; 2003-229219/22

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

Disclosure; SEQ ID NO 3509; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the intiation codon, coding region, 5' or 3' end genomic flanking regions, c initiation codon, coding a polypeptide associated with lung and/or lasal airway dysfunctions a second active agent comprising an attiinflammatory steroid and ubiquinone. A composition of the invention has attiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an prisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an attiframmatory steroid in a subject, for reducing levels of adenosine receptor, producing sensitivity to adenosine, reducing levels of adenosine receptor, producing shonchodilation, increasing levels of ung unflammation, lung allergies, or a respiratory disease or condition. Note: The sequence date for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Gaps ö Score 20; DB 1; Length 20; Pred. No. 1.6e+02; 0; Indels 1.1%; Scc. 100.0%; Pred. No. ... '... 0; Mismatches al Similarity 100. 20; Conservative Query Match Local Best Loca Matches

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RESULT 162

ABZ88565

ABZ88565 standard; DNA; 20

ABZ88565;

17-OCT-2003 (first entry)

Human oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiinflammatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds. 

Homo sapiens.

WO200285308-A2

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC

Katz E, Pabalan J, Aguilar D; Nyce Jw, Li Y, Sandrasagra A,

at ftp.wipo.int/pub/published_pct_sequences 23-APR-2002; 2002WO-US013135. Homo sapiens. ubiquinone ABZ88619 ઠે ద

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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the intistion codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, 5' or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or chasal airway dysfunction and a second active agent comprising an antiinflammatory, antiallergic, antiaschmatic, hypotensive, cantiinflammatory, antiallergic, antiaschmatic, hypotensive, conse in antisense gene therapy. The composition may have a use in antisense gene therapy. The composition may have a use in antisense gene therapy. The composition may have a use in antisense gene therapy. The composition may have a use in antisense gene therapy. The composition may have a use in antisense gene therapy. The composition may have a use in antisense gene therapy. The composition may have a continual antisense sent condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antishammatory steroid in a subject, for reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung suffactant in a subject, a tissue, or treating bronchoconstriction, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed producing the sequence data for this patent is not represented in the printed producing the sequence data for this patent is not represented in the printed producing the sequence data for this patent is not represented in the printed producing the sequence data for this patent is not represented in the printed producing the sequence data for this patent is not represented in the printed producing the sequence data for this patent is not represented in the printed producing the sequence data for this patent is not represented in the printed producing the printed producing the producing the printed producing the producing the printed p
                                                                                                                                                                                                                                                                                                                                treating ailments associated with impaired
                                                                                                                                                                                                                                                                                                                        Pharmaceutical composition for treating ailments associated with impair respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 3807; 872pp; English
Shahabuddin S,
                                                                                                                                                            WPI; 2003-229219/22.
        Tang L,
Miller S,
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Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Gaps ö 1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; tive 0; Mismatches 0; Indels Best Local Similarity 100. Matches 20; Conservative

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ABZ88619 standard; DNA; 20 BP

17-OCT-2003 (first entry)

Human oligonucleotide sequence.

antinflammatory steroid; ubiquinone; antinflammatory; antiallergic; antianterprices antianthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds. Human; antisense; lung dysfunction; nasal airway dysfunction;

WO200285308-A2

31-OCT-2002

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC

Pabalan J, Aguilar D; Katz E, Li Y, Sandrasagra A, Nyce JW,

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the intiation codon, coding region, 5, or 3 end genomic flanking regions, 5 and 3 interon-exon junctions, 5 or 2 end genomic flanking regions, 5 interon-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or masal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiathmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing levels of copeting sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of adenosine creeptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject, a respiratory disease or condition, lung allergies, or a respiratory disease or condition. Note: The sequence data for this parent is not represented in the printed specification, but was obtained in electronic format directly from WIPO Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or Gaps ö 1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; tive 0; Mismatches 0; Indel8 Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other; at ftp.wipo.int/pub/published_pct_sequences Disclosure; SEQ ID NO 3861; 872pp; English. 1736 AAAAAAAAAAAAAAAAAA 1755 Shahabuddin S; 1 AAAAAAAAAAAAAAA 20 20; Conservative Query Match Best Local Similarity Tang L, WPI; 2003-229219/22 ubiquinone. Miller S, Matches ð 셤

RESULT 164 ABZ8970

ABZ89705 standard; DNA; 20 BP

ABZ89705;

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Human oligonucleotide sequence. 17-OCT-2003 (first entry) 

Human, antisense; lung dysfunction, nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Homo sapiens

WO200285308-A2

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC

Pabalan J, Aguilar D; Katz E, Nyce JW, Li Y, Sandrasagra A,

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first accided residue to a lighted phasimaceutical composition, which has a initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory steroid and ubiquinone. A composition of the invention and antiinflammatory steroid and ubiquinone. A composition of the invention immunosuppressive, and cytostatic activity. The composition may have a immunosuppressive, and cytostatic activity. The composition may have a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing levels of adenosine receptor, producing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject stissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from MIPO
                                                                                                               Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                                                                                   The invention relates to a novel pharmaceutical composition, which has
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                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 4947; 872pp; English.
   Tang L, Shahabuddin S
                                                         WPI; 2003-229219/22
                                                                                                                                                                                                    ubiquinone
Miller S,
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Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

. 0 1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels 20; Conservative Query Match Best Local Similarity Matches ઠ

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ABZ88816 standard; DNA; 20 17-OCT-2003 (first entry) ABZ88816; RESULT 165
ABZ88816
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BP.

Human oligonucleotide sequence.

antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchodiolation; bronchodiation; lung allergy; lung inflammation; respiratory disease; ds. Human; antisense; lung dysfunction; nasal airway dysfunction;

Homo sapiens

WO200285308-A2.

31-OCT-2002.

23-APR-2002; 2002WO-US013135

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC

Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D; Nyce JW,

Tang L, Shahabuddin S; Miller S,

WPI; 2003-229219/22

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone

Disclosure; SEQ ID NO 4058; 872pp; English

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' end genomic flanking regions, 5' and 3' end genome flanking regions, 6' and 3' intron-excn junctions or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory attended as second active agent comprising on the antiinflammatory, antiallargic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a cuse in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of antiinflammatory steroid in a subject, for reducing of denosine ceptor, producing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung inflammation, lung allergies, or a respiratory disease or condition. Und allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

ö Gapa ö 1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels Local Similarity 100. 1es 20; Conservative Query Match Best Loca Matches

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Gaps

ABZ88881 standard; DNA; 20 BP RESULT 166 ABZ88881

17-OCT-2003 (first entry)

ABZ88881;

Human oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds. 

Homo sapiens.

WO200285308-A2

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC.

Katz E, Pabalan J, Aguilar D; Nyce JW, Li Y, Sandrasagra A,

Shahabuddin S

Tang L,

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the intitation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a cuse in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or mailgnant disease or condition, also preventing a respiratory, lung or mailgnant disease or condition, also continiflammatory steroid in a subject, for reducing or depleting levels of antiinflammatory steroid in a subject, for reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO Pharmaceutical composition for treating ailments associated with impaire respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or at ftp.wipo.int/pub/published_pct_sequences Disclosure; SEQ ID NO 4123; 872pp; English WPI; 2003-229219/22 ubiquinone. Miller S, ò

ö Gaps ö 1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; tive 0; Mismatches 0; Indels Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other; 1736 AAAAAAAAAAAAAAAAAA 1755 Query Match
Best Local Similarity 100.
Matches 20; Conservative

1 AAAAAAAAAAAAAAA 20 셤

ABZ89706 standard; DNA; 20 BP ABZ89706; 

17-OCT-2003 (first entry)

Human oligonucleotide sequence

antinflammatory steroid, ubiquinone, antiinflammatory; antiallergic; antiantesthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds. Human; antisense; lung dysfunction; nasal airway dysfunction;

Homo Bapiens

WO200285308-A2

31-OCT-2002

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC

Pabalan J, Aguilar D; Katz E, Li Y, Sandrasagra A, Nyce JW,

Shahabuddin S; Tang L, Willer S,

WPI; 2003-229219/22

treating ailments associated with impaired

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

Disclosure, SEQ ID NO 4948; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the intiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a cuse in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing levels of denosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung allergies, or a respiratory disease or condition. Ung inflammation, lung allergies, or a respiratory disease or condition. Specification, but was obtained in electronic format directly from WIPO ftp.wipo.int/pub/published_pct_sequences 

Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Gaps ö 1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.(

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ABZ88620 standard; DNA; 20 BP ABZ88620; ABZ88620

(first entry) 17-OCT-2003

Human oligonucleotide sequence.

antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds. Human; antisense; lung dysfunction; nasal airway dysfunction; 

Homo sapiens

40200285308-A2

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC

Pabalan J, Aguilar D; Nyce JW, Li Y, Sandrasagra A, Katz E,

WO200285308-A2 Homo sapiens. 31-OCT-2002. ubiquinone ABZ88814; RESULT 169 ABZ88814 ò g 

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or Disclosure; SEQ ID NO 3862; 872pp; English. Shahabuddin WPI; 2003-229219/22 Tang L, Miller S,

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation coodon, coding regaion, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an extisting sensitivity to adenosine, reducing or depleting levels of or interpretation increasing levels of adenosine receptor, producing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO ftp.wipo.int/pub/published_pct_sequences

Seguence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Gaps ö 1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; tive 0; Mismatches 0; Indels Query Match Best Local Similarity 100.0 Matches 20, Conservative

ABZ88814 standard; DNA; 20 17-OCT-2003 (first entry)

B

Human oligonucleotide sequence.

antinflammatory steroid, ubiquinone, antinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchodonstriction; lung allergy; lung inflammation; respiratory disease; ds. Human; antisense; lung dysfunction; nasal airway dysfunction;

23-APR-2002; 2002WO-US013135

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC

Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D; Nyce JW,

Tang L, Shahabuddin S; Miller S,

WPI; 2003-229219/22

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone

Disclosure; SEQ ID NO 4056; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5, or 3, end genomic flanking regions, 5, initiation codon, coding region, 5, or 2, end genomic flanking regions, 5, intron-exon junctions, 7 or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallargic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a presenting a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an artisinflammatory steroid in a subject, for reducing levels of continione or ceceptor, producing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung inflammation, lung allergies, or a respiratory disease or condition, lung inflammation, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

ö Gaps ö 1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.0
Matches 20; Conservative

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ABZ89241 standard; DNA; 20 ABZ89241; RESULT 170 ABZ89241

BP.

17-OCT-2003 (first entry)

Human oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory; antiallergic; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds. 

Homo sapiens.

WO200285308-A2

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC.

Katz E, Pabalan J, Aguilar D; Nyce JW, Li Y, Sandrasagra A,

ABZ90650 standard; DNA; 20 BP 23-APR-2002; 2002WO-US013135 W0200285308-A2 Homo sapiens. 31-OCT-2002. ubiquinone ABZ90650; Query Match 셤 8

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding regalon, 5' or 3' end genomic flanking regions, c' and 3' intron-exon junctions or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antialregic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an artifilammatory steroid in a subject, for reducing or depleting levels of or reducing sensitivity to adenosine, reducing levels of ung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ftp.wipo.int/pub/published_pct_sequences Disclosure; SEQ ID NO 4483; 872pp; English. Shahabuddin WPI; 2003-229219/22 Tang L, Miller S,

Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Gaps ö 1.1%; Score 20; DB 1; Length 20; 100.0%; Pred: No. 1.6e+02; 0; Indels 0; Mismatches Best Local Similarity 100. Matches 20; Conservative

Human oligonucleotide sequence. 17-OCT-2003 (first entry)

Human; antisense; lung dysfunction; nasal airway dysfunction; antinflammatory steroid; ubiquinone; antinflammatory; antiallergic; antiathmatic; phypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC

Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D; Nyce JW,

Shahabuddin S; Tang L, Miller S,

WPI; 2003-229219/22

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

Disclosure; SEQ ID NO 5892; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the intiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or namal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention can antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition may have a use in antisense gene therapy. The composition may have a use in antisense year therapy. The composition may have a use in antisense year therapeutic respiratory effect of an autisinflammatory steroid in a subject, for reducing or depleting levels of continuous or ceceptor, producing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing levels of adenosine current in a subject, stissue, or treating bronchocomstriction, lung allergies, or a respiratory disease or condition, or the stinted process or condition, the sequence data for this patent is not represented in the printed appearance of the printed process. ftp.wipo.int/pub/published_pct_sequences 

Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

ö Gaps ö 1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; Live 0; Mismatches 0; Indels Local Similarity 100. nes 20; Conservative Query Match Matches

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ABZ88618 standard; DNA; 20 AB288618

ВР

(first entry) 17-0CT-2003

ABZ88618;

Human oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction; antinflammatory steroid; ubiquinone; antinflammatory; antiallergic; antiasthmatic; hypotensive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Ношо варіепв

40200285308-A2

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P. 

(EPIG-) EPIGENESIS PHARM INC.

Katz E, Pabalan J, Aguilar D; Nyce JW, Li Y, Sandrasagra A, Tang L, Shahabuddin S;

Miller S,

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first active agent comprising an oligomucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallargic, antiathmation of the invention is useful for treating or preventing a respiratory, lung cativity. The composition may have a preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antifalammatory steroid in a subject, for reducing or depleting levels of of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed of specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                Disclosure, SEQ ID NO 3860; 872pp; English.
 Tang L, Shahabuddin
                                    WPI; 2003-229219/22
                                                                                                                             ubiquinone.
 Miller S,
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RESULT 174
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                                                                                                                                                                                                                                                                                   Human, antisense; lung dysfunction, nasal airway dysfunction, antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; Mypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
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1.1%; Score 20; DB 1; Length 20;
100.0%; Pred. No. 1.6e+02;
iive 0; Mismatches 0; Indels
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                                                                                                                                                                  ABZ88815 standard; DNA; 20
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               Best Local Similarity 100.
Matches 20; Conservative
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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a compart in a supersection of the invention of preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of adenosine creeptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO cat fip.wipo.int/pub/published_pct_sequences
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Pred. No. 1.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-OCT-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                                      WPI; 2003-229219/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200285308-A2
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                                                                                                                                                                                              ubiquinone
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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions or regions within 2-10 nucleotides of junctions of genee encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an intinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, and cytostatic activity. The composition may have a preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antipartory steroid in a subject, for reducing or depleting levels of or reducing sensitivity to adenosine, reducing levels of ubiquinone or ung surfactant in a subject, for reating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence date for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or at ftp.wipo.int/pub/published_pct_sequences Claim 15; SEQ ID NO 553; 872pp; English. Shahabuddin S; WPI; 2003-229219/22 Tang L, ubiquinone. Miller S, 

Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

ö 1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels 1736 AAAAAAAAAAAAAAAAA 1755 Local Similarity 100. Query Match Matches 8

20 AAAAAAAAAAAAAAAA 1 셤

ABZ85435 standard; DNA; 20 BP 17-OCT-2003 (first entry) ABZ85435; ABZ885/6 ABZ885/6 ABZ885/6 AAC ABZ88 
Human oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchodialiation; bronchodination; lung allergy; lung inflammation; respiratory disease; ds.

Homo sapiens

WO200285308-A2

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC

Katz E, Pabalan J, Aguilar D; Li Y, Sandrasagra A, Nyce JW,

Shahabuddin S; Tang L, Miller S,

WPI; 2003-229219/22

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

Claim 15; SEQ ID NO 677; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antifinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallargic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a cuse in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antisinflammatory steroid in a subject, for reducing levels of continion and producing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing levels of adenosine lung surfactant in a subject of tissue, or treating bronchocinetion, lung allergies, or a respiratory disease or condition. Uning allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences 

Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Gaps ö 1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; Live 0; Mismatches 0; Indels al Similarity 100. 20; Conservative Query Match Local Matches

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Gaps

RESULT 176 ABZ88817

ВÞ ABZ88817 standard; DNA; 20 ABZ88817; 

Human oligonucleotide sequence.

(first entry)

17-0CT-2003

Human, antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory; antiallergic; antiinflammatory; antiallergic; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Homo sapiens

WO200285308-A2

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC.

Pabalan J, Aguilar D; Katz B, Nyce JW, Li Y, Sandrasagra A,

Miller S, AESULT 177
AES8939
XX
AC ABZ8893
XX
AC ABZ8893
XX
DT 17-OCTXX
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Human;
XW antian;
XW ે

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or Disclosure, SEQ ID NO 4059; 872pp; English. Shahabuddin WPI; 2003-229219/22 Tang L, ubiquinone

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonuclectide antisense to the intiation codon, coding reggion, 5' or 3' end genemic flanking regions, 5' and 3' intron-exon junctions or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal alrway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallargic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an preventing sensitivity to adenosine, reducing levels of adenosine ceptor, producing bronchodilation, increasing levels of ubiquinone or lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed of specification, but was obtained in electronic format directly from WIPO are first and an electronic format directly from WIPO ftp.wipo.int/pub/published_pct_sequences

Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Gaps . Score 20; DB 1; Length 20; Pred. No. 1.6e+02; 0; Indels 1.1%; Scc. 100.0%; Pred. No. 1... Query Match
Best Local Similarity 100..
Local Similarity 100..

ABZ88939 standard; DNA; 20 17-OCT-2003 (first entry) ABZ88939;

BP.

Human oligonucleotide sequence.

antinfilammatory steroid, ubiquinone, antinfilammatory; antiallergic, antiantesthmatic; hypotensive; immunosuppressive; cytostatic; gane therapy; antiense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds. Human; antisense; lung dysfunction; nasal airway dysfunction;

Homo sapiens

WO200285308-A2

31-OCT-2002.

24-APR-2001; 2001US-0286137P.

23-APR-2002; 2002WO-US013135

(EPIG-) EPIGENESIS PHARM INC

Aguilar D; Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J,

Tang L, Shahabuddin S; Miller S,

WPI; 2003-229219/22

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

Disclosure; SEQ ID NO 4181; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5, or 3, end genomic flanking regions, 5, and 3, intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a cuse in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or therapeutic respiratory effect of an activitiammatory steroid in a subject, for reducing or depleting levels of or reducing sensitivity to adenosine, reducing levels of denosine receptor, producing bronchodilation, increasing levels of ubiquinnon or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung allergies, or a respiratory disease or condition. Ung allergies, or a respiratory disease or condition. Second antismmation, lung allergies, or a respiratory disease or condition. Second subject in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Gaps ô Score 20; DB 1; Length 20; Pred. No. 1.6e+02; 0; Indels 100.0%; Preα. κν. - ive 0; Mismatches 1.1%; Query Match Best Local Similarity 100.0 ----has 20; Conservative

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RESULT 178

ABZ89302 standard; DNA; 20 BP ABZ89302

17-OCT-2003 (first entry) ABZ89302; 

Human oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory; antiallergic; antianflammatory; antiallergic; antiatethmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Homo sapiens.

WO200285308-A2

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC.

Katz E, Pabalan J, Aguilar D; Nyce JW, Li Y, Sandrasagra A,

Shahabuddin S;

Tang L,

Miller S,

23-APR-2002; 2002WO-US013135 AB288566 ઠે 셤

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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the intistion codon, coding region, 5' or 3' end ganomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or neasal airway dysfunction and a second active agent comprising an antiinflammatory, antiallergic, antiasthmatic, hypotensive, and allergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antislammatory steroid in a subject, for reducing levels of adenosine or neglocing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject, a tissue, or treating bronchoconstriction, lung allergies, or a respiratory disease or condition. Once: The sequence data for this patent is not represented in the printed propertication, interesting format directly from WIPO
                                                                                                         Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 4544; 872pp; English.
WPI; 2003-229219/22
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Gaps ö 1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other; Best Local Similarity 100. Matches 20, Conservative Query Match

Human oligonucleotide sequence. ABZ88566 standard; DNA; 20 BP 17-OCT-2003 (first entry) ABZ88566;

Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiatehmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodiation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Homo sapiens.

WO200285308-A2

31-OCT-2002

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC

Pabalan J, Aguilar D; Li Y, Sandrasagra A, Katz E, Nyce JW,

Shahabuddin S; Tang L, Miller S,

WPI; 2003-229219/22

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

Disclosure; SEQ ID NO 3808; 872pp; English

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation coodon, coding regains, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an entilflammatory steroid and ubjquinone. A composition of the invention has antilflammatory, antiallergic, antiathmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an preventing sensitivity to adenosine, reducing sensitivity to adenosine, reducing sensitivity to adenosine, reducing sensitivity to adenosine, reducing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactent in a subject's tissue, or treating bronchocomstriction, lung surfactent in a subject's tissue, or treating bronchocomstriction, note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published_pct_sequences 

Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Gaps ö 1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; tive 0; Mismatches 0; Indels 20; Conservative Local Similarity Query Match Matches

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Human oligonucleotide sequence. ABZ89086 standard; DNA; 20 BP 17-OCT-2003 (first entry) ABZ89086; ABZ89086 

Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory; antiallergic; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Homo sapiens

#0200285308-A2

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC

Pabalan J, Aguilar D; Katz E, Nyce JW, Li Y, Sandrasagra A,

lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences WO200285308-A2 Homo sapiens. ubiquinone ABZ85533; Query Match Matches RESULT 181 ò 셤

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation coodon, coding region, 5 or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an entilnflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallargic, antiasthmatic, hypotenaive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is seful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing levels of, or reducing sensitivity to adenosine, reducing levels of denosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction. Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or Disclosure; SEQ ID NO 4328; 872pp; English Tang L, Shahabuddin WPI; 2003-229219/22 Miller S,

Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

ö Gaps ö 1.1%; Score 20; OB 1; Length 20; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels Local Similarity 100. nes 20; Conservative

Human oligonucleotide sequence. ABZ85533 standard; DNA; 20 17-OCT-2003 (first entry)

Human; antisense; lung dysfunction; nasal airway dysfunction;

antinflammatory steroid, ubiquinone, antinflammatory; antiallergic; antianterpressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

31-OCT-2002.

23-APR-2002, 2002WO-US013135

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC

Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D; Nyce JW,

Shahabuddin S; Tang L, Miller S,

WPI; 2003-229219/22

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

Claim 15; SEQ ID NO 775; 872pp; English.

first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory service and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiantenmentory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing bronchocomstriction, lung surfactant in a subject's tissue, or treating bronchocomstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO The invention relates to a novel pharmaceutical composition, which has a at ftp.wipo.int/pub/published_pct_sequences

Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Gaps ; 0 Score 20; DB 1; Length 20; Pred. No. 1.6e+02; 0; Indels 1.1%; SCC. 100.0%; Pred. No. 1... Local Similaricy hes 20; Conservative Query Match Matches

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ò 셤 RESULT 182 ABZ8901

ABZ89015 standard; DNA; 20 ABZ89015; 

17-OCT-2003 (first entry)

Human oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory; antiallergic; antiinflammatory; antiallergic; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Homo sapiens.

WO200285308-A2

31-0CT-2002

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC

Katz E, Pabalan J, Aguilar D; Nyce JW, Li Y, Sandrasagra A,

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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding regaion, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, and cytostatic, artiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a immunosuppressive, and cytostatic activity. The composition may have a cuse in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an autient activity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of biquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                         Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 4257; 872pp; English.
  Shahabuddin S
                                                     WPI; 2003-229219/22
     Tang L,
                                                                                                                                                                                        ubiquinone.
  Miller S,
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Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Gaps ö 1.1%; Score 20; DB 1; Length 20; 00.0%; Pred. No. 1.6e+02; 0; Indels 0; Mismatches 100.08; Best Local Similarity 100. Matches 20; Conservative Query Match

1736 AAAAAAAAAAAAAAAAAA 1755

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1 AAAAAAAAAAAAAA 20 셤

Human oligonucleotide sequence. ABZ89441 standard; DNA; 20 BP ABZ89441; 

17-OCT-2003 (first entry)

Human, antisense, lung dysfunction, nasal airway dysfunction, antinflammatory steroid; ubiquinone; antinflammatory, antiallergic; antiasthmatic; hypotensive; immunosuppressive, cytostatic; gene therapy, antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchodilation; lung allergy; lung inflammation; respiratory disease; ds.

Homo sapiens.

WO200285308-A2

31-OCT-2002.

23-APR-2002; 2002WO-US013135

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC

Pabalan J, Aguilar D; Li Y, Sandrasagra A, Katz E, Nyce JW,

Shahabuddin S; Tang L, WPI; 2003-229219/22 Miller S,

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

Disclosure, SEQ ID NO 4683; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antinflammatory steroid and ubsquinone. A composition of the invention has antinflammatory, antialergic, antiachmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing levels of adenosine of the recondition shall a subject, for reducing levels of adenosine contraction in the composition is a second distant antial and antial antial and antial antial and antial antial and antial antial antial and antial antial antial antial antial ant receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences 

Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Gaps ö 1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; tive 0; Mismatches 0; Indels Matches 20; Conservative Best Local Similarity Query Match

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ABZ89016 standard; DNA; 20 BP 17-OCT-2003 (first entry) ABZ89016; ABZ8901 

Human oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiinsthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Homo sapiens

WO200285308-A2

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC.

Nyce Jw, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

WO200285308-A2 ubiquinone ABZ89120; Matches RESULT 185 ABZ8912 ठे 임

Tang L, Shahabuddin Miller S,

WPI; 2003-229219/22

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

Disclosure; SEQ ID NO 4258; 872pp; English.

first active agent comprising an oligonuclectide antisense to the initation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nuclectides of junctions of genee encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an initial numaricy steroid and ubiquinone. A composition of the invention has antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallargic, antiasthmatic, hypotenaive, immunosuppressive, and cytostatic activity. The composition may have a immosuppressive and cytostatic activity. The composition may have a preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an infillammatory steroid in a subject, for reducing levels of adenosine of receptor, producing pronchodilation, increasing levels of adenosine or receptor, producing pronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, ung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO The invention relates to a novel pharmaceutical composition, which has a at ftp.wipo.int/pub/published_pct_sequences

Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Gaps ; 0 Score 20; DB 1; Length 20; Pred. No. 1.6e+02; 0; Indels 1.1%; Scor. 100.0%; Pred. No. ... 0; Mismatches Local Similarity 100. Query Match

ABZ89120 standard; DNA; 20

17-OCT-2003 (first entry)

Human oligonucleotide sequence.

Human, antisense, lung dysfunction, nasal airway dysfunction, antiinflammatory; antiallergic; antiinflammatory; antiallergic; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds

Homo sapiens.

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC

Aguilar D; Pabalan J, Li Y, Sandrasagra A, Katz E, Nyce JW,

Tang L, Shahabuddin S, Miller S,

WPI; 2003-229219/22

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone

Disclosure; SEQ ID NO 4362; 872pp; English

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a cuse in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or therapeutic respiratory effect of an oriniflammatory steroid in a subject, for reducing or depleting levels of or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchodilation, increasing levels of ubiquinone or lung suffammation, lung allergies, or a respiratory disease or condition. Und suffammation, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Gaps . 0 1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels Best Local Similarity 100. Matches 20; Conservative Query Match

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RESULT 186 ABZ89704

ABZ89704 standard; DNA; 20 BP ABZ89704;

17-OCT-2003 (first entry)

Human oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory; antiallergic; antiinflammatory; antiallergic; antiinsthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Homo sapiens.

WO200285308-A2

31-OCT-2002.

23-APR-2002; 2002WO-US013135. 

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC.

Katz E, Pabalan J, Aguilar D; Nyce JW, Li Y, Sandrasagra A,

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12-OCT-2001; 2001US-00976378
                                                                                                                                                      15-OCT-2003 (first entry)
                                                                                                       Query Match
Best Local Similarity 100.
Matches 20, Conservative
      WPI; 2003-229219/22
                                                                                                                                                                                                             US2002155461-A1
                                                                                                                                                                                             modified_base
                                                                                                                                                                                                                   24-OCT-2002
                     ubiquinone.
Miller S,
                                                                                                                                                                                    Synthetic
                                                                                                                                               ACD27320;
                                                                                                                                   RESULT 187
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This invention relates to a novel method for detecting a nucleic acid having 2 portions. The method comprises providing nanoparticles having coligonucleotides attached, where the oligonucleotide on each nanoparticle has a sequence complementary to a sequence of 2 portions of nucleic acid. The nucleic acid and nanoparticle with two or more portions of nucleic acid and observing a detectable change brought about by the control of the oligonucleotide on the nanoparticle with two or more portions of nucleic acid and observing a detectable change brought about by the chyptidisation. The method of the irrention is useful for separating a selected nucleic acid having 2 portions, from other nucleic acids, and for detecting nucleic acids having 2 portions. The method of the irrention is useful for detecting any type of nucleic acids which may be used for diagnosis of disease and in sequencing of nucleic acids for preferably, the method is useful for detecting nucleic acids for diagnosis and/or monitoring of viral diseases (human immunodeficiency virus), bacterial diseases, sexually transmitted diseases, inherited diseases, in forensics, in DNA sequencing, for paternity testing, for cell line authentication, for monitoring gene therapy, etc. This method disponences detecting nucleic acids based on observing a colour change with the naked eye so is cheap, fast, simple and robust, and does not require specialised expensive equipment. The present sequence represents a thiol modified oligonucleotide sequence used to demonstrate the method of the
                                                                                                                                                                                                                                                                                                                                                                                         Detecting nucleic acids having 2 portions e.g. for detecting disease, comprises use of nanoparticles which have oligonucleotides attached to them that are complementary to portions of the nucleic acid sequence.
                                                                                                                                                                                                                                                 Storhoff JJ, Elghanian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
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                       97WO-US012783.
99US-00240755.
99US-00344667.
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                                                                                                        26-APR-2000; 2000US-0200161P.
26-JUN-2000; 2000US-00603830.
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                                                                                                                                                                                                                                                 Mirkin CA, Letsinger RL,
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nes 20; Conservative
                                                                                                                                                                                         (NANO-) NANOSPHERE INC.
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                          21-JUL-1997;
29-JAN-1999;
                                                                                 25-JUN-1999;
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                                                                                                                                                                                                                                                                                            The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the intitation coodon, coding regains, 5' or 3' end ganomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubjquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an artificammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of sudenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                     Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nanotechnology; ss; nucleic acid detection; nanoparticle; virus detection; human immunodeficiency virus; HIV; hepatitis; herpes; cytomegalovirus; Epstein-Barr virus; bacterial disease; DNA sequencing; sexually transmitted disease; inherited disorder; forensic; paternity testing; cell line authentication.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 20; DB 1; Length 20;
Pred. No. 1.6e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 4946; 872pp; English
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Shahabuddin S
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Tang L,
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Gaps

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0; Indels

Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour; OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis; inflammation; therapy; hyperproliferative disorder; infection; cancer; chromosome 7q22; ZRP-1; phosphorothioate; ss.

'note = "OTHER = Thiol modified"

'mod base≈ OTHER

Synthetic

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The invention relates to antisense compounds targetted to a nucleic acid encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22. Antisense compounds of the invention are useful for modulating the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for indiamostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as research reagents and kins and in distinguishing between functions of various members of a biological pathway. The are also useful in antisense therapy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.
                                                                                                                                 /mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
                                                                                                                                                                                          /*tag= b
/mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides'
16. .20
                                                                                                                                                                                                                                                                 /*tag= c
/mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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100.0%; Pred. No. 1.6e+02;
iive 0; Mismatches 0; Indels
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chromosome 7q22; ZRP-1; phosphorothioate; ss.
                                                                                 ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 76; 111pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                   05-NOV-2002; 2002WO-US035479
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                                                                                                                  *tag=
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                                                                                  Key
modified_base
                                                                                                                                                                                     modified base
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                                  sapiens.
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                                                   Synthetic
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ACC82919/c
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Matches
                                  Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.
                                                /mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour; OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis; inflammation; therapy; hyperproliferative disorder; infection; cancer;
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                                                                                                                                 /mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides
                                                                                                                                                                                                                  /note= "2'-methoxyethyl (2'-MOE) nucleotides
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                                                                                 are 5-methylcytidines"
 cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 TTCAAGACCGCTGTCTGGAG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 76; 111pp; English.
                                                                                                                                                                                                   /mod_base= OTHER
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ses 20; Conserv
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   Key
modified_base
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ACC82896/C
XX
AC ACC8288
XX
DT 27-AUG-
XX
XX
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KW Human;
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KW Human;
KW Human;
KW Human;
KW Human;
KW Human;
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New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.
                 Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour; OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis; inflammation; therapy; hyperproliferative disorder; infection; cancer; chromosome 7q22; ZRP-1; phosphorothioate; ss.
Human TRIP6 antisense oligonucleotide ISIS #198791.
                                                                                                                                                                                                                                                                                                                                                                                               Example 15; Page 77; 111pp; English.
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                                                                                                modified_base
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                                                                                                                                                                                modified_base
                                                              sapiens
                                                                                                                                                                                                                                                15-MAY-2003
                                                                        Synthetic
                                                              Ношо
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/mod_base= OTHER /note= "Phosphorothioate backbone; All cytidine residues are 5-methylcytidines"

Location/Qualifiers

/mod_base= OTHER /note= "2'-methoxyethyl (2'-MOE) nucleotides" 16. .20

*tag= b

/mod_base= OTHER /note= "2'-methoxyethyl (2'-MOE) nucleotides"

*tag= c

The invention relates to antisense compounds targetted to a nucleic acid encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its expression. TRIP6 is also known as Oph.interacting protein.1 (OIP-1) and zyxin.related protein.1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22. Antisense compounds of the invention are useful for modulating the expression of TRIP6 and for treating diseases or conditions associated with the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as tressarch reagents and in distinguishing between functions of various amembers of a biological pathway. The are also useful in antisense therapy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention Sequence 20 BP; 4 A; 7 C; 6 G; 3 T; 0 U; 0 Other;

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Gaps
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 1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels
Query Match
Best Local Similarity 100.
Matches 20; Conservative
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Gaps

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1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels

GCCAGAAAAGTTTTCTTT 65 20 GCCAGAAAAGTTTTCTTTT 1

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20; Conservative

Query Match Pest Local Similarity

ACC82889 standard; DNA; 20 BP RESULT 191 ACC82889/c ID ACC8288

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New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.
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/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
                                                                                                               Human, antisense; thyroid hormone receptor interactor 6; TRIP6; tumour; OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis; inflammation; therapy; hyperproliferative disorder; infection; cancer; chromosome 7q22; ZRP-1; phosphorothioate; ss.
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                                                                             Human TRIP6 antisense oligonucleotide ISIS #198761.
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1. .20
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/*tag= c
/mod_base=
                                               (first entry)
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/mod_ba
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                 ACC82889;
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Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour; OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis; inflammation; therapy; hyperproliferative disorder; infection; cancer; chromosome 7q22; ZRP-1; phosphorothioate; ss.
                                                                Human TRIP6 antisense oligonucleotide ISIS #198779.
                                                                                                                                                                                                                      /note= "2'-methoxyethyl (2'-MOE)
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                                                                                                                                                                                           are 5-methylcytidines"
                                                                                                                                                  Location/Qualifiers
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/mod_base= OTHER
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                                                                                                                                  Synthetic.
                                ACC82907;
RESULT 192
       ACC82907
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Query Match Best Local Similarity

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The invention relates to antisense compounds targetted to a nucleic acid encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and zyxin-related protein-1 (IZRP-1). TRIP6 DNA is located on chromosome 7q22. Antisense compounds of the invention are useful for modulating the expression of TRIP6 and for treating diseases or conditions associated with the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as tesearch reagents and kits and in distinguishing between functions of various members of a biological pathway. The are also useful in antisense therapy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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to prevent or delay infection, inflammation or tumour formation, as research reagents and kits and in distinguishing between functions of avarious members of a biological pathway. The are also useful in antisense therapy. The present sequence is an antisense oligo targetted to human TRIPE DNA. This oligo is used in the exemplification of the invention
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are 5-methylcytidines"
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                                                                                    Length 20;
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                            20 BP; 9 A; 7 C; 3 G; 1 T; 0 U; 0 Other;
                                                                                    DB 1; Le
                                                                                 1.1%; Score 20; DB
100.0%; Pred. No. 1.6
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/mod_base= OTHER
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                       1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                     Human; antisense; thyroid hormone receptor interactor
                                                                                                                                                                                                                                                          Human TRIP6 antisense oligonucleotide ISIS #198772.
Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
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/note= "2'-methoxyethyl (2'-MOE)
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                                        Similarity
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RESULT 197
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zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22. Antisense compounds of the invention are useful for modulating the expression of TRIP6 and for treating diseases or conditions associated with the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as research reagents and kits and in distinguishing between functions of various members of a biological pathway. The are also useful in antisense therapy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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Pred. No. 1.6e+02;
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100.0%; Pred. No. 1..
... 0; Mismatches
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Best Local Similarity 100.0
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1D ACC82905/C
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                                                 The invention relates to antisense compounds targetted to a nucleic acid encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and zyxin-related protein-1 (CIP-1) and zyxin-related protein-1 (CIP-1) and attiense compounds of the invention are useful for modulating the expression of TRIP6 and for treating diseases or conditions associated with the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as research reagents and kits and in distinguishing between functions of various members of a biological pathway. The are also useful in antisense therapy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention
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/mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels
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Example 15; Page 76; 111pp; English.
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/mod_base= OTHER
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              New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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100.0%; Pred. No. 1.6e+02;
rative 0; Mismatches 0; Indels
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                                                                   New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.
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/note= "Phosphorothioate backbone; All cytidine residues
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/mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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16. .20
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Human TRIP6 antisense oligonucleotide ISIS #198793.
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The invention relates to antisense compounds targetted to a nucleic acid encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22. Antisense compounds of the invention are useful for modulating the expression of TRIP6 and as hyperproliferative disorders (e.g. cancer). They are useful for tisansenses or conditions associated with the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as research reagents and kits and in distinguishing between functions of various members of a biological pathway. The are also useful in antisense therappy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention
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/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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Pred. No. 1 66+02;
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                     /note= "Phosphorothioate backbone; All cytidine residues are 5-methylcytidines"
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16. .20
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/mod_base= OTHER
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/mod base= OTHER
                                                                                                                                                                       OTHER
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/mod base=
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Best Local Similarity 100.'
Matches 20, Conservative
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                                                                                                  modified base
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RESULT 205
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ID ACC8:
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                                                                                                                                                                                                                                                                                                                                                  New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.
                                                             /note= "Phosphorothioate backbone; All cytidine residues are 5-methylcytidines"
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                                                                                                                                                        /mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides'
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Pred. No. 1.6e+02;
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                      Location/Qualifiers
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                                                       /mod_base= OTHER
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                                                                                                                                                                                          WO2003040328-A2
                      Key
modified_base
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/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
OPA-interacting protein-1, OIP-1, zyxin-related protein-1, prophylaxis, inflammation, therapy, hyperproliferative disorder, infection, cancer, chromosome 7q22, ZRP-1, phosphorothioate, 88.
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/mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides'
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/mod basse OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides'
16. .20
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ACC82952 standard; DNA; 20
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/*tag=
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                                                                                                                                                                             Synthetic.
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The invention relates to antisense compounds targetted to a nucleic acid encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22. Antisense compounds of the invention are useful for modulating the expression of TRIP6 and for treating diseases or conditions associated with the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as tressarch reagents and kits and in distinguishing between functions of various members of a biological pathway. The are also useful in antisense therapy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention
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/note= "Phosphorothioate backbone, All cytidine residues
are 5-methylcytidines"
                                                                   Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour; OPA-linteracting protein-1; OIP-1; zyxin-related protein-1; prophylaxis; inflammation; therapy; hypertproliferative disorder; infection; cancer; chromosome 7q22; ZRP-1; phosphorothioate; ss.
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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                                    Human TRIP6 antisense oligonucleotide ISIS #198824
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16. 20
/*tag= c
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*tag= a
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*tag= b
(first entry)
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/note= "Phosphorothioate backbone; All cytidine residues are 5-methylcytidines"

Location/Qualifiers

. 20

modified_base

Homo sapiens

Synthetic.

/mod_base= OTHER

/mod_base= OTHER /note= "2'-methoxyethyl (2'-MOE) nucleotides" 16. .20

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modified base

/note= "2'-methoxyethyl (2'-MOE) nucleotides"

base= OTHER

/*tag= c

nodified_base

05-NOV-2002; 2002WO-US035479. 08-NOV-2001; 2001US-00008789.

WO2003040328-A2

L5-MAY-2003

(ISIS-) ISIS PHARM INC

Dobie K;

Bennett CF,

WPI; 2003-430662/40.

Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour; OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis; inflammation; therapy; hyperproliferative disorder; infection; cancer; chromosome 7q22; ZRP-1; phosphorothioate; ss.

Human TRIP6 antisense oligonucleotide ISIS #198825.

(first entry)

27-AUG-2003

ACC82953;

ACC82953 standard; DNA; 20 BP

ACC82953/c

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Gaps

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1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; ... ive 0; Mismatches 0; Indels

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Query Match

1683 CAAATGCTGTCTTCTTTC 1702 CAPATGCTGTCTTCTCTTTC 1

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Location/Qualifiers

1. 20
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//md_base= OTHER
//note= "Phosphorothioate backbone, All cytidine residues
are 5-methylcytidines"
                                                                   Human, antisense, thyroid hormone receptor interactor 6, TRIP6, tumour, OPA-interacting protein-1, OIP-1, zyxin-related protein-1, prophylaxis, inflammation, therapy, hyperproliferative disorder, infection, cancer, chromosome 7q22, ZRP-1, phosphorothioate, ss.
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16. .20
/*tag= c
/mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
                          Human TRIP6 antisense oligonucleotide ISIS #198773.
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/*tag= b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.
                                                                                                                                                                                                                                                                                                                          Human, antisense, thyroid hormone receptor interactor 6; TRIP6; tumour; OPA-linteracting protein-1; OIP-1; zyxin-related protein-1; prophylaxis; inflammation; therapy; hyperproliferative disorder; infection; cancer; chromosome 7q22; ZRP-1; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.1%; Score 20; DB 1; Length 20;
100.0%; Pred. No. 1.6e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 4 A; 2 C; 9 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                 Human TRIP6 DNA specific forward PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 13; Page 74; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1001 GCTGCGGAGAAGATGTGGTT 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GCTGCGGAGAAGATGTGGTT 20
                        20 TCAAGAATAATAATCCCTC 1
                                                                                                                                            ВP
05-NOV-2002; 2002WO-US035479.
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                                                                                                                                       ACC82881 standard; DNA; 20
                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bennett CF, Doble K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                     27-AUG-2003
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                                                                                                                                                                                       ACC82881;
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ACC82901/c
ID ACC829
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AC ACC829
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DT 27-AUG
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                                                                                              RESULT 207
                                                                                                                 ACC82881

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New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.
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Pred. No. 1.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 4 A; 8 C; 6 G; 2 T; 0 U; 0 Other;
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100.0%; Pred. No. 1...
                                                                                                                                                     Example 15; Page 76; 111pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               714 GCGGGGAGCCTCTCAGGCTT
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ACC82904/c
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BP.

ACC82901 standard; DNA; 20

ACC82901;

27-AUG-2003 (first entry)

20 ATAGGAGCCAGAGAGACCA 1

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(first entry)

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The invention relates to antisense compounds targetted to a nucleic acid encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and zyxin-related protein-1 (ZRP-1). TRIP6 NM is located on chromosome 7q22. Antisense compounds of the invention are useful for modulating the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as research reagents and kits and in distinguishing between functions of various emphase of a biological pathway. The are also useful in antisense therapy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.
                                                                                                                               Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour; OPA-linteracting protein-1; OIP-1; zyxin-related protein-1; prophylaxis; inflammation; therapy; hyperproliferative disorder; infection; cancer; chromosome 7q22; ZRP-1; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 1.1%; Score 20; DB-1; Length 20; Local Similarity 100.0%; Pred. No. 1.6e+02; Nes 20; Conservative 0; Mismatches 0; Indels
                                                                                                   Human TRIP6 antisense oligonucleotide ISIS #198776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 1 A; 7 C; 4 G; 8 T; 0 U; 0 Other;
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ACC82904 standard; DNA; 20 BP
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                                                                                                                                                                                                                                                                     Key
modified_base
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                                                                                                                                                                                                                  Homo sapiens.
Synthetic.
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                                                                  27-AUG-2003
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                                 ACC82904
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Dobie K;

/note= "Phosphorothioate backbone; All cytidine residues are 5-methylcytidines"

Location/Qualifiers

1. .20 /*tag= a /mod_base= OTHER

/mod_base= OTHER /note= "2'-methoxyethyl (2'-MOE) nucleotides" 16. .20

*tag= b

'n

/note= "2'-methoxyethyl (2'-MOE) nucleotides"

mod_base= OTHER

U

*tag=

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New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.
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                                                                                                                                                                                                                                                                                                                                               /note= "Phosphorothioate backbone; All cytidine residues are 5-methylcytidines"
1. .5
                                                                                                                                            Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour; OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis; inflammation; therapy; hyperproliferative disorder; infection; cancer; chromosome 7q22; ZRP-1; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                /mod_base= orHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
/mod_base= orHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
                                                                                                               Human TRIP6 antisense oligonucleotide ISIS #198784.
                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 77; 111pp; English.
                                                                                                                                                                                                                                                                                                                                   /mod base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-NOV-2002; 2002WO-US035479.
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             standard; DNA; 20
                                                                              (first entry)
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                                                                                                                                                                                                                                                                                 Key
modified_base
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                                                                                                                                                                                                                                Homo sapiens.
Synthetic.
                                                                            27-AUG-2003
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ACC82912 :
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ACC82912
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Gaps

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Sequence 20 BP; 8 A; 5 C; 4 G; 3 T; 0 U; 0 Other;

Best Loca Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Phosphorothioate backbone; All cytidine residues are 5-methylcytidines"
                                                                                                                                                                                                                                                                                      Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour; OPA-linteracting protein-1; OIP-1; zyxin-related protein-1; prophylaxis; inflammation; therapy; hyperproliferative disorder; infection; cancer; chromosome 7q22; ZRP-1; phosphorothioate; ss.
                    Gaps
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/mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
                0; Indels
                                                                                                                                                                                                                                                          Human TRIP6 antisense oligonucleotide ISIS #198811.
100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 15; Page 77; 111pp; English
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                                                1073 TIGIALGITCIACATGCCGG 1092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mod_base= OTHER
                                                                 20 TIGTATGTTCTACATGCCGG 1
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                                                                                                                                                            ACC82939 standard; DNA; 20
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                20; Conservative
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 Best Local Similarity
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modified_base
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                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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                  Matches
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                                                                                                                           RESULT 21
ACC82939/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Phosphorothioate backbone; All cytidine residues are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                       Human, antisense; thyroid hormone receptor interactor 6; TRIP6; tumour; OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis; inflammation; therapy; hyperproliferative disorder; infection; cancer; chromosome 7q22; ZRP-1; phosphorothioate; ss.
TRIP6 DNA. This oligo is used in the exemplification of the invention
                                                                                          Gaps
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/mod_base= OTHER
/not== "2'-methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "2'-methoxyethyl (2'-MOE) nucleotides'
6. .20
                                                          1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                             Human TRIP6 antisense oligonucleotide ISIS #198764.
                              Seguence 20 BP; 5 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 15; Page 76; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                         1508 CGCTGGATGGCCACATCTTG 1527
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/mod_base= OTHER
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                                                                                                                                         20 CGCTGGATGGCCACATCTTG
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ID ACC82892 standard; DNA; 20 BP.
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                                                                        Best Local Similarity 100.
Matches 20; Conservative
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*tag=
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Synthetic.
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                                                             Query Match
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cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as research reagents and kits and in distinguishing between functions of various members of a biological pathway. The are also useful in antisense therapy. The present sequence is an antisense oligo targetted to human TRIPE DNA. This oligo is used in the exemplification of the invention
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/note= "Phosphorothioate backbone, All cytidine residues
are 5-methylcytidines"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour; OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis; inflammation; therapy; hyperproliferative disorder; infection; cancer; chromosome 7q22; ZRP-1; phosphorothioate; ss.
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/mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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                                                                                                                                      1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; ative 0; Mismatches 0; Indels
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                                                                                                           Sequence 20 BP; 1 A; 5 C; 9 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                     259 CACGGAGCAGCACTCCAGCC 278
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/mod_base= OTHER
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1es 20; Conservative
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ACC82916/0
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expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22. Antisense compounds of the invention are useful for modulating the expression of TRIP6 and for treating diseases or conditions associated with the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as research reagents and kits and in distinguishing between functions of various members of a biological pathway. The are also useful in antisense therapy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention
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/note= "Phosphorothioate backbone; All cytidine residues
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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16. .20
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/mod_base= OTHER
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                                                                                    The invention relates to antisense compounds targetted to a nucleic acid encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and zyxin-related protein-1 (ORP-1). TRIP6 DNA is located on chromosome 7q22. Antisense compounds of the invention are useful for modulating the expression of TRIP6 and for treating diseases or conditions associated with the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as tesearch reagents and kits and in distinguishing between functions of various members of a biological pathway. The are also useful in antisense therapy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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                              Claim 3; Page 77; 111pp; English.
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                                 New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.
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/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
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'note= "2'-methoxyethyl (2'-MOE) nucleotides'
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Pred. No. 1.6e+02;
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                                                                                                   Claim 3; Page 77; 111pp; English.
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WPI; 2003-430662/40.
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The invention relates to antisense compounds targetted to a nucleic acid encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and Jayxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22. Antisense compounds of the invention are useful for modulating the expression of TRIP6 and for treating diseases or conditions associated with the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as research reagents and kits and in distinguishing between functions of various members of a biological pathway. The are also useful in antisense therapy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention
                                                                                                                                                                                                                                                                          New antisense oligonucleotides targeted to nucleic acids encoding thyroid
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
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100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0; Indels
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/note= "Phosphorothioate backbone, All cytidine residues
are 5-methylcytidines"
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
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Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0;
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The invention relates to antisense compounds targetted to a nucleic acid encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its expression. TRIP6 is also known as OPA-interacting protein-1 (OID-1) and zyxin-related protein-1 (ORP-1). TRIP6 DNA is located on chromosome 7q22. Antisense compounds of the invention are useful for modulating the expression of TRIP6 and for treating diseases or conditions associated with the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as research reagents and kits and in distinguishing between functions of various members of a biological pathway. The are also useful in antisense therapp. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention
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/note= "Phosphorothioate backbone, All cytidine residues
are 5-methylcytidines"
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                               /note= "2'-methoxyethyl (2'-MOE) nucleotides"
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100.0%; Pred. No. 1.6e+02;
vative 0; Mismatches 0; Indels
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The invention relates to antisense compounds targetted to a nucleic acid encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22. Antisense compounds of the invention are useful for modulating the expression of TRIP6 and for treating diseases or conditions associated with the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as research reagents and kits and in distinguishing between functions of various members of a biological pathway. The are also useful in antisense therapy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                  New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
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/note= "2'-methoxyethyl (2'-MOE) nucleotides'
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Pred. No. 1.6e+02;
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New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.
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                                                                                                                                                   /note= "Phosphorothioate backbone; All cytidine residues are 5-methylcytidines"
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16. 20
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100.0%; Pred. No. 1.6e+02;
iive 0; Mismatches 0; Indels
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                                                                 Location/Qualifiers
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/mod_base= OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.
           /mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
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/*tag= b
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/note= "2' -methoxyethyl (2'-MOE) nucleotides"
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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100.0%; Pred. No. 1.6e+02;
ative 0; Mismatches 0;
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Best Loca Matches

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Gaps ö us10008789-3.rng

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The invention relates to antisense compounds targetted to a nucleic acid encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its expression. TRIP6 is also known as OPA-interacting protein-1 (OID-1) and zyxin-related protein-1 (ORP-1). TRIP6 DNA is located on chromosome 7q22. Antisense compounds of the invention are useful for modulating the expression of TRIP6 and for treating diseases or conditions associated with the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as research reagents and kits and in distinguishing between functions of various members of a biological pathway. The are also useful in antisense therapy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention
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                 OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis; inflammation; therapy; hyperproliferative disorder; infection; cancer; chromosome 7q22; ZRP-1; phosphorothloate; ss.
antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
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                                                                                           Homo sapiens.
Synthetic.
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are 5-methylcytidines"

modified base

/*tag= b /mod_base= OTHER

Location/Qualifiers 1..20

Key modified_base

sapiens

Synthetic

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*tag=

/note= "2'-methoxyethyl (2'-MOE) nucleotides"

/*tag= c /mod_base= OTHER

modified base

05-NOV-2002; 2002WO-US035479 08-NOV-2001; 2001US-00008789

WO2003040328-A2

15-MAY-2003

(ISIS-) ISIS PHARM INC

WPI; 2003-430662/40.

Bennett CF,

/note= "2'-methoxyethyl (2'-MOE) nucleotides¹ 16. .20

Human, antisense, thyroid hormone receptor interactor 6, TRIP6, tumour, OPA-interacting protein-1, OIP-1, zyxin-related protein-1, prophylaxis, inflammation, therapy, hyperproliferative disorder, infection, cancer; chromosome 7q22; ZRP-1, phosphorothioate; ss.

Human TRIP6 antisense oligonucleotide ISIS #198796.

(first entry)

27-AUG-2003

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100.0%; Pred. No. 1.6e+02;
ive 0; Mismatches 0; Indels
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Query Match Best Local Similarity

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899 20

CCCTGAGCCAGCCTCCAGAG 1

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ACC82924 standard; DNA; 20 BP

ACC82924;

ACC82924/ ID ACC8: XX AC ACC8:

Score 20; DB 1; Length 20; Pred. No. 1.6e+02;

New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.

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The invention relates to antisense compounds targetted to a nucleic acid encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22. Antisense compounds of the invention are useful for modulating the expression of TRIP6 and for treating diseases or conditions associated with the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as tresearch reagents and kits and in distinguishing between functions of various members of a biological pathway. The are also useful in antisense therapy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention
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/note= "Phosphorothioate backbone, All cytidine residues
                                                                                                                                                                             Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour; OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis; inflammation; therapy; hyperproliferative disorder; infection; cancer; chromosome 7q22; ZRP-1; phosphorothioate; ss.
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16. .20
/*tag= c
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                                                                                                                                          Human TRIP6 antisense oligonucleotide ISIS #198803.
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/mod_base= OTHER
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                                     ACC82931 standard; DNA; 20 BP
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                                                                       ACC82931;
RESULT 224
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New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.
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                                                                                                                                                                                                                                                                                                                                              Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour; OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis; inflammation; therapy; hyperproliferative disorder; infection; cancer; chromosome 7q22; ZRP-1; phosphorothioate; ss.
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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    GTGAGAATTGTTGCTCTGGA 1424
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                    GIGAGAATIGITGCTCTGGA 1
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                                                                                                           ACC82932 standard; DNA; 20
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/*tag= b
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                                                                                                                                                                                                                                                                                                                             /note= "Phosphorothioate backbone; All cytidine residues
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
         Length 20;
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  DB 1; Le...
                                                                                                                                                                                 Human TRIP6 antisense oligonucleotide ISIS #198809.
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       1.1%; Score 20; DB
100.0%; Pred. No. 1.6
:ive 0; Mismatches
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                                                1410 AATTGTTGCTCTGGATCGAA 1429
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                                                            20 AATTGTTGCTCTGGATCGAA 1
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        Query Match
Best Local
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various members of a biological pathway. The are also useful in antisense therapy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention
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/mod_base= OTHER
/mode= "2'-methoxyethyl (2'-MOE) nucleotides".
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/mod base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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                                                                                                                            Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 U; 0 Other;
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expression of TRIP6 and for treating diseases or conditions associated with the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as research reagents and kits and in distinguishing between functions of various members of a biological pathway. The are also useful in antisense therapy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
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Pred. No. 1.6e+02;
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                                                                                                                                      Sequence 20 BP; 3 A; 7 C; 8 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                 152 TCCAGGCCATGTCGGGGCCC 171
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/mod_base= OTHER
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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100.0%; Pred. No. 1.6e+02;
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                                                                                                                                                                                                                            Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACC82930;
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                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 229
ACC82930/c
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Best Local Similarity 100.
Matches 20; Conservative
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ACC82944/C
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The invention relates to antisense compounds targetted to a nucleic acid encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22. Antisense compounds of the invention are useful for modulating the expression of TRIP6 such as hyperproliferative disorders (e.g. with the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as tresearch reagents and kits and in distinguishing between functions of various members of a biological pathway. The are also useful in antisense therapy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention
                                                                                                                                 New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
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note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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100.0%; Pred. No. 1.6e+02;
ive 0; Mismatches 0; Indels
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/mod_base= OTHER
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Chomosome 7q22; ZRP-1; phosphor
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Matches 20; Conservative
Dobie K;
                                                                        WPI; 2003-430662/40.
Bennett CF,
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                                                                                                                                                                   The invention relates to antisense compounds targetted to a nucleic acid encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its expression. TRIP6 is also known as OpA-interacting protein-1 (OIP-1) and zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22. Antisense compounds of the invention are useful for modulating the expression of TRIP6 and for treating diseases or conditions associated with the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as tresearch reagents and kits and in distinguishing between functions of various members of a biological pathway. The are also useful in antisense therapy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention
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hormone receptor interactor 6, useful for diagnosing or treating
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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100.0%; Pred. No. 1.6e+02;
cive 0; Mismatches 0; Indels
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                                  hyperproliferative disorders, such as cancer
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                                                                                                          Page 77; 111pp; English
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RESULT 233
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                                                                                                     New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.
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/note= "2'-methoxyethyl (2'-MOE) nucleotides
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                                                                                                                                                  Claim 3; Page 77; 111pp; English.
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                                 (ISIS-) ISIS PHARM INC
                                                          Dobie K;
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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ACC82895/c
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y 100.0%; Pred. No. 1...
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ACC82950/c
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chromosome 7g22; ZRP-1; phosphorothioate; ss.

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                                                     /note= "Phosphorothioate backbone; All cytidine residues are 5-methylcytidines"
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cocation/Qualifiers
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/mod base= OTHER
                                        mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 76; 111pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 GCACACGCAGGGGCTCCCTG 1
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ID ACC82908 Standard; DNA; 20 BP
XX
XX
ACC82908;
XX
DT 27-AUG-2003 (first entry)
DE Human TRIP6 antisense oligonu
XX
XX
W Human; antisense; thyroid hor
XW OPA-interacting protein-1; Oli
XW inflammation; therapy; hyperp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.
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                                                                                                                                                                   /mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
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/mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                           are 5-methylcytidines"
                                                                                 Location/Qualifiers
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Homo sapiens
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                             Synthetic.
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ACC82927/c
-ID. ACC829;
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AC ACC829;
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DT 27-AUG.
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us10008789-3.rng

ACC82934;

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New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.
                                                                                                                                          /mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
                     Human; antisense; thyroid hormone receptor interactor 6; TRIF6; tumour; OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis; inflammation; therapy; hyperproliferative disorder; infection; cancer; chromosome 7q22; ZRP-1; phosphorothioate; ss.
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
                                                                                                                                                                                                                                                      /note= "2'-methoxyethyl (2'-MOE) nucleotides"
Human TRIP6 antisense oligonucleotide ISIS #198799.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 15; Page 77; 111pp; English.
                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                           base= OTHER
                                                                                                                                                                                                                                                                                                                     05-NOV-2002; 2002WO-US035479.
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                                                                          sapiens
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                                                                                       Synthetic.
                                                                           Homo
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The invention relates to antisense compounds targetted to a nucleic acid encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its expression. TRIP6 is also known as OPA-interacting protein-1 (OID-1) and zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22. Antisense compounds of the invention are useful for modulating the expression of TRIP6 such as Merporproliferative disorders (e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as tesearch reagents and Kits and in distinguishing between functions of various members of a biological pathway. The are also useful in antisense therapy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention

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Gaps
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Score 20; DB 1; Length 20;
Pred. No. 1.6e+02;
                       Indels
        100.0%; Preq. ....
                                              1367 GIGGGCCATAATGCCTGAG 1386
           Local Similarity 100.
nes 20; Conservative
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              Best Loca
Matches
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Gaps

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1427 GAAGTTTTCACATTGGCTGT 1446

Conservative

20;

Matches

Query Match Best Local Similarity

20 GAAGTTTTCACATTGGCTGT

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ACC82934 standard; DNA; 20
RESULT 238
             ACC82934/
ID ACC8
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New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.
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                                                                                                                                                                                                                                                                                   /*tag= a
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                                                                                                             Human, antisense, thyroid hormone receptor interactor 6, TRIP6, tumour, OPA-interacting protein-1, OIP-1, zyxin-related protein-1, prophylaxis, inflammation, therapy, hyperproliferative disorder, infection, cancer,
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/mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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100.0%; Pred. No. 1.6e+02;
ive 0; Mismatches 0; Indels
                                                                                Human TRIP6 antisense oligonucleotide ISIS #198806.
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                                                                                                                                                                  chromosome 7q22; ZRP-1; phosphorothioate; ss
                                                                                                                                                                                                                                                                                                                                    are 5-methylcytidines'
                                                                                                                                                                                                                                                  Location/Qualifiers
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1712 GAAATAATAATCCCTCGAGT 1731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.
                                                                                                                                                                                                                                                                                                                                                                             /mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
                                                                                                                                                                                             Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour; OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis; inflammation; therapy; hyperproliferative disorder; infection; cancer; chromosome 7q22; ZRP-1; phosphorothioate; ss.
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                                                                                                                                                                Human TRIP6 antisense oligonucleotide ISIS #198826.
                                                                                                                                                                                                                                                                                                                                                                                                              are 5-methylcytidines"
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                                                                   ACC82954 standard; DNA; 20
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                                   RESULT 239
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                                                    ACC82954
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Length 20;

1.1%; Score 20; DB 1; Le 100.0%; Pred. No. 1.6e+02;

Best Local Similarity

Query Match

Sequence 20 BP; 5 A; 3 C; 4 G; 8 T; 0 U; 0 Other;

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The invention relates to antisense compounds targetted to a nucleic acid encoding thyroid hormone receptor interactor 6 (TRIB6) to inhibit its expression. TRIP6 is also known as OpA-incracting protein-1 (OIP-1) and syxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22. Antisense compounds of the invention are useful for modulating the expression of TRIP6 and for treating diseases or conditions associated with the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as research reagents and kits and in distinguishing between functions of various members of a biological pathway. The are also useful in antisense therapy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.
                                                                                                                                                                                                                                                                                                                                                                                                  /mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
                                                                                                                                                                                                                Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour; OPA-linteracting protein-1; OIP-1; zyxin-related protein-1; prophylaxis; inflammation; therapy; hyperproliferative disorder; infection; cancer; chromosome 7q22; ZRP-1; phosphorothioate; ss.
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16. 20
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                                                                                                                                                                                 Human TRIP6 antisense oligonucleotide ISIS #198766.
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GAAATAATAATCCCTCGAGT
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/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
                                                                                                                                                                                                                           Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour; OPA-interacting procein-1; OIP-1; zyxin-related protein-1; prophylaxis; inflammation; therapy; hypertproliferative disorder; infection; cancer; chromosome 7q22; ZRP-1; phosphorothioate; ss.
                                                  Gaps
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
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                           Score 20; DB 1; Length 20;
Pred. No. 1.6e+02;
                                                 Indels
                                                                                                                                                                                                        Human TRIP6 antisense oligonucleotide ISIS #198786.
         C; 8 G; 5 T; 0 U; 0 Other;
                                   100.0%; Preα. ....
tive 0; Mismatches
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                                                                     381 ACTCCAGCACACGCAGGGGC 400
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                                                                                                                                           ACC82914 standard; DNA; 20
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         Sequence 20
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                                                                                                                                                               ACC82914;
                            Query Match
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to prevent or delay infection, inflammation or tumour formation, as research reagents and kits and in distinguishing between functions of various embers of a biological pathway. The are also useful in antisense therapy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention
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'note= "Phosphorothioate backbone; All cytidine residues
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Pred. No. 1.6e+02;
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/note= "2'-methoxyethyl (2'-MOE)
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100.0%; Pred. No. 1...
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/mod base=
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Exyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7g22. Antisense compounds of the invention are useful for modulating the expression of TRIP6 and for treating diseases or conditions associated with the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for disonseits, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as research reagents and kits and in distinguishing between functions of various members of a biological pathway. The are also useful in antisense therapy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention
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/note= "Phosphorothioate backbone, All cytidine residues
are 5-methylcytidines"
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/mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. 20
/*tag= c
/mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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100.0%; Pred. No. 1.6e+02;
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nes 20; Conservative
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                           The invention relates to antisense compounds targetted to a nucleic acid encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and yayin-related protein-1 (OIP-1) and Antisense compounds of the invention are useful for modulating the expression of TRIP6 and for treating diseases or conditions associated with the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as research reagents and kits and in distinguishing between functions of various members of a biological pathway. The are also useful in natisense therapy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention
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/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
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100.0%; Pred. No. 1.6e+02;
ive 0; Mismatches 0; Indels
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1. .20
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Claim 3; Page 77; 111pp; English.
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Matches 20; Conservative
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Homo sapiens
                                                  27-AUG-2003
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                                                                Synthetic.
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/*tag= c
/mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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                              Bennett CF,
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ACC82933/c
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                                                                                                       The invention relates to antisense compounds targetted to a nucleic acid encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and zyxin-related protein-1 (ZRP-1). TRIP6 DNI a located on chromosome 7q22. Antisense compounds of the invention are useful for modulating the expression of TRIP6 and for treating diseases or conditions associated with the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as research reagents and kits and in distinguishing between functions of various members of a biological pathway. The are also useful in antisense therapy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention
             New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.
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/note= "Phosphorothioate backbone; All cytidine residues
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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Pred. No. 1.6e+02;
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100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                           788 GCCTGCTATAGGAGCCAG 807
                                                                            Claim 3; Page 76; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 GGCCTGGCTATAGGAGCCAG 1
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                                                                                                                                                                                                                      nucleic acids encoding thyroid
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/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
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/mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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100.0%; Pred. No. 1.6e+02;
ive 0; Mismatches 0; Indels
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1es 20; Conservative
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(ISIS-) ISIS PHARM INC.
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                                                                                                                           New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.
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16. .20
                                                                                                                                                                                                                                                                                                                                                                                      Score 20; DB 1; Length 20;
Pred. No. 1.6e+02;
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/mod_base= OTHER
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/mod_base= OTHER
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            05-NOV-2002; 2002WO-US035479
                                  08-NOV-2001; 2001US-00008789
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                                                        (ISIS-) ISIS PHARM INC
                                                                               Dobie K;
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The invention relates to antisense compounds targetted to a nucleic acid encoding thyroid hormone receptor interactor 6 (TRIF6) to inhibit its expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22. Antisense compounds of the invention are useful for modulating the expression of TRIP6 and for treating diseases or conditions associated with the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as research reagents and kits and in distinguishing between functions of various members of a biological pathway. The are also useful in antisense therapy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention
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    /*tag= a
    /mod base= OTHER
    /note= "Phosphorothioate backbone; All cytidine residues are 5-methylcytidines"
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
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/mod_base= OTHER /note= "2'-methoxyethyl (2'-MOE) nucleotides" 16. .20

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The invention relates to antisense compounds targetted to a nucleic acid encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22. Antisense compounds of the invention are useful for modulating the expression of TRIP6 and for treating diseases or conditions associated with the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as tressearch reagents and kits and in distinguishing between functions of various members of a biological pathway. The are also useful in antisense therapy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention
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                                                                                        /note= "2'-methoxyethyl (2'-MOE) nucleotides"
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100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0; Indels
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                                                                        /mod_base= OTHER
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les 20; Conservative
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Matches
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   /note= "Phosphorothioate backbone; All cytidine residues are 5-methylcytidines"
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/*tag= b
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                                                                                   /mod_base= OTHER
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                                                                                                   /mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
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                                            Location/Qualifiers
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are 5-methylcytidines"
OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis; inflammation; therapy; hyperproliferative disorder; infection; cancer; chromosome 7q22; ZRP-1; phosphorothioate; ss.
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Human, antisense, thyroid hormone receptor interactor 6, TRIF6, tumour; OPA-interacting protein-1, OIP-1, zyxin-related protein-1, prophylaxis; inflammation; therapy; hyperproliferative disorder; infection; cancer; chromosome 7q22; ZRP-1; phosphorothioate; ss.
                                                                                                          Human TRIP6 antisense oligonucleotide ISIS #198785.
ACC82913 standard; DNA; 20 BP.
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                                                   Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour; OPA-linteracting protein-1; OIP-1; zyxin-related protein-1; prophylaxis; inflammation; therapy; hyperproliferative disorder; infection; cancer; chromosome 7q22; ZRP-1; phosphorothioate; ss.
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                                                                                                                                                                                                  Key
modified_base
                                                                                                                                                                                                                                                                                                             modified_base
                                                                                                                                                                                                                                                                                                                                                                                   modified base
                                                                                                                                              варіепв.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bennett CF,
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                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Dobie K;

/mod_base= OTHER /note= "Phosphorothioate backbone; All cytidine residues are 5-methylcytidines"

Location/Qualifiers 1..20 /*tag= a

/mod_base= OTHER /note= "2'-methoxyethyl (2'-MOE) nucleotides"

*tag= b

/note= "2'-methoxyethyl (2'-MOE) nucleotides"

/*tag= c
/mod base= OTHER

16. .20

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                                                                                                                                                                                                                                                                                                                                                            The invention relates to antisense compounds targetted to a nucleic acid encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22. Antisense compounds of the invention are useful for modulating the expression of TRIP6 and for treating diseases or conditions associated with the expression of TRIP6 such as hyperpoliferative disorders (e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as research reagents and kits and in distinguishing between functions of various members of a biological pathway. The are also useful in antisense therapy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention
                                                                                   New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 1.1%; Score 20; DB 1; Length 20; Similarity 100.0%; Pred. No. 1.6e+02; 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 BP; 2 A; 8 C; 8 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                  Example 15; Page 77; 111pp; English.
WPI; 2003-430662/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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RESULT 253

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The invention relates to antisense compounds targetted to a nucleic acid encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22 Antisense compounds of the invention are useful for modulating the expression of TRIP6 and for treating diseases or conditions associated with the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as tesearch reagents and kits and in distinguishing between functions of various members of a biological pathway. The are also useful in antisense therapy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                            /mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
                                                                                                                                                                                                                                     Human; antisense; thyroid hormone receptor interactor 6; TRIF6; tumour; OPA-lineracting protein-1; OIP-1; zyxin-related protein-1; prophylaxis; inflammation; therapy; hyperproliferative disorder; infection; cancer; chromosome 7q22; ZRP-1; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note = "2'-methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "2'-methoxyethyl (2'-MOE) nucleotides"
                                                                                                                                                                                                       Human TRIP6 antisense oligonucleotide ISIS #198787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 20 BP; 3 A; 7 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 15; Page 77; 111pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mod_base= OTHER
ACC82915 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-NOV-2001; 2001US-00008789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-NOV-2002; 2002WO-US035479
                                                                                                                                                                       27-AUG-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                              *tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *tag= b
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                                                                                                                                                                                                                                                                                                                                                                                         modified_base
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                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                      ACC82915;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to antisense compounds targetted to a nucleic acid encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its expression. TRIP6 is also known as OPA-Interacting protein-1 (OIP-1) and zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22. Antisense compounds of the invention are useful for modulating the expression of TRIP6 and for treating diseases or conditions associated with the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as research reagents and kite and in distinguishing between functions of various members of a biological pathway. The are also useful in antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                 Human, antisense; thyroid hormone receptor interactor 6; TRIP6; tumour; OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis; inflammation; therapy; hyperproliferative disorder; infection; cancer; chromosome 7q22; ZRP-1; phosphorothioate; ss.
                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
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 Length 20;
                                  Indels
                                                                                                                                                                                                                                                                                    Human TRIP6 antisense oligonucleotide ISIS #198814.
1.1%; Score 20; DB 1; Le
100.0%; Pred. No. 1.6e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                   GCTACGTGGCCACCCTGGAG 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= c
/mod_base= OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mod_base= OTHER
                                                                                                    GCTACGTGGCCACCCTGGAG 1
                                                                                                                                                                                     BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-NOV-2001; 2001US-00008789
                                                                                                                                                                                     ACC82942 standard; DNA; 20
                                                                                                                                                                                                                                                   (first entry)
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                                    Conservative
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/*tag=
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                   Local Similarity
les 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003040328-A2.
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modified_base
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                                                                                                                                                                                                                                                     27-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
   . Query Match
Best Local Si
Matches 20;
                                                                                                                                                                                                                    ACC82942;
                                                                      1151
                                                                                                    20
                                                                                                                                                                     ACC82942/
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Chiral; phosphorothioate; oligonucleotide synthesis; enantiomer; ss.

Phosphorothioate 20-mer oligonucleotide #1.

(first entry)

08-APR-2003

ABZ22916;

/note= "phosphorothioate linkages"

13-JUN-2002; 2002WO-US018581. 14-JUN-2001; 2001US-00881535.

WO2002102815-A2.

27-DEC-2002

(ISIS-) ISIS PHARM INC

WPI; 2003-157021/15.

Ravikumar VT;

/*tag= a /mod_base= OTHER

. .20 *tag=

Key modified base

Synthetic

Location/Qualifiers

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ABZ22916/c
ID ABZ22916 standard; DNA; 20 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is an example of nucleic acid probes of the invention. The probe may be doubly labelled with non-identical covalently attached dyes, e.g. the fluorescent intercalator ethidium, which serves as the detector dye and the fluorescent dye fluorescent, which serves as the donor dye of a fluorescent resonance energy transfer (FRET) system. A bifunctional linker was used to attach the dyes to the oligonucleotide. The probe generates a fluorescent signal upon hybridisation to a complementary nucleic acid based on the interaction of the intercalator with the formed double-stranded DNA. Nucleic acid probes of the invention can be used in homogeneous assays, real-time PCR monitoring,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detection or quantification of nucleic acid analyte, by hybridizing a nucleic acid probe having non-identical covalently attached dyes, with nucleic acid analyte, and measuring change in fluorescence of the probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transcription assays, expression analysis on nucleic acid microarrays and other microarray applications such as genotyping
 therapy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention
                                                                                Gaps
                                                                                ;
                                                      1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
                                  Sequence 20 BP; 3 A; 7 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 9; Page 32; 110pp; English.
                                                                                                     1543 GCCTGGCGCATCCAGGAGCT 1562
                                                                                                                                                                                                                                                                          Probe; nucleic acid detection; ss.
                                                                                                                          20 GCCTGGCGCATCCAGGAGCT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                     Wolter A;
                                                                                                                                                                                   뮵
                                                                                                                                                                                                                                                                                                                                                                  21-OCT-2002; 2002WO-US033699
                                                                                                                                                                                                                                                                                                                                                                                        19-OCT-2001; 2001US-0336432P
                                                                                                                                                                                  ACC58867 standard; DNA; 20
                                                                   Local Similarity 100.0
tes 20; Conservative
                                                                                                                                                                                                                               08-SEP-2003 (first entry)
                                                                                                                                                                                                                                                    Doubly labelled DNA probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-505122/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Davies M,
                                                                                                                                                                                                                                                                                                                                                                                                               (PROL-) PROLIGO LLC
                                                                                                                                                                                                                                                                                                                      WO2003043402-A2
                                                                                                                                                                                                                                                                                                                                             30-MAY-2003.
                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                        ACC58867;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Bruce I,
                                                        Query Match
                                                                             Matches
                                                                                                                                                             RESULT 256
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Preparing internucleotide phosphorothioate linkage enhanced in Sp/Rp enantiomer, by coupling a synthon with 2'-substituted nucleoside in presence of coupling agent having a pKa that enhances linkage in Sp/Rp

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The present invention describes a method (MI) for preparing an internucleotide phosphorothioate linkage enriched in the Sp or Rp cantioner between a synthon having a hydroxyl moiety at the Sp or Rp and 2'-substituted nucleoside having an activated phosphate moiety at the 3'-position, comprising coupling a synthon with a 2'-substituted nucleoside having an activated phosphate moiety at the 3'-position, comprising coupling a synthon with a 2'-substituted to enhance of the runcleoside in the presence of coupling agent that is selected to enhance internucleotide linkages that is enhanced in the Sp or Rp enantiomer. The internucleotide linkages that is enhanced in the Sp or Rp enantiomer, which involves providing a nucleotide having a hydroxyl moiety at the 5'-position or a growing oligonucleotide having a hydroxyl moiety at the 3'-position in the presence of the coupling agent, and repeating the coupling step until the desired number of linkages is established. The coupling step until the desired number of linkages that is enhanced in the Sp enantiomer is further processed to include another condoner. Oligonucleotide linkages that is enhanced in the Sp and/or Rp enantiomer. Oligonucleotides prepared by the method lead to improved drugs, diagnostics and research reagents. The presents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ugs, diagnostics and research reagents. The present sequence represents oligonucleotide used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
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                                                                          Example 1; Page 31; 65pp; English.
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tes 20; Conserv
enantiomer.
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Matches
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Gaps

; 0

1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; tive 0; Mismatches 0; Indels

1736 AAAAAAAAAAAAAAAA 1755

20; Conservative

Matches

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Local Similarity

Query Match

20 AAAAAAAAAAAAAAAA 1

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The invention relates to a method of detecting a nucleic acid having two portions. The method involves providing nanoparticles having coligonuclectides attached to it which has a sequence complementary to oligonuclectides attached to it which has a sequence complementary to agounclectides attached to it which has a sequence complementary to anoparticles to allow hybridisation of oligonuclectides with two or more portions of nucleic acid and observing a detectable change brought about by hybridisation. The method and aggregate probes are useful for detecting two or more nucleic acids (from a biological source) having at least two portions such as viral RNA, bacterial or fungal DNA, a gene synthetic RNA or DNA, or synthetic or structurally modified natural or synthetic and for preparing a nanoprobe conjugate for detecting an analyte and for detecting a nucleic acid bound to exparating a selected nucleic acid having two portions from other nucleic acids. The present sequence is an oligo used to illustrate the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detecting nucleic acid having two portions, by providing nanoparticles having oligonucleotides attached to it, contacting nucleic acid and nanoparticles to allow hybridization, and observing detectable change.
                                                                                                           Thiol-modified oligo #4 used in the nucleic acid detection method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                               Nucleic acid detection; fabrication; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 18; Page 179; 467pp; English
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AAL61645 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                 09-OCT-2001; 2001US-0327864P.
                                                                                                                                                                                                                                                                                             08-OCT-2002; 2002WO-US032088
                                                                      (first entry)
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Best Local Similarity 100.
Matches 20, Conservative
                                                                                                                                                                                                                                                                                                                                                                                       (NANO-) NANOSPHERE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-430409/40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the invention
                                                                      22-SEP-2003
                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                                                          01-MAY-2003
                                    AAL61645;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 259
ABZ59815/c
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The invention relates to DNA sequences (I) that encode six specific plant proteins: (i) a protein (ABB60425) with mitochondrial carrier protein cativity (IIa); (ii) a protein (ABB60427) with renegeran binding protein activity (IIb); (iii) a protein (ABB60429) with receptor-like protein kinase activity (IIc); (iv) a protein (ABB60429) with non-long carrier troelement reverse transcriptase activity (IIe); or a protein (ABB60429) with non-long terminal repeat retroelement reverse transcriptase activity (IIe); or (vi) a protein (ABB60430) with helicase activity (IIf). (I), also related sequences, derived ribozymes and antisense sequences, expression vectors, encoded proteins and antibodies activity (IIf). (I), also related plants with altered properties, including tolerance of overwatering. The antibodies are also used for isolation of the proteins and in minon inmunoassays. Also (I) or their primer or probe fragments are used to seven for terminators and constitutively, aerobically or anaerobically inducible plant promoters, specifically for use in potatoes and the sequence that encodes (IId) is used to alter the translation profile in plants. Since (I) are derived from potato, their promoters and incompanies are specificity and inducibility, and can also be used to improved tissue specificity and inducibility, and can also be used to control endogenous genes. The present sequence is that of a PCR primer used in the first strand synthesis of cDNAs derived from Potato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New DNA sequences from potato, useful for producing plants with altered properties, e.g. tolerance of flooding, also related proteins, antibodies
               Potato; plant; mitochondrial carrier protein; elongation factor EF-2; transferrin binding protein; receptor-like protein kinase; halicase; non-long terminal repeat retroelement reverse transcriptase; overwatering; transgenic; reverse transcriptase; primer; ss.
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human immunodeficiency virus infection; hepatitis virus infection;
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                                                                                                                                                                                                                                                                                                                                         (MPBC-) MPB COLOGNE GMBH MOLECULAR PLANT & PROTE.
                                                                                                                                                                                                                                                                                                                                                                                 Haussuehl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thio-modified 20dA oligonucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sxample 1; Page 8; 26pp; German.
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                                                                                                                                                                                                                                                        22-MAR-2001; 2001DE-01014063.
                                                                                                                                                                                                                                                                                                  22-MAR-2001; 2001DE-01014063.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and inhibitory sequences.
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                                                                                                                                                                                                                                                                                                                                                                                   Tscharntke M,
                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-041808/04.
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                                                                                                                                                                    DE10114063-A1.
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                                                                                                                                                                                                              10-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                   Buelow L,
                                                                                                                               Synthetic
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ABX79181
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Gaps

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ABZ59815 standard; RNA; 20 BP

ABZ59815;

BXAXEXB

Potato gene PCR primer dT20. 01-APR-2003 (first entry)

(first entry)

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JS2002155462-A1
                      29-JAN-1999;
                   29-JUL-1996;
                     11-JUL-1997;
             24-OCT-2002.
                                 Mirkin CA,
       Synthetic.
                                  Taton TA;
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The invention relates to detecting a nucleic acid (NA) having at least 2 cutached to oligonucleotides (N) (0) on each NP has a sequence complementary to sequence of at least 2 portions of NA), contacting NA and NP to allow hybridisation of (0) on NP with 2 or more portions of NA, condecting NA and NP to allow hybridisation of (0) on NP with NA. The nanoparticle is useful for separating a selected on NP with NA. The nanoparticle is useful for separating a selected on NP with NA. The nanoparticle is useful for separating a selected oncleic acid having at least 2 portions. The method of for detecting nucleic acids and the nucleic acid having at least 2 portions. The method of seaful for detecting on the nucleic acids of disease and in sequencing of nucleic acids for used for diagnosis of disease and in sequencing of nucleic acids for preferably, the method is useful for detecting nucleic acids for diagnosis and/or monitoring of viral diseases (human immunodeficiency virus), begatitis virus, herpes virus, cytomegalovirus and Epstein-Barr virus, hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr virus, begatitis virus, sexually transmitted diseases, inherited diseases, in DNA sequencing for patentity testing, for cell line authentication and for monitoring gene therapy. The method is useful in research and analytical laboratories in DNA sequencing and in the field to detect the presence of specific pathogens. Detecting nucleic acide based on observing a colour change with the naked eye is cheap, easily mean analytical laboratories in DNA sequencing and in the field based to detect the method of the invention

Seguence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

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      Length 20;
                          0; Indels
      Score 20; DB 1; L. Pred. No. 1.6e+02;
1.1%; Sco...
100.0%; Pred. No. ...
0; Mismatches
                          20; Conservative
                Local Similarity
       Query Match
                          Matches
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ABX92177 standard; DNA; 20 ABX92177 RESULT 261 ABX9217

ВЪ.

sequencing; viral infection; human immunodeficiency virus; HIV; hepatitis virus; herpes virus; cytomegalovirus; Epstein-Barr virus; bacterial infection; sexually transmitted disease; inherited disorder; forensic; paternity testing; cell line authentication; gene therapy; ss. Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R; Nonoparticle; nucleic acid detection; hybridisation; diagnosis; Nanoparticle-associated oligonucleotide SEQ ID 55. 28-SEP-2001; 2001US-00967409 (NANO-) NANOSPHERE INC. US2002155458-A1. 26-APR-2000; 26-JUN-2000; 12-MAY-2003 29-JUL-1996; 21-JUL-1997; 29-JAN-1999; 24-OCT-2002 25-JUN-1999 Synthetic. Taton TA; herpes virus infection; cytomegalovirus infection; forensic science; Epstein-Bart virus infection; bacterial disease; gene therapy; sexually transmitted disease; inherited disorder; DNA sequencing; paternity testing; cell line authentication. Detecting nucleic acids having at least 2 portions comprises use of nanoparticles which have oligonucleotides attached to them that are complementary to portions of the nucleic acid sequence. Mucic RC, Storhoff JJ, Elghanian R; Example 18; Page 44; 130pp; English 96US-0031809P. 97WO-US012783. 99US-00240755. 25-JUN-1999; 99US-00344667. 26-APR-2000; 2000US-0200161P. 26-JUN-2000; 2000US-00603830. 12-OCT-2001; 2001US-00976577 Letsinger RL, (NANO-) NANOSPHERE INC. WPI; 2003-198491/19.

ğ Detecting nucleic acids having at least two portions involves use of nanoparticles which have oligonucleotides attached to them that are complementary to portions of the nucleic acid sequence. WPI; 2003-182627/18.

97WO-US012783. 99US-00240755. 99US-00344667. 2000US-0200161P.

96US-0031809P.

Disclosure; Page 59; 130pp; English.

method of the invention

Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Gaps ö 1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; tive 0; Mismatches 0; Indels 20; Conservative Query Match Best Local Similarity Matches 20; Conserva

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1736 AAAAAAAAAAAAAAAAA 1755

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Synthetic.
                                   invention
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                                                                                                   Query Match
                                                                                                                     Local
                                                                                                                                                                                                                                                      RESULT 263
                                                                                                                                   Matches
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88888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to a novel method for detecting a nucleic acid having 2 portions. The method comprises providing nanoparticles having oligonucleotides attached, where the oligonucleotide on each nanoparticle has a sequence complementary to a sequence of 2 portions of nucleic acid and nanoparticle are contacted to allow hybridisation of the nucleic acid and observing a detectable change brought about by the nucleic acid and observing a detectable change brought about by the nucleic acid having 2 portions. From other nucleic acids, and selected nucleic acids having 2 portions. The method of the invention is useful for separating a selected nucleic acids having 2 portions. The method of the cards having 2 portions. The method of the cards of disease and in sequencing of nucleic acids and cord diseases and in sequencing of nucleic acids for used for diseases and in sequencing of nucleic acids for categorial diseases, sexually transmitted diseases, inherited diseases, in forensics, in DNA sequencing, for paternity testing, for call since authentication, for monitoring gene therapy, etc. This method cannot a colour change with the naked eye so is cheap, fast, simple and robust, and does not require
                                                                                                                                                                                                               Nanotechnology; ss; nucleic acid detection; nanoparticle; virus detection; human immunodeficiency virus; HIV; hepatitis; herpes; cytomegalovirus; Epetein-Barr virus; bacterial disease; DNA sequencing; sexually transmitted disease; inherited disorder; forensic; paternity testing; cell line authentication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting nucleic acids having 2 portions e.g. for detecting disease, comprises use of nanoparticles which have oligonucleotides attached to them that are complementary to portions of the nucleic acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mucic RC, Storhoff JJ, Elghanian R;
                                                                                                                                                                                    Nanotechnology nucleic acid detection method associated #54
                                                                                                                                                                                                                                                                                                                                                                                                           /mod_base= OTHER
/note= "OTHER= Thiol modified"
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1 AAAAAAAAAAAAAAAA 20
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99US-00240755.
99US-00344667.
2000US-0200161P.
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                                                                               ACD27255 standard; DNA; 20
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                                                                                                                                                   15-OCT-2003 (first entry)
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26-APR-2000;
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                                                                                                                                                                                                                                                                                                                        Synthetic
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specialised expensive equipment. The present sequence represents a thiol modified oligonucleotide sequence used to demonstrate the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting nucleic acid having two portions, by providing nanoparticles having oligonucleotides attached to it, contacting nucleic acid and nanoparticles to allow hybridization, and observing detectable change, useful in forensics.
                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to a novel method for detecting nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                            Nanotechnology, nucleic acid detection; nanoparticle, ss, fo
DNA sequencing; paternity testing; cell line authentication
                                                                                                    Length 20;
                                                                                                                                    Indela
                                                                    Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                  1.1%; Score 20; DB 1; L
100.0%; Pred. No. 1.6e+02;
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/mod_base= OTHER
/note= "OTHER= Thiol modified"
                                                                                                             100.0%; Prec. ...
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29-JAN-1999; 99US-00240755.
25-JUN-1999; 99US-00340667.
26-APR-2000; 2000US-00603830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-SEP-2001; 2001US-00966312
                                                                                                                                                                                                                                                                                         ACD27125 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                    20; Conservative
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                                                                                                                    Similarity
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modified_base
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          or DNA, or a product of a polymerase chain reaction amplification. Nanoparticles and nanoparticle-oligomucleotide conjugates of the invention are useful for nanofabrication, and for separating a selected nucleic acid having two portions from other nucleic acids. The method of the invention is useful in forensics, DNA sequencing, for paternity testing, cell line authentication, and monitoring gene therapy. Diagnostic assays employing the nanoparticle-oligonucleotide conjugates of the invention improve the sensitivity of the nucleic acid detection assay. The present sequence represents a thiol modified oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detection of nucleic acid for, e.g. research and analytical laboratories in deoxyribonucleic acid sequencing, involves contacting nucleic acid with nanoparticles having oligonucleotides.
modified natural or synthetic RNA
                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                   1.1%; Score 20; DB 1; Length 20;
'100.0%; Pred. No. 1.6e+02;
rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nanoparticle; ss; nucleic acid detection; DNA sequencing;
                                                                                                                                               sequence used to demonstrate the method of the invention
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                                                                                                                                                                         Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
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/note= "OTHER= Thiol modified"
synthetic, or structurally-
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99US-00240755.
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26-APR-2000; 2000US-0200161P.
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                                                                                                                                                                                                                                                                                                                                                                   ACD27385 standard; DNA; 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pathogen detection.
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29-JAN-1999;
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Taton TA;
disease,
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ACD27385
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This invention relates to a novel method for detecting a nucleic acid by contacting a nucleic acid with at least two types of nanoparticles having oligonucleotides attached, allowing hybridisation of the oligonucleotides

Example 18; Page 43; 109pp; English.

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on the nanoparticles, and observing a detectable change. The oligonucleotides on each nanoparticle have a sequence complementary to its respective portion of the sequence of the nucleic acid to be detected. The method of the invention may bused for the detection of a nucleic acid used in, e.g. research and analytical laboratories in DNA sequencing, in the field to detect the presence of specific pathogens, in the doctor's office for quick identification of an infection to assist in prescribing a drug for treatment, and in homes and health centres for inexpensive first-line screening. The method of the invention detects nucleic acids based on observing a colour change with the naked eye. This method is cheap, fast, simple, robust and does not require specialised or expensive equipment. The present sequence represents a thiol modified oligonucleotide sequence used to demonstrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detection of nucleic acid for, e.g. research and analytical laboratories in deoxyribonucleic acid sequencing, involves contacting nucleic acid with nanoparticles having oligonucleotides.
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                                                                                                                                                                                                                                                             1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
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/mod_base= OTHER
/note= "OTHER= Thiol modified"
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99US-00240755.
99US-00344667.
2000US-0200161P.
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                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                  Query Match
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(NANO-) NANOSPHERE INC.
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modified_base
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26-JUN-2000;
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oligonucleotides, allowing hybridisation of the oligonucleotides on the nanoparticles, and observing a detectable change. The oligonucleotides on each nanoparticle have a sequence complementary to its respective portion of the sequence of the nucleic acid. The method of the invention may be used for the detection of a nucleic acid used in, e.g. research and analytical laboratories in DNA sequencing, in the field to detect the presence of specific pathogens, in the doctor's office for quick identification of an infection to assist in prescribing a drug for treatment, and in homes and health centres for inexpensive first-line screening. The inventive method of detecting nucleic acids based on observing a colour change with the naked eye are cheap, fast, simple, robust (the reagents are stable), do not require specialised or expensive equipment, and little or no instrumentation is required. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detection of nucleic acid having -2 portions used to prepare biomaterials and in nanofabrication methods, comprises providing nanoparticles, contacting nucleic acid and nanoparticles, and observing change.
                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        Nanotechnology; nucleic acid detection; nanofabrication; nanoprobe;
                                                                                                                                                                                                                                                                                                                                                                                                  Nanotechnology nucleic acid detection method oligonucleotide #54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Elghanian R;
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                                                                                                                                                                                                      Score 20; DB 1; Length 20;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mucic RC, Storhoff JJ,
                                                                                                                                                                                  Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
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/mod_base= OTHER
/note= "OTHER= Thiol modified" "
                                                                                                                                                                                                            100.0%; Pred. .v.
                                                                                                                                                             demonstrate the method of the invention
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21-JUL-1997; 97WO-US012783.
29-JAN-1999; 99US-00344667.
26-APR-2000; 2000US-0220161P.
26-JUN-2000; 2000US-0200161P.
                                                                                                                                                                                                                                                                                                                               ACD27060 standard; DNA; 20 BP.
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                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Warches 20; Conservative
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modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
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This invention relates to a novel method for detecting nucleic acide. The method comprises providing nanoparticles with oligonucleotides attached to the theory which have a sequence of two portions of nucleic acid, and observing the nucleic acid and nanoparticles to portions of nucleic acid, and observing a detectable change brought about by the hybridisation. The nucleic acid to be detected must have at least two cannoparticle-oligonucleotide conjugate binds the target benefit acid, and observing a detectable change brought about by the hybridisation. The nucleic acid to be detected must have at least two portions and the distances between these are chosen so that when the cannoparticle-oligonucleotide conjugate binds the target sequence a detectable change occurs. The method of the invention is useful for detecting two or more nucleic acids (from a biological source) having at associated with a disease, synthetic, or structurally-modified natural cor synthetic RNA or DNA, or a product of a polymerase chain reaction are useful for preparing a nanoprobe conjugate for detecting an analyte, and for detecting and nanoprobe conjugate for detecting an analyte, and for detecting and nanoprobe conjugate of the invention at useful for nanoparticle conjugates of the invention and cor nanoparticle conjugates improve the senativity of nanoparticle-oligonucleotide conjugates improve the senativity of nucleic acid detection methods and can be used to detect nucleic acids that are present in only small amounts in a sample. The invention also conjugates are the method of the invention abilities. The present sequence represents a thiol modified oligonucleotide sequence used to demonstrate the method of the invention legence of the present and prove invention and prove and prove the sequence of the present and prove the sequence of the invention and prove the sequence of the present and prove the sequence of the invention and prove the sequence of the present and prove the sequence of the invention and prove the sequence of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.1%; Score 20; DB 1; Length 20; 00.0%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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99US-00240755.
99US-00344667.
2000US-0200161P.
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This invention relates to a novel method for detecting nucleic acids. The method comprises providing nanoparticles with oligonucleotides attached co to them, which have a sequence complementary to a sequence of two portions of nucleic acid, contacting the nucleic acid and nanoparticles to allow hybridisation of the oligonucleotides with two or more portions of the nucleic acid, and observing a detectable change brought about by the hybridisation. The mucleic acid to be detected must have at least two portions and the distances between these are chosen so that when the nanoparticle-oligonucleotide conjugate binds the target sequence a detectable change occurs. The method of the invention is useful for carried that or mucleic acids (from a biological source) having at least two portions, such as viral RNA, bacterial or fungal DNA, a gene associated with a disease, synthetic, or structurally, modified natural or synthetic RNA or DNA, or a product of a polymerase chain reaction amplification. Nanoparticle-oligonucleotide conjugates of the invention are useful for preparing a nanoprobe conjugates of the invention are useful for nanofabrication and for separating a selected nucleic acid detection methods and can be used to detect nucleic acids conjugates improve the sensitivity of nucleic acid detection methods and can be used to detect nucleic acids conjugates improve the sensitivity of nucleic acid detection methods and can be used to detect nucleic acids conjugates improve the sensitivity of nucleic acid detection methods and can be used to detect nucleic acids conjugates improve the sensitivity of nucleic acid detection methods and can be used to detect nucleic acids conjugates are stable with tailored hybridisation abilities. The present conjugates are stable with tailored hybridisation abilities. The present conjugates the invention are invention and invention of the invention and provides highly desirable manoparticle-oligonucleotide conjugates are stable with tailored hybridisation abilities of pereconfusers 
                                                                                                                                                                                   Detection of nucleic acid having at least two portions, by contacting nucleic acid and nanoparticles under conditions, which allows hybridization of oligonucleotides on nanoparticles with at least two
                                Elghanian R;
                                Letsinger RL, Mucic RC, Storhoff JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  demonstrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                   Example 18; Page 44; 108pp; English
                                                                                                                                                                                                                                                                                     portions of nucleic acid.
                                                                                                                     WPI; 2003-634854/60.
                             Mirkin CA,
Taton TA;
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Gaps
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0
                          1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02;
                                                     0; Indels
Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
                                  100.0%; Pred. w.
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                                        Local Similarity 100.
1es 20; Conservative
                             Query Match
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Immunostimulatory; antiinflammatory; dermatological; antipsoriatic; antiulcer; gene therapy; vaccine; non-allergic inflammatory disease; psoriasis; eczema; allergic contact dermatitis; latex dermatitis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; se.
                                                                                                  Immunostimulatory nucleic acid #537.
                            ACD99851 standard; DNA; 20
                                                                           (first entry)
                                                                           25-SEP-2003
                                                   ACD99851;
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US2003050268-A1

Synthetic.

13-MAR-2003.

Treating non-allergic inflammatory diseases, such as psoriasis, ecziallergic contact dermatitis, latex dermatitis or inflammatory bowel disease by administering an immunostimulatory nucleic acid.

WPI; 2003-521815/49.

Berg DJ;

Krieg AM,

(KRIE/) KRIEG A M. (BERG/) BERG D J.

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Treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic contact dermatitis, latex dermatitis or inflammatory bowel disease by administering an immunostimulatory nucleic acid.
                                                                                                                                                                                                                                                                                                                             psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
This sequence represents an immunostimulatory nucleic acid
                                                                                                                                                                                                                                                   The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunostimulatory nucleic acid #533.
                                                                                                                                                                                                                          Disclosure; Page 23; 229pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 АААААААААААААААА 20
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29-MAR-2002; 2002US-00112653.
                             29-MAR-2001; 2001US-0279642P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACD99847 standard; DNA; 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                  WPI; 2003-521815/49.
                                                                                                      Krieg AM, Berg DJ;
                                                          KRIEG A M.
                                                                        (BERG/) BERG D J.
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                                                          KRIE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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Disclosure, Page 23; 229pp; English

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Gaps

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Matches 20; Conservative

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Gaps

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The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases, such as psortasis, eczema, allergic context dermatisi, latex dermatitis or inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease. This sequence represents an immunostimulatory nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic contact dermatisi, latex dermatiis or inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease. This sequence represents an immunostimulatory nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunostimulatory; antiinflammatory; dermatological; antipsoriatic; antiulcer; gene therapy; vaccine; non-allergic inflammatory disease; psoriasis; eczema; allergic contact dermatitis; latex dermatitis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating non-allergic inflammatory diseases, such as psoriasis, ecz
allergic contact dermatitis, latex dermatitis or inflammatory bowel
disease by administering an immunostimulatory nucleic acid.
                                                                                                                                                                                                                                                 1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02;
                                                                                                                                                                                                           Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
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100.0%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                         100.0%; Preα. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunostimulatory nucleic acid #218.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-SEP-2003 (first entry)
                                                                                                                                                                                                                                                                 Local Similarity 100.
ses 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Krieg AM, Berg DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (KRIE/) KRIEG A M. (BERG/) BERG D J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2003050268-A1.
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Matches
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Length 20;

Best Local Similarity

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Hairpin sensor useful for detecting a target nucleotide sequence in a sample, comprises a hairpin loop assembly including a complementary probe and a quenchable fluorescing agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention discloses a hairpin sensor comprising a hairpin loop assembly including a complementary probe positioned between a first inverse repeat arm and a second inverse repeat arm, and a quenchable fluorescing agent joined, directly or indirectly, to the end of the second inverse repeat arm of the hairpin loop assembly opposite the complementary probe. Also claimed is a microarray comprising the hairpin sensor, where the end of the first inverse repeat arm opposite the complementary probe is bound, directly or indirectly, to a support, a kit for detecting a target nucleotide sequence in a sample comprising the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hairpin sensor, and support, and hairpin sensor system, in which the particle is conductive or semi-conductive, including at least one of the above hairpin sensor assemblies. The hairpin sensor assemblies the hairpin sensor sessemblies. The hairpin sensor further comprises a functional group joined to the end of the first inverse repeat arm, the functional group selected from amino, carboxyl, inverse repeat arm, the functional group selected from amino, carboxyl, thiol and hydroxyl. Further, the sensor comprises a ligand positioned between the second inverse repeat arm and the quenchable fluorescing agent, where the ligand is selected from mercapto, hydroxyl, amino, nitrile and carboxyl, carboxylic acid, organic acid and amino acid. The second spacer is positioned between the second inverse repeat arm and the quenchable fluorescing agent which comprises a semiconductor nanocrystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /bound_molety= "Hairpin oligonucleotide #2"
/note=_"Forms a doube-stranded region with the hairpin
oligonucleotide shown in examples 3, 4 and 5"
                                                                                                                                                                                                                                                                                                      Hairpin sensor; hairpin loop; complementary probe; inverse repeat arm; quenchable fluorescing agent; microarray; semiconductor; nanocrystal; rhodamine B-labelled dye; detection; gold support; 88.
                                                                                                                                                                                                                                                              Hairpin target sequence, #2, used in an example of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1736 AAAAAAAAAAAAAAAAA 1755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Page 11; 16pp; English.
                                        20 AAAAAAAAAAAAAAAAA 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUN-2001; 2001US-0299460P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Σ
                                                                                                                                          ADA14838 standard; DNA; 20
                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-596312/56.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JS2003013109-A1.
                                                                                                                                                                                                                         06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_binding
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                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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or rhodamine B-labelled dye. Within the microarray the support is capable of accepting a charge. At least one hairpin sensor comprises two or more hairpin sensors. The two or more hairpin sensors include complementary probes that are the same or different and respective quenchable fluorescing agents that are the same or different. The two or more hairpin sensors are arranged in a spatially-defined pattern. The sensor and system are useful for detecting a target nucleotide sequence in a sample. Further, the method involves identifying the target nucleotide sequence by the location of the complementary probe to which the target complementary probes or quenchable fluorescing agents, that are different. The sequence presented is the hairpin sensors include different. The sequence presented is the hairpin oilgonucleotide target sequence, #2, used in an example of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to detecting a nucleic acid (NA) having at least 2 portions comprises providing a type of nanoparticles (NP. e.g. colloidal gold) having oligonuclectides (O) attached (where (O) on each NP has a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ss; nanoparticle; colloidal gold; semiconductor; nanomaterial; nanostructure; viral disease; human immunodeficiency virus infection; hepatitis virus infection; herpes virus infection; cytomegalovirus virus infection; Epstein-Barr virus; bacterial disease; sexually transmitted disease; inherited disorders; paternity testing; cell line authentication; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting nucleic acids having at least 2 portions comprises use of nanoparticles which have oligonucleotides attached to them that are complementary to portions of the target nucleic acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Elghanian R;
                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                          Query Match 1.1%; Score 20; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nanoparticle labelled oligonucleotides, spacer DNA #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mucic RC, Storhoff JJ,
                                                                                                                                                                                                                                                                                   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
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97WO-US012783.
99US-00240755.
99US-00344667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADA06159 standard; DNA; 20 BP
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25-JUN-1999; 99US-00344667.
26-APR-2009; 2000US-0200161P.
26-JUN-2000; 2000US-00603830.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-NOV-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-576420/54.
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21-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADA06159;
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ADA06159
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contacting NA and NP to allow hybridisation of (0) on NP with 2 or more contacting NA and NP to allow hybridisation of (0) on NP with 2 or more contacting NA and observing a detectable change brought about by hybridization of (0) on NP with NA. Also included are aggregate probes, core probes, substrate having NP attached to it, a metallic or core probes, substrate having NP attached to it, anomaterials/manostructures comprising anoparticles and methods of nanofabrication utilising nanoparticles and satellite probes. The methods, probes nucleic acids, nanoparticles and slignouclectides are useful for separating a selected nucleic acid having at least two portions, from other nucleic acids, and for detecting nucleic acids having at least two portions, for detecting any type of nucleic acids which may be used for diagnosis of disease and in sequencing of nucleic acids which may be used for diagnosis of disease and in sequencing of nucleic acids which may be used for diagnosis of disease and in sequencing of nucleic acids preferably, the method is useful for detecting nucleic acids for diagnosis and/or monitoring of viral diseases (human immunodeficiency virus), hepatitis virus, heppes virus, cytomegalovirus and Epstein-Barr virus), abcrearial diseases, sexually transmitted diseases, inherited disorders, in forensics, in DNA corporating acolds based on contour change with the nakehod is useful in research and analytical laboratories in DNA sequencing, in the field to detect the cobserving a colour require specialised expensive equipment. The present cobserving a colour require specialised expensive equipment: The present consequence is a spacer oligonucleotide used to illustrate the method of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nanotechnology; nucleic acid detection; nanofabrication; nanoprobe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nanotechnology nucleic acid detection method oligonucleotide #54.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.1%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
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/note= "OTHER= Thiol modified" "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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29-JAN-1999; 99US-00240755.
25-JUN-1999; 99US-00344667.
26-APR-2000; 2000US-02060161P.
26-JUN-2000; 2000US-00603830.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACD26995 standard; DNA; 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACD26995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACD26995
          859999999999999999999999999
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This invention relates to a novel method for detecting nucleic acids. The method comprises providing nanoparticles with oligonucleotides attached to them, which have a sequence complementary to a sequence of two portions of mucleic acid, contacting the nucleic acid and nanoparticles to allow hybridisation of the oligonucleotides with two or more portions of the nucleic acid, and observing a detectable change brought about by the hybridisation. The nucleic acid to be detected must have at least two portions and the distances between these are chosen so that when the nanoparticle-oligonucleotide conjugate binds the target sequence a confection and the distances between these are chosen so that when the nanoparticle-oligonucleotide conjugate binds the target sequence a detectable change occurs. The method of the invention is useful for detecting two or more nucleic acids (from a biological source) having at least two portions, such as viral RNA, bacterial or fungal DNA, a gene associated with a disease, synthetic, or structurally- modified natural or synthetic RNA or DNA, or a product of a polymerase chain reaction are useful for preparing a nanoprobe conjugate for detecting an analyte, and for detecting a nucleic acid bound to an electrode surface.

Nanoparticles and nanoparticle conjugates of the invention are useful for nanofabrication and for separating a selected nucleic acid having two portions from other nucleic acids. Diagnostic assays employing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nanoparticle-oligonucleotide conjugates improve the sensitivity of nucleic acid detection methods and can be used to detect nucleic acids that are present in only small amounts in a sample. The present sequence represents a thiol modified oligonucleotide sequence used to demonstrate the method of the invention
                                                                                                                                      providing nanoparticles
                                                                                                                                                                                             nanoparticles to allow hybridization, and observing detectable change.
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Elghanian
Storhoff JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                   Detecting nucleic acid having two portions, by
Mucic RC,
                                                                                                                                                                                                                                                Example 18; Page 43; 129pp; English.
                                                                                                                                                                   igonucleotides attached
Letsinger RL,
                                                                                WPI; 2003-615795/58
                      raton TA;
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Gaps ö Length 20; Indels Query Match
1.1%; Score 20; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0;

ADB36933 standard; DNA; 20 BP RESULT 274 ADB36933 

04-DEC-2003 (first entry)

Immunostimulatory nucleic acid #547.

ds; allergy; asthma; poly-G nucleic acid; aerosol formulation; hypo-responsive subject; immunostimulatory.

Synthetic

US2003087848-A1.

08-MAY-2003

02-FEB-2001; 2001US-00776479.

03-FEB-2000; 2000US-0179991P.

(BRAT/) BRATZLER R L. (PETE/) PETERSEN D M.

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The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G nucleic acid in an aerosol formulation. The methods and compositions of the present invention are useful for diagnosing and/or treating asthma and allergy especially in a hypo-responsive subject. The present sequence represent an immunostimulatory nucleic acid of the invention.
                                                                                                                 Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.
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                                                                                                                                                                                                                                                                                                                                                                                     1.1%; Score 20; DB 1; Length 20;
100.0%; Pred. No. 1.6e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                     Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
                                      Fouron Y;
                                                                                                                                                                          Disclosure; Page 13; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1736 AAAAAAAAAAAAAAAAA 1755
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                                      Bratzler RL, Petersen DM,
                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
Les 20; Conservative
                                                                           WPI; 2003-657977/62
(FOUR/) FOURON Y.
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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ds; allergy; asthma; poly-G nucleic acid; aerosol formulation; hypo-responsive subject; immunostimulatory. Immunostimulatory nucleic acid #215. (first entry) 04-DEC-2003 

ADB36601 standard; DNA; 20

RESULT 275 ADB36601/c

ADB36601;

Synthetic

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US2003087848-A1.

38-MAY-2003.

)2-FEB-2001; 2001US-00776479.

03-FEB-2000; 2000US-0179991P.

'nΣ (BRAT/) BRATZLER R (PETE/) PETERSEN D (FOUR/) FOURON Y. Fouron Y; Bratzler RL, Petersen DM,

WPI; 2003-657977/62

Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.

Disclosure; Page 8; 221pp; English

The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G nucleic acid in an aerosol formulation. The methods and compositions of the present invention are useful for diagnosing and/or treating asthma and allergy especially in a hypo-responsive subject. The present sequence represents an immunostimulatory nucleic acid of the invention.

Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

04-DEC-2003

ADB36929

RESULT 276 ADB36929/c

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
                                                                                                                                                                                                                                                                                                                      Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          method can be used to analyse gene expression rapidly and easily
           Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Analysis; gene expression; reverse transcription; primer; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.1%; Score 20; DB 1; Length 21; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                 (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 6; 11pp; Japanese.
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Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                   WPI; 1995-018287/03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-APR-1993;
                                                                                                   JP06303997-A
                                                                                                                                                                            16-APR-1993;
                                                                                                                                                                                                               16-APR-1993;
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                                                                                                                                        01-NOV-1994.
                                                                     Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G nucleic acid in an aerosol formulation. The methods and compositions of the present invention are useful for diagnosing and/or treating asthma and allergy especially in a hypo-responsive subject. The present sequence represents an immunostimulatory nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.
                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                        ds; allergy; asthma; poly-G nucleic acid; aerosol formulation; hypo-responsive subject; immunostimulatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reverse transcription primer used in cDNA analysis technique.
 DB 1; ne.._
0. 1.6e+02;
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 20; DB 1; Length 20;
Pred. No. 1.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
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100.0%; Pred. No. 1...
             1.1%; Score 20; DB 100.0%; Pred. No. 1.6; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Petersen DM, Fouron Y;
                                                                                                                                                                                                                                                                                                                      Immunostimulatory nucleic acid #543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 13; 221pp; English.
                                                                                    1736 AAAAAAAAAAAAAAAAAA 1755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-FEB-2001; 2001US-00776479.
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                                                                                                                                                                                                               ADB36929 standard; DNA; 20
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Matches 20; Conservative
                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BRAT/) BRATZLER R L.
(PETE/) PETERSEN D M.
(FOUR/) FOURON Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-657977/62.
             Query Match
Best Local Similarity
Matches 20; Conserv
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04-AUG-1995

AAQ75643;

BXXXXX

AAQ75643,

Query Match

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Gaps

3' ribonucleoside; self-addressable electronic device;

(first entry)

/*tag= a /note= "3' ribonucleoside terminal"

*tag=

94WO-US012270.

Location/Qualifiers

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CP-1 (synthetic DNA probe with 3'ribonucleoside terminal #2)
                                     AAQ90391 standard; DNA; 21 BP
                                                                                                                                             CP-1; HLA; dQa; 3' ribos
SAED; hybridisation; ss
                                                                                                                                                                                                                                                                                                                                      26-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1993;
                                                                                                                                                                                                                              misc_feature
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                                                                                                                                                                                                                                                                                                           11-MAY-1995.
                                                                                           08-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                      Heller MJ,
                                                                                                                                                                                       Synthetic
                                                                AAQ90391;
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Matches
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            RESULT 280
                          AA09039
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                      A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-057598) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Analysis of cDNA and gene expression - by amplification of mRNA followed
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                        Reverse transcription primer used in cDNA analysis technique.
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                                                                                                                                                                        Length 21;
                                                                                                                                                                                                  0; Indels
                                                                                                                                             Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                      1.1%; Score 20; DB 1; Le
100.0%; Pred. No. 1.6e+02;
                                                                                                                                                                               100.0%; Preα. ....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               by digestion with restriction enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 6; 11pp; Japanese.
Page 6; 11pp; Japanese.
                                                                                                                                                                                                                             1733 TACAAAAAAAAAAAAAA 1752
                                                                                                                                                                                                                                                      20 TACAAAAAAAAAAAAAA 1
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                                                                                                                                                                                                                                                                                                                         AAQ75645 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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nes 20; Conservative
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                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                               RESULT 279
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                                                                                                                                                                                                                                New self-addressable electronic devices - used for multi-step and multiplex reactions such as DNA hybridisation(s), clinical diagnostics and bio:polymer synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sensitivity of these reactions are greatly improved at micro-locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gapa
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100.0%; Pred. No. 1.6e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 40; 86pp; English.
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93US-00146504
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                                                                                                                                                                         NPI; 1995-185870/24.
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                                                    (NANO-) NANOGEN INC.
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Gaps

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are used in the construction of the electronically self-addressable device (ED) of the invention. The ED comprises a substrate, an electrode or opt. a number of electrodes supported by the substrate, a current source operatively connected to the electrode and an attachment layer permeable to a molecule capable of insulating or binding to the electrode which is permeable to a counterion but not permeable to a molecule capable of insulating or binding to the electrode. The attachment layer is capable of attaching a macromolecule. The ED is used for genetic typing and comprises a number of electrodically addressable locations each comprising an electrode, and a binding entity, such as one of these probes, attached to each of the locations capable of electrodic the presence of a genetic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypervariable region; ENV protein; vaccinia virus; gag gene; retrovirus; vaccines; infection; protection; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                   Electronically self-addressable device - used for electronic control of,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences given in AAT10742-67 are synthetic oligonucleotides which
Electronically self-addressable device; ED; electrode; current source; attachment layer; permeable; counterion; genetic typing; probe; detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.1%; Score 20; DB 1; Length 21;
100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0; Indels
                                                                                                                               /*tag= a
/note= "3'-ribonucleoside terminus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 1 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                       Sosnowski RG;
                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 60; 155pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                    e.g. nucleic acid hybridisation.
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                                                                                                                                                                                                                                         95WO-US008570
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                                                                                                                                                                                                                                                                        94US-00271882
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                                                                                                                                                                                                                                                                                                        (NANO-) NANOGEN INC.
                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-097582/10.
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Best Local Similarity
                                                                                              Key
modified_base
                                                                                                                                                                                                                                       05-JUL-1995;
                                                                                                                                                                                                                                                                        07-JUL-1994;
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                                                                                                                                                                             WO9601836-A1
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                                                                Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Microelectronic device; multi-step reaction; microscopic format; ion-permeable permeation layer; electrode; electrical control; transport; attachment; binding; DNA/RNA hybrid; probe; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Edman CF;
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                                                                                                                                                                                                                                                                                                                                                                       Recombinant vaccinia virus containing fusion HIB gag gene -
production in host cells of gag protein for use as vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.1%; Score 20; DB 1; Length 21; 100.0%; Pred. No. 1.6e+02; tive 0; Mismatches 0; Indels
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                                                                                                                                 (NINA-) JAPAN NAT INST INFECTIOUS DISEASES (JAPG ) NIPPON ZEON KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 66; 84pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1735 CAAAAAAAAAAAAAAAAAA 1754
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                                                                                                                                                                                                                                  Yasuda A;
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97WO-JP004216.
                                                                  96JP-00323412.
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Matches 20; Conservative
                                                                                                                                                                                                                                      Kojima A, Kurata T,
                                                                                                                                                                                                                                                                                                        WPI; 1998-312481/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NANO-) NANOGEN INC
19-NOV-1997;
                                                                  19-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX81302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX81302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PART SERVICE S
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Gaps ö

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Watson MA,
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                      AAX26973,
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                                                                                                                                                                                                                                                                                        The specification describes a self-addressable, self-assembling microelectronic device which is designed to actively carry out and control multi-step and multiplex molecular biological reactions in microscopic formats. A key aspect of this inventions is played by the ion permeable permeation layer which overlies the electrode. This permeation layer which overlies the electrode. This permeation layer allows attachment of nucleic acids to permit immobilization but also separates the attached oligonucleotides and hybridized target DNA sequences from the highly reactive electrochemical environment generated immediately at the electrode surface. The microelectronic device is separation, dispositics and biopolymer synthesis. The device can be preparation, diagnostics and biopolymer synthesis. The device can electronically control the transport and attachment of specific binding entities, such as nucleic acids and polypeptides, to specific microlocations. The device can subsequently control the transport and reaction of analytes or reactants at the addressed specific microlocations. The
                                                                                                             New microelectronic device designed to carry out and control multi-step and multiplex molecular biological reactions in microscopic format.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       device is able to concentrate analytes and reactants, remove non-specifically bound molecules, provide stringency control for DNA hybridization reactions and improve the detection of analytes. The present sequence represents a probe used to exemplify the invention
                                                                                                                                                                                                                               Example 1; Page 89; 179pp; English
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Gaps ö Query Match 1.1%; Score 20; DB 1; Length 21; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 20; Conservative 0; Mismatches 0; Indels Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 1 U; 0 Other; 1736 AAAAAAAAAAAAAAAA 1755

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20 AAAAAAAAAAAAAAAA

AAX26973 standard; cDNA; 21 BP 25-JUN-1999 (first entry) AAX26973;

Primer used to reverse transcribe mammaglobin RNA

Human; mammary-specific protein; mammaglobin; antigen; vaccine; mammaglobin-expressing cancer; breast cancer; autologous tumor lymphocyte; diagnosis; marker; primer; 88.

Synthetic.

409914230-A1

98WO-US017991 18-SEP-1998; 97US-00933149 18-SEP-1997;

(UNIW ) UNIV WASHINGTON.

Fleming TP;

WPI; 1999-244021/20.

Mammaglobin, secreted protein overexpressed in breast cancer.

1.1%; Score 20; DB 1; Length 21; 100.0%; Pred. No. 1.6e+02;

Best Local Similarity

Query Match

Example 2; Page 55; 60pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   have antimicrobial, cytostatic and immunosuppressive activity. The oligomucleotides are useful for binding to and preventing or inhibiting the biological function of a protein kinase or a target molecule and for detecting the presence or absence of a target molecule in biological samples. The oligomucleotides are also useful for prophylactic and therapeutic treatment of diseases unch as cancer, autoimmune diseases and diseases caused by pathogenic microorganisms. This sequence represents a primer used in the method of the invention
The present primer was used to reverse transcribe RNA encoding a human demmary-specific protein, designated mammaglobin. The specification describes a procein comprising a mammaglobin antigen that is recognized by B and/or Tc cells specific for the natural, secreted and glycosylated form of mammaglobin polypeptide. This protein, or recombinant vectors that express it, are used in vaccines for treating mammaglobin-expressing cancers, specifically of the breast. Such cancers can also be treated using autologous tumor lymphocytes activated ex vivo with an mammaglobin antigen, then returned to the patient. Expression of mammaglobin is elevated in 27% of stage I primary breast cancers, so it represents a marker useful for diagnosis of this disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotides inhibiting protein kinase, useful for treating diseases such as cancer and autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes novel purified aptameric oligonucleotides which
                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antimicrobial; cytostatic; immunosuppressive; protein kinase; prophylactic; therapy; treatment; cancer; autoimmune disease; pathogenic microorganism; primer; 88.
                                                                                                                                                                                                                                                                                                       1.1%; Score 20; DB 1; Length 21;
100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                    Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein kinase inhibiting primer #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 8; Col 27-28; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   1736 AAAAAAAAAAAAAAAAA 1755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ44350 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
ses 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neckers L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-104623/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-APR-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ44350;
                                                                                                                                                                                                                                                                                                              Query Match
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Branched compounds useful in e.g. nucleic acid synthesis reaction comprises nucleic acid moieties optionally extended by a polymerase.
                                                                                                                      Branched chain compound; nucleic acid synthesis; primer extension; reverse transcription; nucleic acid hybridization; nucleic acid amplification; ss.
                                                                                             Oligonucleotide used to produce branched chain compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schmidt W, Hiller R, Huber M,
 AAH42480/c
ID AAH42480 standard; DNA; 21 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-466959/51.
                                                                                                                                                                                                                    modified base
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                                                                                                                                                                                                                                                                                                     misc feature
                                                                   01-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                    27-JUN-2001
                                                                                                                                                                              Synthetic
                                          AAH42480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (LION-) 1
(VBCG-) 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      response. The method comprises administering an immunostiamulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immunostiamulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immunostimulatory. The presponse. The present sequence is one such immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae, haemophilus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is slab useful for preventing cancer, asthma, infectious disease, alleryy or immune deficiency. The present sequence can also be used to redirect a Th2 to a Th1 immune response and to activate immune cells. Note: the
                                                                                                                                                                                                                                 anti-parasitic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.
  Gaps
                                                                                                                                                                                                                                                                           88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a method for stimulating an immune
                                                                                                                                                                                                                              Vaccine, cytostatic, virucidal, bactericidal, fungicidal, anti-par immunostimulatory, tumour, viral infection; bacterial infection; fungal infection; cancer, asthma, infections disease, allergy, immune deficiency; phosphorothioate;
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 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present sequence may have a phosphorothioate backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;
 0; Mismatches
                                                                                                                                                                                                      Immunostimulatory nucleic acid #823.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 101; Page 56; 338pp; English.
                          1736 AAAAAAAAAAAAAAAAA 1755
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                                                    21 AAAAAAAAAAAAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                          25-SEP-1999; 99US-0156113P.
27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
                                                                                                                                                                                                                                                                                                                                                                                25-SEP-2000; 2000WO-US026383
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IOWA ) UNIV IOWA RES FOUND.
(COLE-) COLEY PHARM GMBH.
                                                                                                                     AAF99707 standard; DNA; 21
                                                                                                                                                                          (first entry)
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schetter C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-273485/28.
                                                                                                                                                                                                                                                                                                                           WO200122972-A2
                                                                                                                                                                            12-JUN-2001
                                                                                                                                                                                                                                                                                                                                                      05-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Krieg AM,
                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                               AAF99707;
                                                                                          Matches
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Mueller M;

a "NH2-C6 attached" b "NH2-C6 attached"

/*tag= /note=

Location/Qualifiers

(first entry)

/*tag= c
/note= "branch present"

6. .7 /*tag= *tag= /note=

99EP-00125484. 99EP-00125484.

LION BIOSCIENCE AG.

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                                             The specification describes branched compounds containing nucleic acid moieties optionally extended by a polymerase. The branched chain compounds of the invention are used in nucleic acid synthesis reaction, primer extension reaction, reverse transcription reaction of RNA into DNA, nucleic acid hybridization experiment (for identifying sequence of a nucleic acid, and nucleic acid amplification experiment (for analysing the expression pattern of genes). The compounds are also used in solid-phase enzymatic reactions. The present sequence was used in the course of the invention to produce branched chain compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                1.1%; Score 20; DB 1; Length 21;
100.0%; Pred. No. 1.6e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                             Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 10; 31pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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ID ABS7
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AC ABS7
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Gaps

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1.1%; Score 20; DB 1; Length 21; 100.0%; Pred. No. 1.68+02; tive 0; Mismatches 0; Indels

1736 AAAAAAAAAAAAAAAA 1755

20; Conservative

Matches

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Local Similarity

Query Match

AAAAAAAAAAAAAAA 2

21

/*tag= a /mod_base= OTHER /note= "phosphorothioate backbone"

WO200197843-A2

27-DEC-2001.

22-JUN-2001; 2001WO-US020154. 22-JUN-2000; 2000US-0213346P.

(IOWA ) UNIV IOWA RES FOUND.

Location/Qualifiers

modified base

Synthetic.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antiangiogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antianglogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lesion, rheumatoid archritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic
                                                                                                                                                                                                                                                                                                                                                                                                   Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
                                                Anglogenesis inhibitor; ss; anglogenesis; solid tumour growth; tumour metestasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasis; rubeosis; Osler-Webber Syndrome; myocardial anglogenesis; plaque meovascularisation; telangiectasia; haemophiliac joint; anglofibroma; wound granulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibody-induced cell lysis; cancer; immunostimulatory; CD20; angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunostimulatory nucleic acid SEQ ID NO: 840.
                           Angiogenesis inhibitory oligonucleotide #912.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1736 AAAAAAAAAAAAAAAAAAA 1755
                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 35; 276pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 AAAAAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                   (COLE-) COLEY PHARM GROUP INC
                                                                                                                                                                                                                                                              14-DEC-2001; 2001WO-US048458
                                                                                                                                                                                                                                                                                          14-DEC-2000; 2000US-025534P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL39404 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-APR-2002 (first entry)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-566690/60.
                                                                                                                                                                                                         WO200253141-A2.
                                                                                                                                                                                                                                                                                                                                                3ratzler RL;
13-DEC-2002
                                                                                                                                                                                                                                    11-JUL-2002
                                                                                                                                                                               Synthetic.
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ID ABL3
AC ABL3
XX ABL3
XX I6-A
XX IMMU
XX AAL1
XW AAL1
XX ANL1
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The present invention relates to methods for treating or preventing cancer, involving administering to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies. The methods are useful for creating or preventing cancer such as basal call carcinoma, bladder cancer, bone cancer, brain and central nervous system (CNS) cancer, corphageal cancer, colon and rectum cancer, connective tissue cancer, cesophageal cancer, eye cancer, kidney cancer, larynx cancer, leukaemia, liver cancer, luy cancer, Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin cancer, stomach cancer, testicular cancer, rhabdomyosarcoma, skin cancer, stomach cancer i testicular cancer, and uterine cancer. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laminitis; viral disease; vaccine; bacterial disease; primer; epistaxis; gastritis; gastric ulcer; respiratory ailment; fracture; joint disease; musculoskeletal damage; ss.
                                                                                                                     Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies to a subject having or at risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Regular oligo dT primer used to illustrate the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.1%; Scor.
100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                  Disclosure; Page 309; 312pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1736 AAAAAAAAAAAAAAAAAA 1755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 AAAAAAAAAAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD51323 standard; DNA; 21 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20; Conservative
Hartmann G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                              WPI; 2002-154611/20.
                                                                                                                                                                                                                                 developing cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-APR-2003
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Weiner G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD51323;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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WO200290579-A1

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WPI; 2003-521815/49.
                                                    Berg DJ;
   (KRIE/) KRIEG A M. (BERG/) BERG D J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                    Krieg AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB37209;
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BRAT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PETE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 292
ADB37209/c
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                              The invention relates to a method for assessing a condition of a performance animal. The method involves determining in sample abundance of expressed target nucleic acid; transmitting digital sample signal to cor expressed target nucleic acid; transmitting digital sample signal to cor endoced database to correlate digital signal with digital at remotely corected database to correlate digital signal with digital information and correlate digital signal with digital information and correlate digital signal with digital information and condition of a performance animal preferably human, dog cor camel. The condition can be an athletic ability and a condition that enhances, hinders, impedes or does not change an expected ability of the correlation; and also normal, pre-clinical, overt progress and/or stage of disease, undiagnose of unclassified conditions, presence of chugs, response to exercise, response to vaccines, therapies, nutritional states and response to environmental conditions. Diseases assessed by the invention include laminitis, lameless, viral or bacterial disease,

Catage astrictis, gastric ulcers, respiratory ainments, fractures, epistaxis, musculoskeletal damage or disorders and joint diseases. The present

Catage as primer used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                Assessing condition e.g. athletic ability, stage of disease, presence of drugs, response to exercise, response to vaccines, therapies, nutritional states, of performance animal involves analyzing nucleic acid expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunostimulatory; antiinflammatory; dermatological; antipsoriatic; antiulcer; gene therapy; vaccine; non-allergic inflammatory disease; psoriasis; eczema; allergic contact dermatitis; latex dermatitis; lafilammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 20; DB 1; Length 21;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
1.1%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 1.6
Matches 20; Conservative 0; Mismatches
                                                                                                                (GENO-) GENOMICS RES PARTNERS PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunostimulatory nucleic acid #881.
                                                                                                                                                                                                                                                                                    Disclosure; Page 46; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1736 AAAAAAAAAAAAAAAAA 1755
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                                 03-MAY-2002; 2002WO-AU000553
                                                                04-MAY-2001; 2001AU-00004809.
29-JUN-2001; 2001US-00896941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACH03246 standard; DNA; 21
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                                                                                                                                                                                  WPI; 2003-120558/11.
14-NOV-2002
                                                                                                                                                 Brandon RB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACH03246;
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                                                                                                                             The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases, such as pportains, eccama, allergic contact dermatitis, latex dermatitis or inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease. This sequence represents an immunostimulatory nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G nucleic acid in an aerosol formulation. The methods and compositions of the present invention are useful for diagnosing and/or treating asthma and allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                              allergic contact dermatitis, latex dermatitis or inflammatory bowel
disease by administering an immunostimulatory nucleic acid.
Treating non-allergic inflammatory diseases, such as psoriasis, allergic contact dermatitis, latex dermatitis or inflammatory h
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ds; allergy; asthma; poly-G nucleic acid; aerosol formulation; hypo-responsive subject; immunostimulatory.
                                                                                                                                                                                                                                                                                                                                                                    Score 20; DB 1; Length 21;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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                                                                                                                                                                                                                                                                                                                                                   1.1%; Scc...
100.0%; Pred. No. ...
0; Mismatches
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                                                                                            Disclosure; Page 33; 229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunostimulatory nucleic acid #823.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 17; 221pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-FEB-2001; 2001US-00776479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-FEB-2000; 2000US-0179991P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADB37209 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                              20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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PETERSEN D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (FOUR/) FOURON Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS2003087848-A1
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29-MAR-2002; 2002US-00112653. 29-MAR-2001; 2001US-0279642P

US2003050268-A1 13-MAR-2003.

Synthetic.

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13-MAR-2001
                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                              AAF16627;
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                                                                                                                                                          Query Match
                                                                                                                                                                         Matches
                                                                                                                                                                                                                                       AAF16627
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especially in a hypo-responsive subject. The present sequence represents an immunostimulatory nucleic acid of the invention.
                                                                                                                                                                                               Human interleukin-6 gene, herpes simplex; AIDS; modified; HIV; RSV; HPV; malignancy; hepatitis; inflammation; ss.
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New oligomers contg. modified bases - which form a triplex with G-C doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis, herpes malignancy and inflammation.
                                                       ;
0
                                                                                                                                                                               Oligomer IL6805 for forming triplex with HUMIL6 target duplex.
                                     1.1%; Score 20; DB 1; Length 21; 100.0%; Pred. No. 1.6e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                   *tag= d
note= "o-xyloso dimer synthon linkage"
                                                                                                                                                                                                                                                      /*tag= a
/mod base= OTHER
/note= "OTHER= N4 N4 ethanocytosine"
/1. .12
                                                                                                                                                                                                                                                                                                                                                 /mod_base= OTHER
/note= "OTHER= N4 N4 ethanocytosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matteucci MD, Milligan J;
                      Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                           /*tag= c
/label= inverted_polarity_region
/note= "see comments"
                                                                                                                                                                                                                                     Location/Qualifiers
                                                                    1736 AAAAAAAAAAAAAAAAA 1755
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                                                                                    AAAAAAAAAAAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                     90US-00617907.
91US-00643382.
91US-00683420.
91US-00686544.
91US-00686546.
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                                                                                                                           AAQ30432 standard; DNA; 23
                                                                                                                                                         (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                          *tag= b
                                                     20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Froehler B, Krawczyk S,
                                                                                                                                                                                                                                                                                                   12. .23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GILE-) GILEAD SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1992-217083/26.
                                     Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                      Key
modified_base
                                                                                                                                                                                                                                                                                                                                  modified base
                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                         WO9209705-A1
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                                                                                                                                                        25-MAR-2003
07-DEC-1992
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18-JAN-1991;
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27-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                        11-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                       38-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                              17-APR-1991
17-APR-1991
                                                                                                                                                                                                                       Synthetic
                                                                                                                                         AAQ30432;
                                                                                                          RESULT 293
AAQ30432/c
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The synthetic oligomer is capable of forming a triplex at physiological physic a purine rich target sequence by coupling into the major groove of the duplex. The specific target sequence of this oligomer is the human interleukin 6 gene untranslated sequence contg. a purine rich sequence concd. on one strand of the duplex. The oligomer, and others like it are useful in diagnosis and therapy of diseases characterised by specific DNA duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant thus assays may be carried out without subjecting the test specimen to harsh conditions. The oligomer contains an inverted polarity region formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso (nucleotides have the 3'positions of xylose augars linked via the o-xyloso close table to nucleotides are coupled through a xylone residue to conjecute table to nuclease activity. The oligomer is able to finhibit gene expression, as verified by in vitro systems. See also AAQ25452-25501 and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treating gastric acid disturbance by administering an oligonucleotide which modulates the activity of a polypeptide involved in gastric acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gastric acid production inhibiting oligonucleotide SEQ ID NO: 114.
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Kane MD, Dombkowski AA, Nagel AC;
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                                                                                                       31-MAY-2000; 2000CN-00116266.
                                                                                                                          31-MAY-2000; 2000CN-00116266
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                                                                                                                                                                                                                                                                                                                                                                                                                             20; Conservative
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Best Local Similarity
                                                                                                                                                                                       WPI; 2002-196660/26.
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                                                                                                                                                                     Xie Y;
                                          Homo sapiens
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                                                            CN1325900-A.
                                                                                 12-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .0-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK86172;
                                                                                                                                                                   Mao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides the protein and coding sequences of human serine/thronine protein kinase 48. The sequences can be used in the treatment of cancer and HIV infection. The present sequence is a PCR primer for the coding sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                     New human serine/threonine protein kinase 48 and its encoding polynucleotide, useful for treating cancer and human immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human gonadotropin-releasing hormone 10 RT-PCR primer, SEQ ID NO:4.
                                                                                                                                                                                                                               Human; serine/threonine protein kinase 48; cancer; HIV infection; gene therapy; PCR primer; 88.
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                                                                                                                                                                                                            Human serine/threonine protein kinase 48 cDNA PCR primer #2
                          ch 1.1%; Score 20; DB 1; Length 23; 1.1 Similarity 100.0%; Pred. No. 1.8e+02; 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.1%; Score 20; DB 1; Length 24; Best Local Similarity 100.0%; Pred. No. 1.8e+02; Matches 20; Conservative 0; Mismatches 0; Indels
        Sequence 23 BP; 1 A; 0 C; 0 G; 22 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24 BP; 3 A; 1 C; 3 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Page 17(Disclosure); 33pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                        (BODE-) BODE GENE DEV CO LTD SHANGHAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1731 TTTACAAAAAAAAAAAA 1750
                                                                      1736 AAAAAAAAAAAAAAAAA 1755
                                                                                          23 AAAAAAAAAAAAAAAAAAA 4
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                                                                                                                                                                                                                                                                                                                                99CN-00125686
                                                                                                                                                                                                                                                                                                                                                    99CN-00125686
                                                                                                                                              AAI64873 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL55130 standard; DNA; 24
                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-530471/59.
                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            virus infection
                                                                                                                                                                                                                                                                                                                                                                                             Mao Y, Xie Y;
                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                       04-DEC-2001
                                                                                                                                                                                                                                                                                                                                                    22-DEC-1999;
                                                                                                                                                                                                                                                                                     CN1300831-A.
                                                                                                                                                                                                                                                                                                           27-JUN-2001.
                                                                                                                                                                   AAI64873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
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                             Query Match
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ABL55130/c
1D ABL55130/c
X AC ABL5512
XX
DT 31-MAY
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DE Human 9
                                                  Matches
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Human; gonadotropin-releasing hormone 10; recombinant production; cancer; HIV infection; human immunodeficiency virus; gene therapy; cytostatic; anti-HIV; reverse transcription-PCR; RT-PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polypeptide-human gonadotropin-releasing hormone 10 and polynucleotide encoding it.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 20; DB 1; Length 24;
Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligo dT primer; gene expression analysis; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 17 (Disclosure); 32pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.1%; Scor.
100.0%; Pred. No. ...
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Human, PDZ protein 11.99, 88; malignant tumour; haemopathy; cancer;
HIV infection; human immunodeficiency virus; immunological disease;
Inflammation; primer; RT-PCR; reverse transcriptase.
                                                                                                                                                                                                                                   Sequence 24 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                   Human PDZ protein 11.99 cDNA RT-PCR primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
                                                                                                                                                                                                                                                                            Example 1; Page 15; 45pp; English
                                                                                                                                                                                                                                                                                        24 AAAAAAAAAAAAAAAA S
                                                                                                                                                                                                                                                                                                                          ABS56855 standard; DNA; 24 BP
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WPI; 2002-508123/54.
                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                     29-JAN-2003
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                                                                                                                                                                                                                                                                                                                                        ABS56855;
                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                            RESULT 298
                                                                                                                                                                                                                                                              Matches
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Length 24; 0; Indels

Score 20; DB 1; Le Pred. No. 1.8e+02;

1.1%; Scc. No. 100.0%; Pred. No. ... 0; Mismatches

Conservative

(first entry)

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                                                                                                                                                                                                                                       diseases such as malignant tumours, haemopathy, HIV infection, immunological disease and various inflammations. This sequence represents a reverse transcriptase PCR (RT-PCR) primer used in isolation of cDNA encoding the human PDZ protein 11.99
                                              Novel polypeptide-human PDZ protein 11.99 and polynucleotide for encoding said polypeptide.
                                                                                                                                                                  The invention relates to the human PDZ protein 11.99, a polynucleotide encoding the polypeptide and a method for producing the polypeptide using DNA recombination technology. The polypeptide is used for curing several
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides the protein and coding sequences of human vyclophilin-40-12.54. The sequences can be used in the treatment of immunopathy and cancer. The present sequence is a PCR primer for the coding sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptide-human cyclophilin-40-12.54 and polynucleotide for coding it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cyclophilin-40-12.54; immunopathy; cancer; PCR; primer; 88.
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                                                                                                                                                                                                                                                                                                                                                                                                                         1.1%; Score 19.8; DB 1; Length 24; 91.3%; Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cyclophilin-40-12-54 coding sequence PCR primer #2.
                                                                                                                                                                                                                                                                                                                                                                           Sequence 24 BP; 15 A; 0 C; 9 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24 BP; 2 A; 1 C; 2 G; 19 T; 0 U; 0 Other;
                                                                                                                      Sxample 2; Page 16 (Disclosure); 32pp; Chinese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 17 (Disclosure); 33pp; Chinese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAL47515 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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  WPI; 2002-539316/58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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AAL47515/c
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δ
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                                                                                                                                                                                                                                       of gene expression in one or more samples, comprising an identifier having a specific oligo-dT primer sequence, where the identimer comprises a detectable marker at its 5' end. The system is useful for identifying any or all genes expressed in a given in vivo or in vitro RNA sample, as well as the relative differences in mRNA between 2 or more samples, where that represented at different levels between 2 or more samples. The new system or method addresses limitations of prior methods by comprising compositions and systems that incorporate new strategies where molecular or biochemical assay compositions and systems are linked to DNA or RNA sequence databases for optimal resource efficiency in assaying gene cypression. The system has the following advantages over existing methods: (a) prior sequence information or clone library construction is not needed to enable the assay; (b) provides immediate sequence information to information to level and mRNA isocit, to determine mRNA expression level and mRNA isocit.

In one assay; (c) generates cDNA fragments from all mRNAs present in the sample for subsequent investigation by common molecular biology companisms lacking significant genomic sequence in formation. The present in the present in the present in the method of the organism lacking significant genomic sequence in the method of the
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                                                                                                                                                                                                                        The invention relates to systems for identification and characterisation
                                              Identifying and characterizing gene expression in samples, for identifying myNNs expressed at different levels, comprises employing an identimer having a oligo-dT primer of a specific sequence and a detectable marker at its 5' end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Human, T-type calcium channel; CACNAIG; cytosine methylation; CpG island; cellular proliferative disorder; colorectal cancer; age related disease; applipoprotein B, APOB; caudal type homeobox transcription factor 2; CDX2; epidermal growth factor receptor; EGFR; fibrillin-1; FBNI; G protein-coupled receptor 37; GPR37; heat shock 70kD protein 6; HSP70B'; HSPAG; RasGAP-related protein; IQGAP2; proteinse-activated receptor 2; PAR2; paired-like homeodomain transcription factor 2; PITX2; klotho; KL; patched A; patched B; PTCHA; syndecan 1; syndecan 4; SDC1; SDC4; chromosome 17; PCR primer; 88.

Human MINT31/CACNA1G region 6 bisulfite GM6 reverse PCR primer.

(first entry)

18-JUL-2001

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The invention relates to a novel chemically modified oligonucleotide having no more than about 27 nucleic acid base units. The oligonucleotide modulates mammalian telomere length. The chemically modified oligonucleotide of the invention may be useful for modulating the telomere length of a mammalian chromosome, inhibiting the division of a maingnant mammalian cell or modulating the effects of aging of a mammalian cell. The oligonucleotides may also useful for treating diseases associated with abnormal telomere length such as aging and thyperproliferative conditions including cancer. The current sequence is that of the G4 phosphorothicate oligonucleotide 2 (alternative) of the invention which was used to modulate telomere length.
                                                                                                                                                                                                                                                                                                                                                                                                   New chemically modified oligonuclectides, useful for modulating telomere length of a mammalian chromosome, inhibiting the division of a malignant mammalian cell, or modulating the effects of aging of a mammalian cell.
                                                                                        G4 phosphorothioate oligonucleotide 2a used to modulate telomere length.
                                                                                                             telomere length; aging; hyperproliferative condition; cancer; ss; G4
                                                                                                                                                                                                                                                                                                                                                  Brown-Driver VL;
                                                                                                                                                                                                                                                                                                                                                  Chiang M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 24 BP; 0 A; 0 C; 16 G; 7 T; 0 U; 1 Other;
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Wyatt JR;
                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 6; 10pp; English.
                                                                                                                                                                                             /note= "Inosine"
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93WO-US009297.
95US-00403888.
                            ADB68055 standard; DNA; 24 BP.
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                                                                    04-DEC-2003 (first entry)
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Ecker DJ, Vickers TA, W
                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                                                                                             (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-606442/57.
                                                                                                                                                                                                                US2003096776-A1
                                                                                                                                                              modified base
                                                                                                                                 Unidentified
                                                                                                                                                                                                                                                                                       29-SEP-1993;
                                                                                                                                                                                                                                                                                                12-JUN-1995;
                                                                                                                                                                                                                                                                                                         23-APR-1999;
                                                                                                                                                                                                                                    22-MAY-2003
                                                ADB68055
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New nucleic acid molecule for use as a marker for screening cancer, comprises the coding region for a T-type calcium channel and regulatory sequences associated with the channel.

(UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE

WPI; 2001-244777/25.

Issa J;

99US-00398522

15-SEP-1999;

14-SEP-2000; 2000WO-US025479

WO200119845-A1. Homo sapiens.

22-MAR-2001

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The present sequence for bisulfite GM6 reverse PCR primer is used to study the methylation state of region 6 in human MINT31/T-type calcium channel CACMA16 which map to chromosome 17. The methylation state of specific regions within CpG islands associated with the CACMA1G gene correlate with several cancerous phenotypes involving various tissue and cell types. Since aberrant methylation of normally unmethylated CpG islands is often observed in immortalised and transformed cells, CACMA1G is implicated in cellular proliferative disorders e.g. leukaemis, colorectal, lung, breast and other cancers. The nucleic acid coding for CACMA1G is useful as marker for screening cancer and age related diseases. A diagnostic kit containing primers (AAS0154-AAS01623) for amplification of a CpG-containing primers (AAS0157-AAS0163) for be used for detecting aberrant methylation. The CpG island sequences (AAS01677-AAS01692) are selected from genes encoding CACMA1G, apolioportein B (APOB), caudal type homeobox transcription factor 2 (CDX2), epidermal growth factor receptor (EGFR), fibrillin-1 (FBN1), G protein-coupled receptor 37 (GPR37), heat shock 70kp protein 6 (HSP70B', HSPA6), paired receptor 2 (PAR2), paired protein (IQGAP2), paired receptor 2 (PAR2), paired protein (IQGAP2), paired receptor 2 (PAR2), paired-like homeodomain transcription factor 2 (PITX2), patched A and B (PTCHA, PTCHB) and syndecan 1 and 4 (SDC1;
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Pred. No. 2.2e+02;
1; Mismatches 0; Indels
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Claim 21; Page 35; 125pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (PITX2), patched A and B SDC4) or a MINT31 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 95.0%
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RESULT 302 AAS01577

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Gaps

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Length 24; 3; Indels

Score 19.8; DB 1; Pred. No. 1.9e+02; 0; Mismatches

Query Match 1.1%; Best Local Similarity 87.5%;

21; Conservative

Matches

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AAS01617 standard; DNA; 26

AASO1617 ID AASO XX AC AASO

RESULT 301

AAS01617

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AAS01577 standard; DNA; 26
                  22-MAR-2001
 AAS01577;
                         Івва Ј;
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Human; T-type calcium channel; CACNAIG; cytosine methylation; CpG island; cellular proliferative disorder; colorectal cancer; age related disease; apolipoprotein B. APOB; caudal type homeobox transcription factor 2; CDX2; epidermal growth factor receptor; EGFR; fibrillin-1; FBNI; G protein-coupled receptor 37; GPR37; heat shock 70kD protein 6; HSP70B; HSPA6; RasGAP-related protein; IQGAP2; proteinsse-activated receptor 2; PAR2; paired-like homeodomain transcription factor 2; PITX2; klotho; KL; patched A; patched B; PTCHA; PTCHB; syndecan 1; syndecan 4; SDC1; SDC4; chromosome 17; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid molecule for use as a marker for screening cancer, comprises the coding region for a T-type calcium channel and regulatory sequences associated with the channel.
                                                                                          Human T-type calcium channel CACNAIG R6 3'-bisulfite PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 21; Page 34; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-SEP-2000; 2000WO-US025479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-00398522
18-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-244777/25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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The present sequence for 3'-bisulfite PCR primer is used to study the methylation state of region R6 in a novel human T-type calcium channel CACNAIG which maps to chromosome 17. The methylation state of specific regions within CpG islands associated with the CACNAIG gene correlate with several cancerous phenotypes involving various tissue and cell cypes. Since aberrant methylation of normally unmethylated CpG islands is often observed in immortalised and transformed cells. CACNAIG is confident of normally unmethylated CpG islands is conformed in cellular proliferative disorders e.g. leukaemia, colorectal, lung, breast and other cancers. The nucleic acid coding for cancers and useful as a market contenting primers (AASO157-AASO1623) for amplification of a CpG-containing nucleic acid, where the primer hybridises with a target polymucleotide sequence (AASO167-AASO167), can be used for detecting abstrant methylation. The CpG island sequences (AASO167-AASO1692) are selected from genes encoding CACNAIG, apolipoprotein B (APOB), caudal type homeobox transcription factor 2 (CDX2), epidermal growth factor receptor (BGRN), fibrillin-1 (FBN1), Grotein-coupled receptor 37 (GPR37), heat shock 70kb protein 6 (HSP70B'; HSPA6), patred receptor 2 (PAX2), paired protein (IQGAP2), patred procein (IQGAP2), protein-coupled acceptor 2 (PAX3), paired-like homeodomain transcription factor 2 (PIXX2), patrend A and B (PTCHA, PTCHB) and syndecan 1 and 4 (SDC1; SDC4) or a MINT31 sequence

Sequence 26 BP; 18 A; 3 C; 0 G; 4 T; 0 U; 1 Other;

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Query Match
1.1%; Score 19.6; DB 1; Length 26;
Best Local Similarity 95.0%; Pred. No. 2.2e+02;
Matches 19; Conservative 1; Mismatches 0; Indels
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Gaps

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1734 ACAAAAAAAAAAAAAAAA 1753

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The present sequence for human MINT31/T-type calcium channel CACNAIG
region 6 reverse target sequence is used to study the methylation state
CC region 6 in MINT31/CACNAIG which map to chromosome 17. The methylation
state of regions within CGG islands associated with the CACNAIG
state of specific regions within CGG islands associated with the CACNAIG
concernate with several cancerous phenotypes involving various tissue
cc and cell types. Since aberrant methylation of normally unmethylated CpG
islands is often observed in immortalised and transformed cells,
cs implicated in cellular proliferative disorders e.g. leukaemia,
cc islands is useful as a marker for screening cancer and age related
cd issasses. A diagnostic kit containing primers (AASO1574-AASO1632) for
amplification of a CpG-containing primers (AASO1674-AASO1676), can
cc (AASO1677-AASO1692) are selected from genes encoding CACNAIG,
cc (AASO1677-AASO1692) are selected from genes encoding CACNAIG,
cc (CDX2), epidermal growth factor receptor (EGRR), fibrillin-1 (PBN1), G
cc (CDX2), epidermal growth factor receptor (EGRR), fibrillin-1 (PBN1), G
cc (CDX2), epidermal growth factor receptor (EGRR), fibrillin-1 (PBN1), G
cc (CDX2), pacced protein (IQCAP2), klotho (KL), proteinaee-
cativated receptor 2 (FAR2), paired-like homeodomain transcription factor
cc (PDX2), parched A and B (PTCHA, PTCHB) and syndecan I and 4 (SDC1;
cc SDC4) or a MINT31 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                Human; T-type calcium channel; CACNAIG; cytosine methylation; CpG island; cellular proliferative disorder; colorectal cancer; age related disease; apolipoprotein B; APOB; caudal type homeobox transcription factor 2; CDX2; epidermal growth factor receptor; EGFR; fibrillin-1; FBNI; G protein-coupled receptor 37; GPR37; heat shock 70KD protein 6; HSP70B'; PARS; paried-like homeodomain transcription factor 2; PITX2; Klotho; Ki; patched A; patched B; PTCHB; syndecan 1; syndecan 4; SDC1; SDC4; chromosome 17; ds.
                                                                                                                                                                     Human MINT31/CACNAIG region 6 reverse target sequence for bisulfite PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid molecule for use as a marker for screening cancer, comprises the coding region for a T-type calcium channel and regulatory sequences associated with the channel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.1%; Score 19.6; DB 1; Length 26; 95.0%; Pred. No. 2.2e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26 BP; 4 A; 0 C; 3 G; 18 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; Page 36; 125pp; English.
                                          AAS01670 standard; DNA; 26 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-SEP-2000; 2000WO-US025479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-00398522
                                                                                                                          (first entry)
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SBest Local Similarity 95.07
Matches 19, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      API; 2001-244777/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200119845-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-MAR-2001.
                                                                                                                             18-JUL-2001
                                                                                    AAS01670;
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RESULT 303
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93JP-00112515.

93JP-00112515

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A method for the analysis of cDNA comprises (a) preparing an aggregate of McDLA-extranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEC files AA075547-075798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the adouble-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The
                                                                                                                                                                        Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
                                                                                                                                                                                                                                                                                                                                                                                      method can be used to analyse gene expression rapidly and easily
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21 BP; 3 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
                                                                                                      (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1732 TTACAAAAAAAAAAAAAA 1752
                                                                                                                                                                                                                              Disclosure; Page 7; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 95.2
nes 20; Conservative
                                                                                                                                       WPI; 1995-018287/03.
                                  16-APR-1993;
                                                                     16-APR-1993;
01-NOV-1994.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - by amplification of mRNA followed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    double stranded cDNAs by using an aggregate of mRNAs and a plural type clabelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                             Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
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                                                                                                                                                                                                            Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.1%; Score 19.4; DB 1; Length 21; Best Local Similarity 95.2%; Pred. No. 2e+02; Matches 20; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Analysis of cDNA and gene expression - by digestion with restriction enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1732 TTACAAAAAAAAAAAAAAA 1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 6; 11pp; Japanese.
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                  ACRAAAAAAAAAAAAAAA
                                                                                                        BP.
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                                                                                                        21
                                                                                                                                                                           (first entry)
                                                                                                      AAQ75648 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                   JP06303997-A.
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                                                                                                                                                                                                                                                                                                  Synthetic
                  56
                                                                                                                                         AAQ75648;
                                                                   RESULT 304
                                                                                       AAQ75648,
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Gaps

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1.1%; Score 19.4; DB 1; Length 21; 95.2%; Pred. No. 2e+02; ive 0; Mismatches 1; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 double-stranded cDNAs by using an aggregate of mRNAs and a plural type labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A method for the analysis of CDNA comprises (a) preparing an aggregate
                                                                                                                                                                                  gene expression; reverse transcription; primer; cDNA; restriction enzyme; 88.
                                                                                                                                                       Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                                                                                                                                                                                                                                                         (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 6; 11pp; Japanese.
TTATAAAAAAAAAAAAA
                                                                  AAQ75660 standard; DNA; 21 BP
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                                                                                                                            (first entry)
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                                                                                                                                                                                      gene
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                                                                                                                              04-AUG-1995
                                                                                                                                                                                                  aggregate;
                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                   Analysis;
21
                                                                                                  AAQ75660;
                                           RESULT 306
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pene expression; reverse transcription; primer; cDNA; restriction enzyme; ss.

gene

Analysis;

aggregate;

Synthetic

JP06303997-A.

Reverse transcription primer used in cDNA analysis technique.

(first entry)

04-AUG-1995

AAQ75676

BP.

AAQ75676 standard; DNA; 21

RESULT 305

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expression - by amplification of mRNA followed
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                                                                                                                                                                                                                                                                                                                                                                               A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of ababled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
                                               Analysis; gene expression; reverse transcription; primer; cDNA;
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                  Reverse transcription primer used in cDNA analysis technique.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.1%; Score 19.4; DB 1; Length 95.2%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                              (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
                                                                                                                                                                                                                                                                                                                        by digestion with restriction enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1732 TTACAAAAAAAAAAAAAAA 1752
                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 5; 11pp; Japanese.
                                                             aggregate; restriction enzyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 TTCCAAAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP
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                                                                                                                                                                                                                                                                                                           gene
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                                                                                                                                                                                                                                                                                                          Analysis of cDNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                            4PI; 1995-018287/03
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                                                                                                                                                                                  6-APR-1993;
                                                                                                                                                                                                                16-APR-1993;
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                                                                                           Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amplification of mRNA followed
electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                    expression; reverse transcription; primer; cDNA;
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                                                                                                                                                                                                                                                                                                                                        Reverse transcription primer used in cDNA analysis technique.
                                                                          DB 1; Length 21;
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                                                                                                        1; Indels
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                                             Seguence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
                                                                          1.1%; Score 19.4; DB 1 ilarity 95.2%; Pred. No. 2e+02; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Analysis of cDNA and gene expression - by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             by digestion with restriction enzymes
                                                                                                                                      1732 TTACAAAAAAAAAAAAAA 1752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 6; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                    aggregate; restriction enzyme; ss
                                                                                                                                                     21 TGACAAAAAAAAAAAAAA 1
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AAQ75612/C
LD AAQ75612 standard; DNA; 21 BE
XX
AC AAQ75612;
XX
DT 04-AUG-1995 (first entry)
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                                                                                                                                                                                                                                            AAQ75652 standard; DNA; 21
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                                                                                      Best Local Similarity
Matches 20, Conserv
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les 20; Conser
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Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
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                                                                                                                                             AAQ75628 standard; DNA; 21
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                                                                                  RESULT 31:
AAQ75628/c
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                                                                                                                A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
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                                                                                                                                                                                                                                                                                  seperate lanes. The
                                                                                                                                        double-stranded cDNAs by using an aggregate of mENAs and a plural type labelled reverse transcription primers (GENBESO files AAQ75547-Q75798) and using the aggregate of mENAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the duble-stranded CDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of CDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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                                                                                                                                                                                                                                                                                                                                                                                                                             1.1%; Score 19.4; DB 1; Length 21; 55.2%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                           Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;
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by digestion with restriction enzymes.
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                                                        Disclosure, Page 6; 11pp; Japanese.
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Best Local Similarity
Matches 20; Conserv
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
                                                                                                                                            Analysis of cDNA and gene expression - by amplification of mRNA followed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 U; 0 Other;
                                              (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
                                                                                                                                                                        by digestion with restriction enzymes.
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                                                                                                                                                                                                                      Disclosure; Page 6; 11pp; Japanese.
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nes 20; Conservative
                                                                                              WPI; 1995-018287/03
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16-APR-1993;
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Best Local Similarity 95.2 Matches 20; Conservative

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AAQ75712 standard; DNA; 21
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Best Local Similarity 95.2
Matches 20; Conservative
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                       WPI; 1995-018287/03
                                                                                                                                                        Analysis; gene
   16-APR-1993;
          16-APR-1993;
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                                                                                                                                   AAQ75712
                                                                                                                     RESULT 313
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Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
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method can be used to analyse gene expression rapidly and easily
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Pred. No. 2e+02;
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                                           Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
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nes 20; Conservative
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AAQ75673/c
                                                                                                                                                                                                                                                                                           RESULT 314
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                                                                                                                                                                                                 - by amplification of mRNA followed
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Pred. No. 2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
                                                                                                            (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
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                                                                                                                                                                                                                           by digestion with restriction enzymes.
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Reverse transcription primer used in cDNA analysis technique.

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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AAQ75640/c
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digestion with restriction enzymes.
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                                                                                                           A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of abablled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting acts of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                                                                                                                                                                                                                                        1.1%; Score 19.4; DB 1; Length 21; 95.2%; Pred. No. 2e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                     Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
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Matches

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The present sequence is a DNA probe used in a novel method of analysis or assay for nucleotides, which comprises: (i) digesting DNA with a restriction enzyme; (ii) discriminating a difference in sequences of the DNA fragments obtained around the 3' termini with a DNA probe and extending the DNA probe by a complementary strand synthesis to the compare the DNA fragments into groups; and (iii) measuring lengths of the DNA fragments which belong to the groups, or length of the extended DNA probe, and using the lengths obtained for the fragments around the 3' termini as fingerprints. Where polyA is present, the presence of recognition sequence GCG is critical for clarifying the terminal site, this is because the length of polyA cannot be controlled. The method is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              this is because the length of polyA cannot be controlled. The method is useful for assaying a large number of cDNA molecules or DNA fragments and for assaying long DNA sequences
               probe; screening; fingerprinting; assay; 3' termini; hybridisation; ss.
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/note= "this base represents an unspecified number of
bases"
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                                                                                                                                                                                                                                                                                                                                                   Nucleic acid assay methods - based on restriction fragment length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 1.1%; Score 19.4; DB 1; Length 24; 1 Similarity 95.2%; Pred. No. 2.2e+02; 20; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fragment of a plasmid used to detect somatic instability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24 BP; 0 A; 2 C; 1 G; 19 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1735 CAAAAAAAAAAAAAAAAA 1755
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                                                                                                                                                                 96EP-00118921.
                                                                                                                                                                                                     95JP-00311949
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/note=
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                                                                                                                                                                                                                                                                            Kambara H, Okano K,
                                                                                                                                                                                                                                                                                                                 WPI; 1997-300347/28
                                                                                                                                                                                                                                          (HITA ) HITACHI LTD
                                                                                                                                                                                                                                                                                                                                                                        determination.
                                                                                                                                                                 26-NOV-1996;
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                                                                                                                                                                                                     30-NOV-1995;
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                                                                                          EP778351-A2
                                                                                                                              11-JUN-1997
                                                     Synthetic.
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Analysis of cDNA and gene expression - by amplification of mRNA followed
                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                       Analysis, gene expression, reverse transcription; primer, cDNA, aggregate, restriction enzyme; ss.
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Pred. No. 2e+02;
0; Mismatches 1; Indels
                                                     Length 21;
                                                                                          1; Indels
                 Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;
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                                                     DB 1;
                                                 Score 19.4; DB 1
Pred. No. 2e+02;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               by digestion with restriction enzymes.
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                                                                                                                            1735 CAAAAAAAAAAAAAAAAAA 1755
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                                                                                                                                                                 21 CAACAAAAAAAAAAAAAA 1
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                                                     1.1%;
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nes 20; Conservative
                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-018287/03.
                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                  04-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-APR-1993;
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                                                                                          20;
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                                                     Query Match
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AAT68615/C
ID AAT6861
XX
AC AAT6861
XX
XX
DT 20-FEB-
XX
DE DNA pro
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DNA probe used in fingerprinting technique.

20-FEB-1998 (first entry)

Best Loca Matches

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Gaps

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The specification describes a method for determining whether a product of a gene is involved in preventing a replication error in a cell. The method comprises providing the cell with a specific inhibitor for the product and determining the level of functional expression of a marker gene in the cell, where the level of expression of the marker gene is dependent on the occurrence of the replication error. The method is used for determining whether a product of a gene is involved in preventing a replication error in a cell. The identified genes are useful for manipulate cells on the basis of the presence or absence of function of the gene. ABZ2535-36 represents fragments of plasmids used to detect somatic instability, in the course of the invention
                                                                                                                                                                                                                               Determining whether a product of a gene is involved in preventing a replication error in a cell comprises providing a specific inhibitor for the product and determining the level of expression of a marker gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.1%; Score 19.4; DB 1; Length 25; 87.0%; Pred. No. 2.3e+02; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "OTHER= calix(4)arene nucleoside"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 25 BP; 21 A; 0 C; 1 G; 1 T; 0 U; 2 Other;
                                                                                  (NEVW-) KONINK NEDERLANDSE AKAD VAN WETENSCHAPPE.
(TIJS/) TIJSTERMAN M.
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/mod_base= OTHER
                                                                                                                                                                                                                                                                                                                      3xample 1; Fig 3; 47pp; English.
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                                            22-MAY-2001; 2001EP-00201936.
  22-MAY-2002; 2002WO-NL000322.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JAN-2002; 2002KR-00002316.
                                                                                                                                                  Plasterk RHA, Tijsterman M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACF79235 standard; DNA; 25
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/*tag= a
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Best Local Similarity 87.0'
Matches 20; Conservative
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                                                                                                                                                                                            WPI; 2003-129440/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         The specification describes a method for determining whether a product of a gene is involved in preventing a replication error in a cell. The method comprises providing the cell with a specific inhibitor for the product and determining the level of functional expression of a marker gene in the cell, where the level of expression of the marker gene is dependent on the occurrence of the replication error. The method is used for determining whether a product of a gene is involved in preventing a replication error in a cell. The identified genes are useful for manipulate cells on the basis of the presence or absence of function of the gene. ABZ2335-36 represents fragments of plasmids used to detect somatic instability, in the course of the invention
                                                                                                                                                                                                                                                                                                                 Determining whether a product of a gene is involved in preventing a replication error in a cell comprises providing a specific inhibitor for the product and determining the level of expression of a marker gene.
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/note= "this base represents an unspecified number of
bases"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fragment of a plasmid used to detect somatic instability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 24 BP; 20 A; 0 C; 1 G; 1 T; 0 U; 2 Other;
                                                                                                                                                                      (NEVW-) KONINK NEDERLANDSE AKAD VAN WETENSCHAPPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.1%; Score 19.4; DB 1; Best Local Similarity 87.0%; Pred. No. 2.2e+02; Matches 20; Conservative 0; Mismatches 3
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                                                                               22-MAY-2002; 2002WO-NL000322
                                                                                                                            22-MAY-2001; 2001EP-00201936
                                                                                                                                                                                                                                  Plasterk RHA, Tijsterman M;
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/note= '
bases"
                                                                                                                                                                                            (TIJS/) TIJSTERMAN M.
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WO200295071-A2.
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                                                                                   The present sequence is that of a calix(4) arene-oligonucleotide hybrid of the invention, which includes a calix(4) arene-nucleoside (preferably thymidine) derivative. The calix(4) arene-oligonucleotide hybrid functions as a DNA hairpin structure minic. It effectively recognises DNA or RNA through triplex formation by bonding between the calix(4) arene-containing cavity and a biologically active substance. The hybrid has a certain level of both rigidity and flexibility, is stable in vivo, has high cell permeability and can be mass-produced. It can be used as a DNA sensor or
                                New calix(4) arene-nucleoside hybrid useful in gene therapy has at least one nucleoside attached to a calix(4) arene group through amide bonding, and is derived from a calix(4) arene having amino groups.
                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                             1.1%; Score 19.4; DB 1; Length 25; 90.9%; Pred. No. 2.3e+02; Live 0; Mismatches 2; Indels
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/mod_base= OTHER
/note= "OTHER= locked nucleic acid"
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/note= "OTHER= locked nucleic acid"
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'note= "OTHER= locked nucleic acid"
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/note= "OTHER= locked nucleic acid"
                                                                                                                                                                                                                                                                                                                                                                    Locked nucleic acid; LNA; gene therapy; primer; ss
                                                                                                                                                                            Sequence 25 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                  Locked nucleic acid anchored oligo(I) primer ON12
                                                                                                                                                                                                                                  1734 ACAAAAAAAAAAAAAAAAAA 1755
                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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/mod_base= OTHER
                                                                                                                                                                                                                                                 Claim 7; Page 20; 16pp; English
                                                                                                                                                                                                                                                                                              ACC48482 standard; DNA; 21
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                                                                                                                                                                                                      Local Similarity 90.9
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               WPI; 2003-627375/59.
                                                                                                                                                             for gene therapy
Kim SJ;
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modified_base
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Matches
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The present sequence is that of pyrene-anchored locked nucleic acid (LNA) coligo(dT) primer ON12, which was used in first-strand cDNA synthesis from eukaryotic mRNA. It includes compound '17d' at its 3' end, which is based on an LNA-type 2'-0,4'-C-methylene-beta-D-ribofuranosyl moiety. It is come of a set of such primers (see also ACC48480-85) that were used in an example from the invention to demonstrate improved reverse transcription of mRNA using pyrene-LNA anchored oligo(T) primers. The following results were observed: efficient priming on mRNAs with short poly(A) tails; efficient anchoring of the oligo(T) primer by pyrene-LNA and LNA-C/G/T counts resulting in an improved T20-VM anchor primer and thus avoiding reverse transcription of long poly(A) tracts; and improved reverse transcription of enkaryotic poly(A) tracts; and improved reverse transcription of enkaryotic poly(A) tracts; and improved reverse transcription of enkaryotic poly(A) tracts; and improved reverse transcription of abses groups. Desirable mucleobase and nucleosidic comprise unique base groups. Desirable nucleobase and nucleosidic into nucleic acid strands. The novel LNA compounds can be used e.g. as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acid comprising a locked nucleic acid unit having a modified base that comprises an optionally substituted carbocyclic aryl moiety, or modified nucleobase or nucleosidic base other than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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19; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                       /*tag= j
/mod_base= OTHER
/note= "OTHER= locked nucleic acid"
                                                                                                                                                                                                     /*tag= i
/mod_base= OTHER
/note= "OTHER= locked nucleic acid"
'note= "OTHER= locked nucleic acid"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mod_base= OTHER
/note= "OTHER= Compound 17d"
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22-SEP-2001; 2001US-0323967P.
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                                                                      *tag=
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ACC99729;

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The sequences given in AAQ73325-81 represent oligonucleotides which hybridise specifically with DNA or RNA from a herpes virus gene corresponding to one of the open reading frames ULS, -8, -9, -20. 29, -30, -42, -52 or IE175 of herpes simplex virus type I (HSV-1). These oligos pref. hybridise with a translation initiation site, a coding region or a 5' untranslated region. These oligos may be used in compositions for the treatment and diagnosis of herpes viral infection, by contacting the virus or the animal, or its cells, tissues or body fluids with the oligo. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New oligonucleotide(s) hybridising with DNA or RNA of herpesvirus gene are used in the treatment and diagnosis of herpes simplex virus, cytomegalovirus, Epstein Barr virus and varicella zoster infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhibition; replication; herpes simplex virus; HSV; HIV; human cytomegalovirus; influenza virus; inflammation; neurological disorders; phospholipase A2 activity; hyperproliferation; malignancy; cardiovascular diseses; snake bite; malignancy; telant; retard; aging; ss.
                                                                                                                                                                                                                                                                                                                                                                                    Crooke ST, Mirabelli CK, Ecker DJ, Hanecak R;
Brown-Driver VL, Wyatt JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.1%; Score 19.2; DB 1; Length 24; Best Local Similarity 87.5%; Pred. No. 2.3e+02; Matches 21; Conservative 0; Mismatches 3; Indels
                                                  Hybridise; herpes simplex virus; HSV; open reading frame;
translation initiation site; coding region; 5' UTR; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 24 BP; 0 A; 0 C; 16 G; 8 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1019 TTGGGGATGGGGTTGTGG 1042
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(first entry)
Anti-HSV-1 G4 oligo #5651.
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/*tag=
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misc_feature
                                                                                                                                                                                                                                                                                                                                                                                    Draper KG, C:
Anderson KP,
                                                                                                                                                               W09419945-A1
                                                                                                                                                                                                                                                       17-MAR-1994;
                                                                                                                                                                                                                                                                                                 12-MAR-1993;
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04-NOV-1994
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                                                                                                                   Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a multiplex real-time quantitative PCR method for determining the relative copy number of a group of target mucleic acid molecules present in a sample. The method comprises: (1) performing a first PCR in a PCR mixture; (2) performing a second PCR in a PCR mixture; (2) performing a second PCR in a PCR mixture; (2) performing a second PCR in a PCR mixture; (3) performing a second PCR in a PCR mixture; (1) a performing a second PCR in a proup of target nucleic acid product present in the sample containing the target nucleic acid molecule. Also described: (1) quantifying the copy number of a group of target nucleic acid as asmple; and (2) determining whether a subject is at risk of acquiring Alzheimer's disease. The method is nucleic acid molecules present in a sample for determining whether subject is at risk of acquiring Alzheimer's disease. ACC99520 to ACC99730 represent PCR primer used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Determining the relative copy number of a group of target nucleic acid molecules present in a sample by performing a first or second PCR in a PCR mixture and quantifying the number of copies of the second target
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                                                                                                                                                                                                                                                     quantitative PCR; PCR primer; copy number;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 2 Other;
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                                                                       ACC99729 standard; DNA; 21 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-DEC-2002; 2002WO-US038806.
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Best Local Similarity 95.0
Matches 19; Conservative
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Alzheimer's disease; ss
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                                                                                                                                                                                                           Oligonucleotide
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02-MAY-1995
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/note= "Phosphorothionate intersugar linkages"

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                                                                                                                                                  New modified oligo-nucleotide contg guanine quartet - inhibits activity of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length of chromosomes.
                                                                                                                                                                                                                       which contain a G4 or two G3 stretches and which may be used for inhibiting replication of herpes simplex virus (HSV). Oligonuclectides such as these may also be used for inhibiting activity of HIV, human cytomegalovirus or influenca virus, or for treating inflammatory and neurological disorders caused by phospholipase A2 activity in cases of hyperproliferation, malignancy, cardiovascular disease and snake bite. They may also be used for inhibiting division of malignant cells by modualting telomere length, which may also retard aging. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                               sequences given in AAQ61825-50 and AAQ61886-906 are oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibition; replication; herpes simplex virus; HSV; HIV; retard; human cytomegalovirus; influenza virus; inflammation; telomere length; neurological disorders; phospholipase A2 activity; hyperproliferation; malignancy; cardiovascular disease; snake bite; malignancy; aging; ss.
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                                                                                                  Brown-Driver VL;
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/note= "Phosphorothionate intersugar linkages"
                                                                                                                                                                                                                                                                                                                                             Length 24;
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                                                                                                 P, Bennett CF, Chiang M, Wyatt JR, Imbach JL;
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                                                                                                                                                                                                                                                                                                                                             Score 19.2; DB 1;
Pred. No. 2.3e+02;
0; Mismatches 3;
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                                                                                                                                                                                            Disclosure; Page 19; 144pp; English
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                                         93WO-US009297
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                                                          92US-00954185
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                                                                                                  , Anderson KP,
Vickers TA, W
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                                                                              (ISIS-) ISIS PHARM INC
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                                                                                                                                WPI; 1994-135613/16
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                                       29-SEP-1993;
                                                           29-SEP-1992;
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 WO9408053-A1
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                     14-APR-1994
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                                                                                                Hanecak RC,
                                                                                                              Ecker DJ,
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AAQ61990
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New modified oligo-nucleotide contg guanine guartet - inhibits activity of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length of chromosomes.
                                                                                                                                                                                                                                                                                                                                                                                          The sequences given in AAO61990-2001 are oligonucleotides which contain G4 or G3 stretches and which may be used for inhibiting replication of herpes simplex virus (HSV), activity of HIV, human cytomegalovirus or influenza virus, or for treating inflammatory and neurological discoders caused by phospholipase A2 activity in cases of hyper- proliferation, malignancy, cardiovascular disease and snake bite. Oligonucleotides such modualting telomere length, which may also retard aging. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhibition; replication; herpes simplex virus; HSV; HIV; human cyromegalovirus; influenza virus; influenza virus; ortomegalovirus; influenza virus; influenza virus; interclogical disorders; phospholipase A2 activity; hyperproliferation; malignancy; cardiovascular disease; snake bite; malignancy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                          Brown-Driver VL;
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/note= "Phosphorothionate intersugar linkages"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.1%; Score 19.2; DB 1; Length 24; 87.5%; Pred. No. 2.3e+02; ive 0; Mismatches 3; Indels
                                                          Chiang M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24 BP; 0 A; 0 C; 16 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSV replication inhibiting oligomer, ISIS no 5651.
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J, Vickers TA, Wyatt JR, Imbach JL;
                                                       Bennett CF, Chian
att JR, Imbach JL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   telomere length; retard; aging; ss
                                                       Hanecak RC, Anderson KP, Bennett
Ecker DJ, Vickers TA, Wyatt JR,
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(first entry)
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(ISIS-) ISIS PHARM INC.
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04-NOV-1994
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The sequences given in AAQ61825-50 and AAQ61886-906 are oligonucleotides which contain a 4d or two G3 stretches and which may be used for inhibiting replication of herpes simplex virus (HSV). Oligonucleotides such as these may also be used for inhibiting activity of HIV, human orthogological disorders orine, or for treating inflammatory and neurological disorders caused by phospholipaes A2 activity in cases of hyperproliferation, malignancy, cardiovascular disease and snake bite. They may also be used for inhibiting division of malignant calls by modualizing telomere length, which may also retard aging. (Updated on 25-MAR-2003 to correct PN field.)
             New modified oligo-nucleotide contg guanine quartet - inhibits activity of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibition, replication, herpes simplex virus, HSV, HIV, retard, human cytomegalovirus, influenza virus, influenze length, neurological disorders; phospholipses A2 activity, hyperproliferation, malignancy; cardiovascular disease; snake bite; malignancy; aging; ss.
                                                                                                                                                                                                                                                                                                                           Gaps
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/note= "Phosphorothionate intersugar linkages"
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                                                                                                                                                                                                                                                                Sequence 24 BP; 0 A; 0 C; 16 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guanine quartet containing oligomer, #8.
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/*tag= a
                                                                      Claim 5; Page 19; 144pp; English
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(first entry)
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Matches 21, Conservative
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04-NOV-1994
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New modified oligo-nucleotide contg guanine quartet - inhibits activity of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length

Disclosure; Page 107; 144pp; English.

of chromosomes.

Brown-Driver VL

Chiang M,

Bennett CF, Chian att JR, Imbach JL;

RC, Anderson KP, Bennett I, Vickers TA, Wyatt JR,

Ecker DJ,

Hanecak

WPI; 1994-135613/16.

92US-00954185

29-SEP-1992;

(ISIS-) ISIS PHARM INC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /notes "at least one (and preferably all) of the backbone subunits are composed of N-acetyl N-(2-aminoethyl)glycine peptide residues, the nucleobase being attached covalently to the acetyl group and the peptide linkage being formed by condensation of the glycine carboxy group of one residue with the amino group of the 2-aminoethyl moiety in the next residue"
The sequences given in AAO61990-2001 are oligonucleotides which contain G4 or G3 stretches and which may be used for inhibiting replication of herpes simplex virus (HSV), activity of HIV, human cytomegalovirus or influence avirus, or for treating inflammatory and neurological disorders caused by phospholipase A2 activity in cases of hyper- proliferation, malignancy, cardiovascular disease and snake bite. Oligonucleotides such modualting telomere length, which may also retard aging. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligomer hybridisable to HIV sequence and contg. peptide nucleic acid sub:unit - binds in complementary manner to DNA and RNA, and useful for modulating HIV viral activity, e.g. in treating AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New peptide nucleic acid (PNA) oligomers are provided which (a) consist of naturally occurring nucleobases covalently bound to a polyamide backbone and (b) hybridise to the translation initiation AUG region, 5' untranslated region (5' UTR), 3' untranslated region (3' UTR), splice junctions or coding sequence of a human immunodeficiency virus gene
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide nucleic acid; PNA; HIV; human immunodeficiency virus; AIDS; antiviral; antisense; triple helix; ss.
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                                                                                                                                                                                                                   ch 1.1%; Score 19.2; DB 1; Length 24; 1 Similarity 87.5%; Pred. No. 2.3e+02; 21; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide nucleic acid oligomer targetting HIV gene.
                                                                                                                                                                                    Sequence 24 BP; 0 A; 0 C; 16 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                             1019 TTGGGGATGGGGCTGGGGTTGTGG 1042
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/*tag=
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                                                                                                                                                                                                                                         Best Local Similarity
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19-OCT-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ97981;
                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                   RESULT 333
                                                                                                                                                                                                                                                        Matches
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chosen from env, gag, pol, rev and tat. The PNAs can be used to target
RNA and single stranded DNA (ssDNA) to produce antisense-type gene
regulation moieties. They have utility as gene-targetted drugs for
modulating HIV processes. They have utility as gene-targetted drugs for
research tools. PNA obligomers have high affinity for complementary single
stranded DNA. They are also useful in diagnostic applications and as
stranded DNA. They are also able to form triple helices in which a first
PNA strand binds with RNA or ssDNA and a second PNA strand binds with the
resulting double helix or with the first PNA strand binds with the
resulting double helix or with the first PNA strand binds with the
resulting double helix or with the first PNA strand binds and uptake. Further, since they contain amides of non-biological amino acids,
they are biostable and resistant to enzymatic degradation by proteases.
The present sequence is a specifically claimed PNA sequence (represented
by the sequence of nucleobases) targetting HIV genes. (Updated on 25-MAR-

Sequence 24 BP; 0 A; 0 C; 16 G; 8 T; 0 U; 0 Other;

Gaps ; 0 1.1%; Score 19.2; DB 1; Length 24; 87.5%; Pred. No. 2.3e+02; 3; Indels 0; Mismatches 1019 TTGGGGATGGGGCTGGGGTTGTGG 1042 1 rrecectrecerrecerreces 24 21; Conservative Local Similarity Query Match Matches 8 g

ADB68048

ADB68048 standard; DNA; 24 ADB68048;

ВÞ

04-DEC-2003 (first entry)

G4 phosphorothioate oligonucleotide 2 used to modulate telomere length.

telomere length; aging; hyperproliferative condition; cancer; ss; G4

Unidentified

US2003096776-A1

22-MAY-2003

02-JAN-2002; 2002US-00038335

92US-00954185. 93WO-US009297. 95US-00403888. 99US-00299058. 29-SEP-1992; 29-SEP-1993; 12-JUN-1995; 23-APR-1999;

(ISIS-) ISIS PHARM INC

Brown-Driver VL; Chiang M, Bennett CF, Wyatt JR; , Anderson KP, Vickers TA, W Hanecak RC, Ecker DJ, 

WPI; 2003-606442/57

New chemically modified oligonucleotides, useful for modulating telomere length of a mammalian chromosome, inhibiting the division of a malignant mammalian cell, or modulating the effects of aging of a mammalian cell.

Example 2; Page 8; 10pp; English.

The invention relates to a novel chemically modified oligonucleotide having no more than about 27 nucleic acid base units. The oligonucleotide modulates mammalian tellomere length. The chemically modified oligonucleotide of the invention may be useful for modulating the telomere length of a mammalian chromosome, inhibiting the division of a mailgnant mammalian cell or modulating the effects of aping of a mammalian cell. The oligonucleotides may also useful for treating diseases associated with abnormal telomere length such as aging and

ö hyperproliferative conditions including cancer. The current sequence is that of the G4 phosphorothicate oligonucleotide 2 of the invention which was used to modulate telomere length. Gaps ö Length 24; 3; Indels Sequence 24 BP; 0 A; 0 C; 16 G; 8 T; 0 U; 0 Other; Score 19.2; DB 1; Pred. No. 2.3e+02; 0; Mismatches 3; 1019 TIGGGGATGGGCTGGGGTTGTGG 1042 1 TTGGGGTTGGGGTTGGGG 24 tch 1.1%; al Similarity 87.5%; 21; Conservative C Query Match Best Local S: Matches 21, 88666 g ò

BP. AAQ61892 standard; DNA; 25 AAQ61892; RESULT 335 AAQ61892 

(first entry) (revised) 25-MAR-2003 04-NOV-1994

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HSV replication inhibiting oligomer, ISIS no 5366.

Inhibition; replication, herpes simplex virus; HSV; HIV; human cytomegalovirus; influenza virus; influenza virus; influenza virus; neurological disorders; phospholipase A2 activity; hyperproliferation; neurological disorders; phospholipase A2 activity; hyperproliferation; telomere length; retard; aging; ss.

Synthetic

/*tag= a /note= "Phosphorothionate intersugar linkages" Location/Qualifiers ...25 *tag= misc_feature

93WO-US009297. WO9408053-A1 29-SEP-1993; 14-APR-1994

92US-00954185. 29-SEP-1992;

(ISIS-) ISIS PHARM INC.

, Anderson KP, Bennett CF, Chiang M, Brown-Driver VL; Vickers TA, Wyatt JR, Imbach JL; Hanecak RC, Ecker DJ,

WPI; 1994-135613/16.

New modified oligo-nucleotide contg guanine quartet - inhibits activity of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length of chromosomes.

Claim 5; Page 19; 144pp; English.

The sequences given in AAQG1825-50 and AAQG1886-906 are oligonucleotides which contain a G4 or two G3 stretches and which may be used for inhibiting replication of herpes simplex virus (HSV). Oligonucleotides such as these may also be used for inhibiting activity of HIV, human cytomegalovirus or influenza virus, or for treating inflammatory and neurological disorders caused by phospholipase A2 activity in cases of hyperproliferation, malignancy, cardiovascular disease and snake bite. They may also be used for inhibiting division of malignant cells by modualting telomere length, which may also retard aging. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 25 BP; 0 A; 0 C; 17 G; 8 T; 0 U; 0 Other;

BP

AAQ97978 standard; DNA; 25

RESULT 337

1 TTGGGGTTGGGGTTGGGG

Peptide nucleic acid; PNA; HIV; human immunodeficiency virus; AIDS; antiviral; antisense; triple helix; 88.

Synthetic.

Peptide nucleic acid oligomer targetting HIV gene.

(revised)
(first entry)

25-MAR-2003 19-OCT-1995

AAQ97978;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New modified oligo-nucleotide contg guanine quartet - inhibits activity of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
                                                                                                                                                                                                                                                                                                                                                       human cytomegalovirus; influenza virus; inflammation;
neurological disorders; phospholipase A2 activity; hyperproliferation;
malignancy; cardiovascular disease; snake bite; malignancy;
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanecak RC, Anderson KP, Bennett CF, Chiang M, Brown-Driver VL; Ecker DJ, Vickers TA, Wyatt JR, Imbach JL;
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/note= "Phosphorothionate intersugar linkages"
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   Length 25;
                                   3; Indels
                                                                                                                                                                                                                                                                                                                                         Inhibition; replication; herpes simplex virus; HSV; HIV;
                                                                                                                                                                                                                                                                                                      HSV replication inhibiting oligomer, ISIS no 5367.
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1.1%; Score 19.2; DB 1;
ilarity 87.5%; Pred. No. 2.4e+02;
Conservative 0; Mismatches 3;
                                                                  1019 TTGGGGATGGGCTGGGGTTGTGG 1042
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                                                                                                                                                                                    AAQ61893 standard; DNA; 25
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(first entry)
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/*tag=
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Ouery Match
Best Local Similarity
Matches 21; Conserv
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04-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
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New peptide nucleic acid (PNA) oligomers are provided which (a) consist of naturally occurring nucleobases covalently bound to a polyamide backbone and (b) hybridise to the translation initiation AUG region, 5' untranslated region (5' UTR), 3' untranslated region (3' UTR), splice intranslated region (5' UTR), 3' untranslated region (3' UTR), splice consent from env. gag, pol, rev and tat. The PNAs can be used to target RNA and single stranded DNA (ssDNA) to produce antisense-type gene regulation HTV processes. Hence they can be used to treat AIDS and other viral infections. They are also useful in diagnostic applications and as reanded DNA. They are also able to form triple helices in which a first PNA strand binds with RNA or ssDNA and a second PNA strand binds with RNA or ssDNA and a second PNA strand binds with the first PNA strand binds with they are significant charge and are water soluble, which facilitates cellular uptake. Further, since they contain amides of non-biological amino acids, they are biostable and resistant to enzymatic degradation by proteases.

The present sequence is a specifically claimed PNA sequence (represented by the sequence of nucleobases) targetting HIV genes. (Updated on 25-MAR-
                                                                                                                                                                                                                                                                                                                           /note= "at least one (and preferably all) of the backbone subunits are composed of N-acetyl N-(2-aminoethyl)glycine peptide residues, the nucleobase being attached covalently to the acetyl group and the peptide linkage being formed by condensation of the glycine carboxy group of one residue with the amino group of the 2-aminoethyl moiety in the next residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligomer hybridisable to HIV sequence and contg. peptide nucleic acid sub:unit - binds in complementary manner to DNA and RNA, and useful for modulating HIV viral activity, e.g. in treating AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25 BP; 0 A; 0 C; 17 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 176; 186pp; English.
                                                                                                                                                                                                                                                                                                               /*tag= a
/note= "at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94WO-US008517.
                                                                                                                                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-082179/11.
                                                                                                                                                                                                                                                                                          misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09504068-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-FEB-1995
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1019 TTGGGGATGGGCTTGGGGTTGTGG 1042

87.5%;

Best Local Similarity 87.5 Matches 21, Conservative

Query Match

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Gaps

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Identifying extendible primers for use in identification, or classification of a nucleic acid of an organism, allele or gene such as class 1/2 HLA comprises identifying all possible nucleotide sequences of
                           DNA sequence analysis; sequencing; protein sequence; protein structure; gene typing; organ donation; bacteria identification; 16s rRNA; HLA; human leukocyte antigen; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a method for identifying a set of extendible primers which can be used in the identification, typing and classification of genes. This can then be used to predict protein sequence and structure, in organ donation to match the organ with the receiver, and to identify bacteria in a sample. The method can be used type the human leukocyte antigen genes (HLA) and 16s rRNA genes in particular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.1%; Score 19.2; DB 1; Length 25; 87.5%; Pred. No. 2.4e+02; tive 0; Mismatches 3; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25 BP; 3 A; 3 C; 5 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1724 CCTCGAGTTTACAAAAAAAAA 1747
                                                                                                                                                                                                                           (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 14; Page 45; 66pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP
 16s rRNA gene PCR primer #41.
                                                                                                                                                                      20-APR-2000; 2000WO-EP003636.
                                                                                                                                                                                                 99EP-00303215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93JP-00112515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93JP-00112515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                549/c
AAQ75549 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21; Conservative
                                                                                                                                                                                                                                                       Wong K;
                                                                                                                                                                                                                                                                                   WPI; 2000-679677/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                      specific length,
                                                                                                               WO200065088-A2
                                                                                                                                                                                                 26-APR-1999;
                                                                                    Homo sapiens
                                                                                                                                                                                                                                                       Ulfendahl P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JP06303997-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L6-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ75549;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a method for identifying a set of extendible primers which can be used in the identification, typing and classification of genes. This can then be used to predict protein sequence and structure, in organ donation to match the organ with the receiver, and to identify bacteria in a sample. The method can be used to type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying extendible primers for use in identification, or classification of a nucleic acid of an organism, allele or gene such as class 1/2 HLA comprises identifying all possible nucleotide sequences of specific length.
                                                                                                                                                                                                                                                                   DNA sequence analysis; sequencing; protein sequence; protein structure; gene typing; organ donation; bacteria identification; 16s rRNA; HLA; human leukocyte antigen; PCR primer; ss.
                           Gaps
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Pred. No. 2.4e+02;
0; Mismatches 3; Indels
 Length 25;
                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25 BP; 3 A; 3 C; 3 G; 16 T; 0 U; 0 Other;
Score 19.2; DB 1;
Pred. No. 2.4e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1727 CGAGTTTACAAAAAAAAAAAA 1750
                                                       1019 TTGGGGATGGGGCTGGGGTTGTGG 1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
                                                                          CGTCTGTACAAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 14; Page 48; 66pp; English
                                                                                                                                                        BP
1.1%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                            20-APR-2000; 2000WO-EP003636.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.1%;
                                                                                                                                                                                                                                       HLA DPA1 gene PCR primer #8
                                                                                                                                                      AAC96251 standard; DNA; 25
                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-2001 (first entry)
                           21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wong K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-679677/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC96074 standard;
              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                      WO200065088-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ulfendahl P,
                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                        26-APR-1999;
                                                                                                                                                                                                            26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                02-NOV-2000.
                                                                                                                                                                                  AAC96251;
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 Query Match
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AAC96074/c
ID AAC9607
XX
AC AAC960
XX
DT 26-FEE
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                                                                        A method for the analysis of cDNA comprises (a) preparing an aggregate of McDLA-estranded cDNAs by using an aggregate of mcNAs and a plural type of labelled reverse transcription primers (GRNESEQ files AAQ75547-C75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequences given in AAT10742-67 are synthetic oligonucleotides which are used in the construction of the electronically self- addressable device (ED) of the invention. The ED comprises a substrate, an electrode or opt- a number of electrodes supported by the substrate, a current source operatively connected to the electrode and an attachment layer adjacent to the electrode which is permeable to a counterion but not
                   Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Electronically self-addressable device - used for electronic control of, e.g. nucleic acid hybridisation.
                                                                                                                                                                                                                                                                                                                                                                                                               Electronically self-addressable device; ED; electrode; current source; attachment layer; permeable; counterion; genetic typing; probe;
                                                                                                                                                                                                                        Gaps
                                                                                                                                                      method can be used to analyse gene expression rapidly and easily
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                                                                                                                                                                                                1.1%; Score 19; DB 1; Length 19; 100.0%; Pred. No. 2e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                          Sequence 19 BP; 0 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/note= "5'-amino terminus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sosnowski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 61; 155pp; English.
                                                    Disclosure; Page 5; 11pp; Japanese.
                                                                                                                                                                                                                                             1734 ACAAAAAAAAAAAAAAA 1752
                                                                                                                                                                                                                                                                  19 ACAAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                         AAT10757 standard; RNA; 19 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94US-00271882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Evans GA,
                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide probe, T-2
                                                                                                                                                                                                                                                                                                                                                                    09-SEP-1996 (first entry)
                                                                                                                                                                                                           Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NANO-) NANOGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-097582/10.
WPI; 1995-018287/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.
E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                     detection; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9601836-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JAN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                               AAT10757;
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permeable to a molecule capable of insulating or binding to the electrode. The attachment layer is capable of attaching a macromolecule. The ED is used for genetic typing and comprises a number of electronically addressable locations comprising an electrode, and a binding entity, such as one of these probes, attached to each of the locations capable of detecting the presence of a genetic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New aminooxy-modified oligonucleotides - which can show improved binding to complementary strands and improved resistance to nuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphorothioate; ras gene; malignant cell growth; aminooxy-modified; nuclease resistance; reporter group; 88.
                                                                                                                                                                                                                                                                                                                                                                            Gарв
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "5-methyl, 2'-aminooxyethoxy-thymidine"
                                                                                                                                                                                                                                                                                                 1.1%; Score 19; DB 1; Length 19;
100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                      Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aminooxy-modified oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                       1736 AAAAAAAAAAAAAAAA 1754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВЪ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-568232/48
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modified_base
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                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 342
AAV07878/c
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AAX81316 standard; DNA; 19 BP.

Microelectronic device; multi-step reaction; microscopic format; ion-permeable permeation layer; electrode; electrical control; transport; attachment; binding; DNA/RNA hybrid; probe; ss.

amino oligonucleotide probe T-2.

(first entry)

20-AUG-1999

AAX81316;

a "amino group attached at 5' terminal"

/note= /*tag=

WO9929711-A1

17-JUN-1999

cocation/Qualifiers

misc_feature

Synthetic

Mon Aug 16 16:46:36 2004

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "these T residues are formed as part of a conventional phosphoramidite oligonucleotide synthesis process but using as the reactant a thymosine nucleoside having at the 3'-position a group of formula -CH2-P(OCH2CH2CN)-N(iPr)2"
                                                                      Gaps
                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New tetra:hydro:furan derivatives - useful in the synthesis of oligo:nucleotide(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide containing modified internucleotide linkage.
Score 19; DB 1; Length 19;
Pred. No. 2e+02;
0; Mismatches 0; Indels
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                                   100.0%; Pred. No. 2e+
ive 0; Mismatches
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      1.18;
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                                      Best Local Similarity
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modified_base
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      Query Match
                                                                Matches
                                                                                                                                                                                                                                                                             RESULT 343
AAV06820/C
ID AAV06820/C
XX AAV06
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XX AAV06
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New microelectronic device designed to carry out and control multi-step and multiplex molecular biological reactions in microscopic format.

Example 1; Page 90; 179pp; English

Edman CF

Heller MJ,

Nerenberg MI,

Ta B,

Sosnowski RG, Butler WF,

(NANO-) NANOGEN INC.

98WO-US025475. 97US-00986065.

01-DEC-1998; 05-DEC-1997;

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The specification describes a self-addressable, self-assembling microelectronic device which is designed to actively carry out and control multi-step and multiplex molecular biological reactions in microscopic formats. A key aspect of this inventions is played by the ion permeable permeation layer which overlies the electrode. This permeation layer which overlies the electrode. This permeation layer which overlies the electrode by the ion separates the attached oligonucleotides and hybridized target DNA sequences from the highly reactive electrochemical environment generated immediately at the electrode surface. The microelectronic device is sendesigned and feabricated to actively carry out and control reactions such as nucleic acid hybridizations, antibody/antigen reactions, sample preparation, diagnostics and biopolymer synthesis. The device can sucleic acids and polypeptides, to specific binding entities, such as nucleic acids and polypeptides, to specific micro-locations. The device can subsequently control the transport and reaction of analytes or reactants at the addressed specific micro-locations. The specifically bound molecules, provide stringency control for DNA specifically bound molecules, provide stringency control for DNA hybridization reactions and improve the detection of analytes. The present sequence represents a probe used to exemplify the invention
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100.0%; Pred. No. 2e+02;
ive 0; Mismatches 0; Indels
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AAX81927/c
ID AAX81927 standard; DNA; 19 BP.
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Best Local Similarity 100.0
Matches 19, Conservative
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DB 1; Length 19; 2e+02; Indels

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19 AAAAAAAAAAAAAAA 1

RESULT 344 AAX81316/c

Score 19; Pred. No.

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RESULT 346 AAZ01358/c

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wavelength from far UV region (350-400 nm) to the 500-600 nm region of the electromagnetic spectrum and reducing the effect of background signal levels of intact reagents. The present sequence is used in the course of
                                                                                                                                                                                                                                                                                                                  Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
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Best Local Similarity 100.(
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                        the invention
    AAX81927;
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Enzyme-specific cleavable polynuclectide substrate;
quenched fluorescent moiety; biological assay; detection; identification;
microorganism; sterilization assurance; nuclease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The specification describes an enzyme-specific cleavable polynucleotide substrate bearing quenched fluorescent moieties. The enzyme-specific cleavable polynucleotide substrate is useful in biological assays for detection and identification of microorganisms, sterilization assurance, biological assays. The method provides a rapid and convenient approach for detection and identification of microorganisms. It can be adapted to sequence-dependent or sequence-independent tests. The invention provides and identification, and overall lower cost in detection and identification, and overall lower cost in detection measured more accuracely and sensitively by red-shifting the emission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= d
/note= "amine-modified C6 derivative of deoxythymidine
(dT)"
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'note= "amine-modified C6 derivative of deoxythymidine
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/note= "amine-modified C6 derivative of deoxythymidine
(dT)"
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note= "amine-modified C6 derivative of deoxythymidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 An enzyme-specific cleavable polynucleotide substrate bearing quenched
                                                            Polynucleotide strand with amino groups.
                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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07-SEP-1999 (first entry)
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                                                                                                                        PGI gene; biallelic marker; PCR primer; PGI-related biallelic marker; cancer; prostate specific antigen; PSA; human; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of a prostate cancer associated gene and biallelic markers derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the organ. A need exists for both a reliable diagnostic procedure which would enable early stage diagnosis, and for preventative and curative treatments of the disease. The PGI gene can be used for detection of prostate cancer, and the risk of developing it in the future, and can also be used to determine therapies for the disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                  PCR primer for PG1 biallelic marker 4-4-187.
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BP
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98US-0099658P.
 AAZ01358 standard; DNA; 19
                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                          (GEST ) GENSET
                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                     WO9932644-A2
                                                                  27-SEP-1999
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                                 AAZ01358;
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hote= "2'-O-[2-N,N-dimethylaminoethyl)oxyethyl-5- methyl
uridine"
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                                                                                                                                                                                                                                                                                                                                               Novel 2'-O-aminoethyloxyethyl modified nucleosides and oligonucleotides used in diagnostic, therapeutic and research reagents.
                                                               l. .19
*tag= a
'note= "nucleosides linked by phosphodiester linkages"
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100.0%; Pred. No. 2e+02;
ive 0; Mismatches 0; Indels
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 nuclease resistance; phosphorothioate; ss.
                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 51; 60pp; English.
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AAC62422 standard; DNA; 19 BP.
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les 19, Conserv
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                                                                                                    modified base
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                                                             misc_feature
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                         Synthetic
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents an uniform phosphodiester oligomuclectide. The specification describes oligomeric compounds containing 2'.O-modified ribosyl nucleosides. The 2'-O-modified nucleosides include ring structures that position the sugar moiety of the nucleosides preferentially in 3' endo geometries. The modified oligomeric compounds have increased binding affinity and increased nuclease resistance. The oligomeric compounds can be used in diagnostic, therapeutic and research reagents
                                                   Oligomeric compound; 2'-0-modified ribosyl nucleoside; 3' endo geometry; nuclease resistance; phosphodiester; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligomeric compound; 2'-O-modified ribosyl nucleoside; 3' endo geometry;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel 2'-O-aminoethyloxyethyl modified nucleosides and oligonucleotides used in diagnostic, therapeutic and research reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2'-O-modified ribosyl oligonucleotide with phosphodiester linkages
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Pred. No. 2e+02;
0; Mismatches 0; Indels
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100.0%; Pred. No. 200.
0; Mismatches
                          Uniform phosphodiester oligonucleotide.
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"2'-modified T"
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/note= "2'-modified T"
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"2'-modified T"
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"2'-modified
                                                                                                                Location/Qualifiers
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19-JUN-2000 (first entry)
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'note=
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                                                                                                                                                                                                                                                                                                                                                                                                                             Cook PD;
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                                                                                                                Key
modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                             Manoharan M,
                                                                                                                                                                                                                                                                                                                                                                            07-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                 36-AUG-1999;
                                                                                                                                                                                                                                                                                                                          17-FEB-2000
                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ61404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ61404/
ID AAZ6
XX
XX AAZ6
XX
DT 19-J
XX
XX XX
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Gaps

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This sequence represents a modified oligonucleotide used in the course of the invention. The invention relates to oligonucleotides comprising nucleotides covalently linked together by internucleotide linkages where at least 1 nucleotide is linked to adjacent nucleotide by a 2',5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "Optionally all 3'-O-(2-methoxyhexyl) or all 2'-O-(2-methoxyethyl)"
                                                                                                                                                                                                                           internucleotide linkage and bears a 3'-substituent. The oligonucleotides can be used in gene therapy and are also useful in antisense methodologies, diagnostics, therapeutics and as research reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antisense oligonucleotide, phosphorothioate; gene therapy, ISIS # 22110; research reagent; therapeutic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= d
/note= "Optionally all phosphorothioate internucleotide
                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel modified oligonucleotides, useful in antisense methodologies, diagnostics, therapeutics and as research reagents.
                                                                 Novel modified oligonucleotides, useful in antisense methodologies,
diagnostics, therapeutics and as research reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *tag= a
note= "Phosphorothioate internucleotide linkage'
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                                                                                                                                                                                                                                                                                                                                   1.1%; Score 19; DB 1; Length 19;
100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                  Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified oligonucleotide #3 ISIS # 22110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                      Example 54; Page 59; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        1736 AAAAAAAAAAAAAAA 1754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mod base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US015886.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-JUL-1998; 98US-00115043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ95240 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linkages"
16. .19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15. .19
/*tag= c
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/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          '*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ISIS-) ISIS PHARM INC.
 Cook PD;
                                  WPI; 2000-182445/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PI; 2000-182445/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
 Manoharan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ95240;
                                                                                                                                                                                                                                                                                                                                                                                                                                           19
                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ95240/
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                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                         The present invention is concerned with methods of determining the nuclease stability of oligomeric compounds using capillary-gel electrophoresis and laser-induced fluorescence. The methods are useful in the polymerase chain reaction (PCR), molecular cloning and disease diagnosis and treatment. The present sequence was used in a demonstration of the methods of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             //note= "Optionally all 3'-0-(2-methoxyhexyl) or all 2'-0-
(2-methoxyethyl)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antisense oligonucleotide, phosphorothioate, gene therapy, ISIS # 22111; research reagent; therapeutic; ss.
                                                                                                                                       Determining the nuclease stability and relative binding affinity of an oligomeric compound comprises capillary gel electrophoresis using laser-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15. 19
/*tag= d
/note= "Optionally all phosphorothioate internucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
note= "Phosphorothioate internucleotide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                      1.1%; Score 19; DB 1; Length 19; 100.0%; Pred. No. 2e+02; Ative. 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Length 19;
                                                                                                                                                                                                                                                                                                                                                                     Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified oligonucleotide #3 ISIS # 22111
                                                                                                                                                                                                            Example 3; Col 19-20; 14pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1736 AAAAAAAAAAAAAAAA 1754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 AAAAAAAAAAAAAAA 1
99US-00234237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ95241 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUN-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inkages"
                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 19; Conservative
                                  (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ISIS-) ISIS PHARM INC
                                                                     Leeds JM, Cummins LL;
                                                                                                                                                                           induced fluorescence.
                                                                                                      WPI; 2000-637737/61.
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200004189-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified base
20-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
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AAZ95241;

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WPI; 2000-672833/65.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oligonuclectides and to oligonuclectides that elicit RNase H for cleavage in a complementary nucleic acid strand. It also relates to oligonucleotides wherein at least some of the nucleotides are functionalised to be nuclease resistent, at least some of the nucleotides include a substituent that potentiates hybridisation of the oligonucleotide to a complementary strand, and at least some of the nucleotides include a 2'-deoxy-erythro-pentofuranosyl sugar moiety. The inclusion of one or more aminooxy moieties in such oligonucleotides
                                  This sequence represents a modified oligonucleotide used in the course of
                                           the invention. The invention relates to oligonucleotides comprising nucleotides covalently linked together by internucleotide linkages where at least I nucleotide is linked to adjacent nucleotide by a 2',5'-internucleotide linkage and bears a 3'-substituent. The oligonucleotides can be used in gene therapy and are also useful in antisense methodologies, diagnostics, therapeutics and as research reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aminooxy-modified nucleosides and oligonucleotides useful in diagnostic, therapeutic and research reagents and for modulating the expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/note= "These nucleotides are substituted with 2'-O-{2-
[N-(2-amino)ethy1-N-(methy1)]aminooxyethy1} group"
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                  Modified nucleoside, aminooxy group,
2'-deoxy-erythro-pentofuranosyl sugar moiety, nuclease resistant,
hybridisation, binding affinity, ss.
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0
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                                                                                                                                    Score 19; DB 1; Length 17,
Pred. No. 2e+02;
O; Indels
                                                                                                                                                                                                                                                                                                                                             Modified T-containing oligonucleotide, SEQ ID NO:14.
                                                                                                                           Seguence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prakash TP, Kawasaki AM;
                                                                                                                                        1.1%; Scor.
100.0%; Pred. No. 20.
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 99; Page 120; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
16. .19
           Example 54; Page 59; 75pp; English.
                                                                                                                                                                                             1736 AAAAAAAAAAAAAAA 1754
                                                                                                                                                                                                                   19 AAAAAAAAAAAAAAA 1
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                                                                                                                                                                                                                                                                           AAA06839 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                        19-JUN-2000 (first entry)
                                                                                                                                                Query,Match 1.1
Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cook PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein in organisms.
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modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Manoharan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                 AAA06839,
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                                              strand. The oligonucleotides of the invention aare used as diagnostic, therapoutitic or research reagents, and can be used to modulate gene expression in organisms. The oligonucleotides containing the modified nucleosides have increased nuclease resistance and increased binding affinity to a complementary strand. The present sequence represents an oligonucleotide containing nucleotides substituted with a 2'-0-{2- [N-(2- N-(2-[N-(2-[N-(2-[N-(2-[N-(2-[N-(2-[N-(2-[N-(2-[N-(2-[N-(2-[N-(2-[N-(2-[N-(2-[N-(2-[N-(2-[N-(2-[N-(2-[N-(2-[N-(n-([N-(2-[N-(1-[N-(2-[N-(2-[N-(2-[N-(2-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-[N-(1-
provides for improved binding of such oligonucleotides to a complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic; dermatological; cytostatic; virucide; antibacterial; fungicide; therapy; diagnosis; DNA-RNA hybrid; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.1%; Score 19; DB 1; Length 19; 100.0%; Pred. No. 2e+02; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= b
|mod_base= OTHER
|note= "2'-0-(2-methoxyethyl)thymidine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "2'-0-(2-methoxyethyl)thymidine"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= d
/mod_base= OTHER
/note= "2'-0-(2-methoxyethyl)uridine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "phosphorothioate linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1736 AAAAAAAAAAAAAAAAA 1754
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/mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= c
/mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 AAAAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-MAY-2000; 2000WO-US011913.
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/label= RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA88952 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide ISIS 22115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .. .15
/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Manoharan M, Mohan V;
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03-MAY-2000; 2000WO-US011913.
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                                                                           Oligonucleotide ISIS 22115 contains a mixed phosphodiester and phosphorothicate backbone and has 2'-O-(2-methoxyethyl) chemistry. It was used in experiments to determine the effects of snake venom phosphodiesterase and liver homogenate on the stability of oligonucleotides. Novel oligonucleotides of the invention have both A- and B-form conformational geometry. The A-form geometry modulates the binding affinity and nuclease resistence of the oligonucleotide. The B-form geometry allows the oligonucleotide to serve as substrate for RNase-used to treat psoriasis and other inflammatory skin conditions, skin cancers and viral, bacterial and fungal infections, and in various
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/note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-
(F), 2'-ara-(OH), -2'-ara-(OMe)"
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//mod_bage= OTHER
//note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-
(F), 2'-ara-(OH), -2'-ara-(OMe)"
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/note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-
(F), 2'-ara-(OH), -2'-ara-(OMe)"
                New oligonucleotides containing sequences with A and B geometry, used treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and bacterial infections, bind to single stranded RNA or DNA.
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                                                                                                                                                                                                                                              Length 19;
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                                                                                                                                                                                                                                             Query Match 1.1%; Score 19; DB 1; Best Local Similarity 100.0%; Pred. No. 2e+02; Matches 19; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                               2'-Modified chimeric oligonucleotide.
                                                           Example 54; Page 69; 132pp; English
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/mod_base= OTHER
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dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
diagnosis; ss.
                                                                                                                                                                      New oligonucleotides containing sequences with A and B geometry, used treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and bacterial infections, bind to single stranded RNA or DNA.
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/mod_base= OTHER
/note= "3'-0-(2-methoxyethy1)thymidine"
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Pred. No. 2e+02;
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/mod_base= OTHER
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(ISIS-) ISIS PHARM INC
                                                         Manoharan M, Mohan V;
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100.0%; Pred. No. 2e+02;
iive 0; Mismatches 0; Indels
/note= "3'-0-(2-methoxyethy1)thymidine"
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/note= "2'-O-(2-methoxyethy1)thymidine"
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/note= "2'-O-(2-methoxyethyl)thymidine"
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*tag= f
note= "phosphorothioate linkage"
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Oligonucleotide ISIS 22113 contains a phosphorothioate backbone and has 2'-O-(2-methoxyethyl) chemistry. It was used in experiments to determine the effects of snake venom phosphodiesterase and liver homogenate on the stability of oligonucleotides. Novel oligonucleotides of the invention have both A- and B-form conformational geometry. The A-form geometry modulates the binding affinity and nuclease resistance of the oligonucleotide. The B-form geometry allows the oligonucleotide to serve as substrate for RNase-H when bound to a target nucleic acid strand. The oligonucleotides can be used to treat psoriasis and other inflammatory skin conditions, skin cancers and viral, bacterial and fungal infections, and in various diagnostic applications
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New oligonucleotides containing sequences with A and B geometry, used treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and bacterial infections, bind to single stranded RNA or DNA.
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100.0%; Pred. No. 2e+02;
ive 0; Mismatches 0; Indels
                                                        /note= "2'-0-(2-methoxyethyl)thymidine"
                                                                                                                                                                                                                                                                /mod_base= OTHER
/note= "2'-0-(2-methoxyethyl)uridine"
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                            OTHER
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AAA88951 standard; DNA; 19 BP.
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/label= RNA
                            pase=
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                                                                                                                                                                                                                                *tag= d
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Les 19; Conservative
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Oligonuclectide ISIS 22110 contains a phosphodiester backbone and has 3'-0-(2-methoxyethyl) chemistry. It was used in experiments to determine the effects of snake venom phosphodiesterase and liver homogenate on the stability of oligonuclectides. Novel oligonuclectides of the invention have both A- and B-form conformational geometry. The A-form geometry modulates the binding affinity and nuclease resistance of the oligonuclectide. The B-form geometry allows the oligonuclectide to serve as substrate for RNase-H when bound to a target nucleic acid strand. The oligonuclectides can be used to treat psoriasis and other inflammatory skin conditions, skin cancers and viral, bacterial and fungal infections, and in various diagnostic applications
     Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic; dermatological; cytostatic; virucide; antibacterial; fungicide; therapy; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New oligonucleotides containing sequences with A and B geometry, used treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and bacterial infections, bind to single stranded RNA or DNA.
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100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                     /mod_base= OTHER
/note= "3'-0-(2-methoxyethy1)thymidine"
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                                                                                                                                                                                                                                                             note= "3'-0-(2-methoxyethyl)thymidine
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                                                                                                                 Location/Qualifiers
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/mod_base= OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide ISIS 22114 contains a mixed phosphodiester and phosphorothioate backbone and has 3'-0-(2-methoxyethyl) chemistry. It was used in experiments to determine the effects of snake venom phosphodiesterase and liver homogenate on the stability of oligonucleotides. Novel oligonucleotides of the invention have both A-and B-form conformational geometry. The A-form geometry modulates the binding affinity and nuclease resistance of the oligonucleotide. The B-form geometry allows the oligonucleotide to serve as substrate for RNase-H when bound to a target nucleic acid strand. The oligonucleotides can be used to treat psoriasis and other inflammatory skin conditions, skin diagnostic applications
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New oligonucleotides containing sequences with A and B geometry, used treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and bacterial infections, bind to single stranded RNA or DNA.
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                                                                                                                                                                                                                                                                                                    /mod_base= OTHER
/note= "3'-0-(2-methoxyethyl)thymidine"
                                                         *tag= a
mod base= OTHER
'note= "3'-0-(2-methoxyethy1)thymidine"
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/mod_base= CTHER
/note= "3'-0-(2-methoxyethyl)thymidine"
                                                                                                                                                                     note= "3'-0-(2-methoxyethyl)thymidine
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     '*tag= e
'note= "phosphorothioate linkage"
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/mod_base= OTHER
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Best Local Similarity 100.º
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mohan V;
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                                          modified base
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Gaps

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ð 요 RESULT 358

Phosphorothioate; primer; oligomer synthesis; antisense therapy; ss.

Phosphorothioate 20-mer primer DNA #1.

(first entry)

14-DEC-2000

AAA71630;

AAA71630 standard; DNA; 19 BP

RESULT 360

AAA71630/

/note= "phosphorothioate linkage"

mod_base= OTHER

ಹ

modified base

Synthetic

"mod_base= OTHER
"note= "2'-0-(2-methoxyethy1)thymidine"

Location/Qualifiers

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tag=

pom/

/mod_base= OTHER /note= "2'-0-(2-methoxyethyl)thymidine"

Д

*tag=

note = "2'-0-(2-methoxyethyl)thymidine"

/*tag= e /label= RNA

J= c base= OTHER

/*tag= /mod_ba

/*tag= d /mod_base= OTHER /note= "2'-O-(2-methoxyethyl)uridine"

EP1028124-A2

06-SEP-1999; 04-FEB-1999; 09-APR-1999;

16-AUG-2000

Location/Qualifiers

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Oligonucleotide ISIS 22111 contains a phosphodiester backbone and has 2'-O-(2-methoxyethyl) chemistry. It was used in experiments to determine the effects of snake venom phosphodiesterase and liver homogenate on the stability of oligonucleotides. Novel oligonucleotides of the invention have both A- and B-form conformational geometry. The A-form geometry modulates the binding affinity and nuclease resistance of the oligonucleotide. The B-form geometry allows the oligonucleotide to serve as substrate for RNase-H when bound to a target nucleic acid strand. The oligonucleotides can be used to treat psoriasis and other inflammatory skin conditions skin cancers and viral, bacterial and fungal infections,
                                                          Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic; dermatological; cytostatic; virucide; antibacterial; fungicide; therapy; diagnosis; DNA-RNA hybrid; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New oligonucleotides containing sequences with A and B geometry, used treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and bacterial infections, bind to single stranded RNA or DNA.
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                              Oligonucleotide ISIS 22111
05-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ISIS-) ISIS PHARM INC
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modified_base
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                                                                                                                    Synthetic
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99US-00303586

Mohan V;

Novel method for the production of oligomers with reduced exocyclic adducts comprises treatment with deprotecting and cleaving reagents.

Cole DL;

Krotz A,

Capaldi DC,

Manoharan M,

Ravikumar VT,

Guzaev A;

WPI; 2000-500332/45.

PHARM INC

SISI (-SISI)

99US-0118564P. 99EP-00307066

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providing a sample comprising a number of oligomers of formula (1); (b) contacting the sample with a deprotecting agent to remove R t groups from the oligomers; and (c) reacting the oligomer with a cleaving reagent. The method is used to produce oligomer compounds for use in antisense and oligonuclectide therapies. The method enables the synthasis of oligomers with a reduction in the number acrylonitrile groups attached.

Acrylonitrile has been demonstrated to be a potent carcinogen in rats. This sequence represents a phosphorothioate 20-mer primer which is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cleavage of nucleic acids from solid supports assay oligonucleotide #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel synthetic method (M) comprising: (a)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.1%; Score 19; DB 1; Length 19;
100.0%; Pred. No. 2e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in the method of the invention
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Best Local Similarity
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Score 19; DB 1; Length 19; Pred. No. 2e+02; 0; Mismatches 0; Indels

100.0%; Pr tive 0;

Conservative

Local Similarity nes 19; Conserv

Best Loca Matches

1.1%;

1736 AAAAAAAAAAAAAAA 1754

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19 AAAAAAAAAAAAAAAA 1

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The present invention relates to nucleotide oligomers comprising monomer units. Oligomers modulate gene expression when hybridized by a single- or double-stranded nucleic acid. They are useful for gene therapy, diagnostic and investigative purposes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New oligomers for use as research reagent, for treating disease caused by undesired production of proteins, and for diagnosing and treating AIDS,
                                                                                                                                            Guanidinium functionalized oligomers prepared from corresponding monomer units, are hybridizable with a specific RNA or DNA sequence, useful for diagnostic and therapeutic purposes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.1%; Score 19; DB 1; Length 19;
100.0%; Pred. No. 2e+02;
ive 0; Mismatches 0; Indels
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                            >
                            Mohan
                                                                                                                                                                                                                                                                         Example 26; Page 54; 108pp; English.
                            Prakash TP,
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tes 19; Conservative
                            PD,
                                                                                      WPI; 2001-138119/14.
                            Cook
   Manoharan M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detaching nucleic acid molecule comprising unconventional nucleotide incorporated at predetermined site from a solid support involves cleaving the nucleic acid molecule at the site of unconventional nucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention is concerned with the cleavage of nucleic acids from solid supports. This is carried out by adding a non-conventional nucleotide into the nucleic acid attached to the support, so that it is recognised and cleaved by a specific DNA glycosylase and the sequence is released. This is useful in many molecular biological procedures such as sequencing, in vitro amplifications, cDNA and template preparation, DNA-based assays, mutagenesis procedures, nucleic acid purification and affinity chromatography. The present sequence is an oligonucleotide used in assays to demonstrate the methods of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                      Nucleic acid cleavage; solid support; DNA-RNA hybrid; affinity chromatography; sequencing; mutagenesis; DNA preparation; nucleic acid purification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 Other;
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                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sxample 3; Page 34; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1736 AAAAAAAAAAAAAAAA 1754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUL-2000; 2000WO-US018609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF31458 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
nes 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GOLD/) GOLDSBOROUGH A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-664908/64.
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                                                                                                                                                                                                                                                                                                                                   WO200058329-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                            05-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JAN-2001
                                                                                                                                               Synthetic
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                                                                                                                                                                                                                                      misc_RNA
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Matches
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Human, RNase H type II, RNase H1 cleavage substrate; antisense therapy; gene therapy; primer; phosphorothioate backbone; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric oligonucleotides that can serve as substrates for human RNase H1, useful for enhancing the effectiveness of antisense gene therapies.
                                                                             Human type II RNase H substrate oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 54; Page 88; 178pp; English.
AAH25737 standard; DNA; 19 BP
                                                                                                                                                                                                                                                                                                                                                                              29-SEP-2000; 2000WO-US026729
                                                                                                                                                                                                                                                                                                                                                                                                                                  (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Crooke ST, Lima WF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-343164/36.
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                                                                                                                                                                           Key
modified_base
                                                                                                                                                                                                                                           modified base
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                                                   14-AUG-2001
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                                                                                                                                                Synthetic
                          AAH25737;
8XCCCCCCX8XXEXEXEXEXEXEXEXEXEXEXEXEXEXXEXEXEX8XXEXEX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a method for preparing phosphorothioate oligonucleotides having at least one nucleoside with a 2' modification. The method comprises phosphitylating the 5'-hydroxyl of a nucleic acid group having at least one nucleoside with a 2' modification in an acetonitrile. The present sequence was used to illustrate the method of the present invention. The method is useful for synthesising sulphurised 2' substituted phosphorothioate oligonucleotides, which may be used in molecular biological research, in applications such as anti-viral therapy, and for determining the stereochemical pathways of certain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Preparing sulfurized 2' substituted phosphorothioate oligonucleotides useful in biological research, comprises phosphitylating the 5'-hydroxyl of a nucleic acid having a nucleoside with a 2' modification.
                                                                                                                                                                                                   Phosphorothioate; anti-viral therapy; stereochemical pathway; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.1%; Score 19; DB 1; Length 19; 100.0%; Pred. No. 2e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                     /*tag= b
/mod_base= OTHER
/note= "Modified with 2'-O-methoxyethyl"
                                                                                                                                                                                                                                                                                              /mod_base= OTHER
/note= "All bases are phosphorothioate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cheruvallath ZS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        enzymes which recognise nucleic acids
                                                                                                                                                                                                                                                         Location/Qualifiers
AAAAAAAAAAAAAAAA 1754
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                         AAAAAAAAAAAAAAA 1
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                                                                                         AAH46460 standard; DNA; 19
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                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-407218/43
                                                                                                                                                                         Oligonucleotide #8.
                                                                                                                                                                                                                                                        Key
modified_base
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                                                                                                                                                                                                                             Synthetic.
                         13
                                                                                                                     AAH46460;
1736
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                                                               AAH46460/
AAH46460/
XXX AAH46
XXX AAH46
XXX AAH60
XXX Syntl
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XXX Syntl
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XXX SYNTl
XXX SXX Syntl
XXX SXX SYNTl
XXX SXX SEXAM
XXX SEXAM
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Manoharan M;

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99US-00409926

/ 16. .19 /*tag= b /mod base= OTHER methoxyethy1)" or 2'-0-(2-methoxyethy1) or 2'-0-(2-

1. .19 /*tag= a /mod_base= OTHER /note= "optionally phosphorothioate backbone"

Location/Qualifiers

(first entry)

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The present invention provides a number of DNA-RNA oligonucleotides which can act as substrates for human RNAses HI (a type II RNase). The sequence consists of two portions, one of which is capable of supporting cleavage of a complementary target RNA and the other of which is incapable of supporting such cleavage. These can be used to enhance the effectiveness of antisense theraples. The present sequence is an RNase H substrate used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, RNase H type II; RNase H1 cleavage substrate; antisense therapy;
                                                                                                                                                                                                                                                                                           Gaps
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0
                                                                                                                                                                                                                              1.1%; Score 19; DB 1; Length 19;
100.0%; Pred. No. 2e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human type II RNase H substrate oligonucleotide #5.
                                                                                                                                                                                              Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                        1736 AAAAAAAAAAAAAAA 1754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH25738 standard; DNA; 19 BP
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                                                                                                                                                                                                                                                                                           19; Conservative
                                                                                                                                                                                                                                                                     Best Local Similarity
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                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH25738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 366
                                                                                                                                                                                                                                                                                           Matches
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Gaps

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1736 AAAAAAAAAAAAAAAA 1754

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Local Similarity 100. 18 19; Conservative

Best Loca Matches

19 AAAAAAAAAAAAAAA 1

RESULT 365 AAH25737/c

gene therapy; primer; phosphorothioate backbone; ss.

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The present invention provides a number of DNA-RNA oligonucleotides which can act as substrates for human RNAse HI (a type II RNAse). The sequence consists of two portions, one of which is capable of supporting cleavage of a complementary target RNA and the other of which is incapable of supporting such cleavage. These can be used to enhance the effectiveness of antisense therapies. The present sequence is an RNase H substrate used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric oligonucleotides that can serve as substrates for human RNase
H1, useful for enhancing the effectiveness of antisense gene therapies.
                                                                                                                                                            /note= "optionally 3'-O-(2-methoxyethyl) or 2'-O-(2-methoxyethyl)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2'-O-N-[2-(dimethylamino)ethylacetamido]-modified oligo ISIS #32335.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2'-O-acetamido; diagnostic; kinase modulator; nuclease resistance; tumour formation; cancer; protein kinase C expression; cell adhesion molecule expression; multidrug resistance; ss.
                                                                                         "mod_base= OTHER
'note= "optionally phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.1%; Score 19; DB 1; Length 19;
100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                     Manoharan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 54; Page 88; 178pp; English
                                                     ocation/Qualifiers
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16. .19
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/mod_base= OTHER
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                                                                                                                                                                                                                                                                                    29-SEP-2000; 2000WO-US026729.
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/*tag= a
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Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                    16. .19
                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                          (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                     Lima WF,
                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-343164/36.
                                                                                                                                                                                                                                WO200123613-A1
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modified_base
                                                              modified base
                                                                                                                    modified base
                                                                                                                                                                                                                                                                                                               30-SEP-1999;
                                                                                                                                                                                                                                                           05-APR-2001
                                                                                                                                                                                                                                                                                                                                                                     Crooke ST,
                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC83664;
                                                                                                                                                                                       misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 367
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The present sequence is a modified oligonucleotide. 2'-O-acetamidomodified nucleosides were used to produce oligonucleotides which have enhanced nucleosides were used to produce oligonucleotides which have enhanced nuclease resistance and superior hybridisation properties than prior art. The oligomeric compounds are useful for identification or quantification of ribonucleic acid and deoxyribonucleic acid or for modulating the activity of an ribonucleic acid or deoxyribonucleic acid or for modulating the appropriated nucleoside monomer and are specifically hybridisable with a preselected nucleotide sequence of a single-stranded or double-stranded target deoxyribonucleic acid or ribonucleic acid or double-stranded target deoxyribonucleic acid or ribonucleic acid molecule. The oligomers are further useful in a ras-lucification and tumour formation. They are useful in abnormal cell proliferation and tumour formation and modulation of expression of protein kinase C and cell adhesion molecules such as ICAM. They are useful in the modulation of proteins related to multidrug resistance and viral genomic nucleic acids such as HOV, herpes viruses, Epstein-Barr virus, cytomegalovirus, papillomavirus, hepatitis C virus and influenza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Target detection, quantitative analysis, probe, medical diagnosis; forensics; bacterial screening, tissue typing; gene expression analysis;
                                                                                                                                                                                                                                                                                                                                    New 2'-0-acetamido modified nucleosides (I) used to produce oligonucleotides which have enhanced nuclease resistance and superior hybridization properties than prior art.
               /mod_base= OTHER
/note= "2'-O-N-[2-(dimethylamino)ethylacetamido]5MeU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid quantitative analysis related oligonucleotide #1.
                                                                                                                                                                                                                                                              Kawasaki AM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.1%; Score 19; DB 1; Length 19; Best Local Similarity 100.0%; Pred. No. 2e+02; Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                              Prakash TP,
                                                                                                                                                                                                                                                              Fraser AS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                Example 12; Col 28; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1736 AAAAAAAAAAAAAAAAA 1754
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                                                                                                                                                99US-00378568.
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AAK98526 standard; DNA; 19
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 /*tag= a
                                                                                                                                                                                                                                                              Cook PD,
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                                                                                                                                                                                                                         (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                   WPI; 2001-069824/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genotyping, ss.
                                                                                                                                                19-AUG-1999;
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modified_base
                                                                                                                                                                                     19-AUG-1999;
                                                                                                                                                                                                                                                              Manoharan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-APR-2002
                                                                        US6147200-A.
                                                                                                             14-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAK98526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 368
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TILLEXSXEMENT
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                                                                                                                                                                                                                                Determining targets by interaction with probe array, useful e.g. for diagnosis, based on detecting formation of precipitate at specific probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2'-0-alkyl oligonucleotide; nuclease resistance; diagnosis; therapy; ss.
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Wagner G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.1%; Score 19; DB 1; Length 19;
100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
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/note= "2'-methyl thioethyl thymidine"
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/note= "2'-methyl thioethyl thymidine'
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/note= "2'-methyl thioethyl thymidine'
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
/note= "modified by thiol"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methyl thioethyl modified oligonucleotide.
                                                                                                                                   (CLON-) CLONDIAG CHIP TECHNOLOGIES GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1736 AAAAAAAAAAAAAAA 1754
                                                                                                                                                                                                                                                                                     Example 5; Page 47; 92pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 AAAAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABA91949 standard; DNA; 19 BP.
                                                                             02-JUL-2001; 2001WO-EP007575
                                                                                                        01-JUL-2000; 2000DE-01033334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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                                                     10-JAN-2002
                                                                                                                                                              Bickel R,
Schulz T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
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The present sequence is that of a chimeric oligonucleotide having some 2'methyl thioethyl modifications. This was compared with oligonucleotides with methoxyrethoxy (see ABA91950) and dimethylaminopropyl (see ABA91951) modifications for resistance to snake venome phosphodiesterase. The assay revealed the nuclease resistance of the modified oligomers. The invention provides methods for the alkylation of alcohols, anines, thiols and their provides methods for the alkylation of alcohols, anines, thiols and their derivatives by cyclic sulfate intermediates. In particular, methods for the alkylation of the 2', 3' or 5'-0-alkyl their analogues with cyclic sulfates to form the 2', 3' or 5'-0-alkyl collate modified compounds are disclosed. Displacement of the 2', 3' or 5'-0-alkyl nucleosides and nucleosides and their analogues. The methods are especially useful for the preparation of 2'-0-alkyl nucleosides, nucleosides and nucleoside currogates that are precursors for the preparation of oligomeric compounds useful as therapeutics, diagnostics and research reagents
                                                                                                                                                                                                                                                                                                Alkylation of alcohols, amines, or thiols, useful for preparing nucleosides that are precursors for preparation of oligomeric compounds beneficial as therapeutics, involves use of cyclic sulfate intermediates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2'-O-alkyl oligonucleotide; nuclease resistance; diagnosis; therapy; ss.
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                                                                                                                                                                                                                              Kawasaki AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.1%; Score 19; DB 1; Length 19;
100.0%; Pred. No. 2e+02;
ive 0; Mismatches 0; Indels
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                /note= "2'-methyl thioethyl thymidine"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dimethylaminopropyl modified oligonucleotide.
                                                                                                                                                                                                                                Jung ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                PD,
                                                                                                                                                                                                                                                                                                                                                                        Example 15; Col 35; 45pp; English
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/mod_base= OTHER
/mod_base= OTHER
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/mod_base= OTHER
                                                                                                                                                                                                                                Cook
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                                                                                                                       99US-00378665.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                Fraser AS, Manoharan M,
                                                                                                                                                                                             (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                 WPI; 2002-235143/29.
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                                                                                                                         20-AUG-1999;
                                                                                                                                                          20-AUG-1999;
                                                                                      21-AUG-2001
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The present sequence is that of a chimeric oligonucleotide having some 2, methoxyethoxy modifications. This was compared with oligonucleotides with hinecthyl thiosethyl (see Aba21949) and dimethylaminopropyl (see Aba21949) and dimethylaminopropyl (see Aba21951) modifications for resistance to snake venom phosphodiseterase. The assay revealed the nuclease resistance of the modified oligomers. The invention provides methods for the alkylation of alcohols, amines, thiols and their derivatives by cyclic sulfate intermediates. In particular, methods for the alkylation of the 2', 3' or 5'-hydroxy position of nucleosides and their analogues with cyclic sulfates to form the 2', 3' or 5'-O-alkyl sulfate with a nucleophile provides 2', 3' or 5'-O-ankyl sulfate with a nucleophile provides 2', 3' or 5'-O-ankyl sulfate with a nucleophile provides 2', 3' or 5'-O-ankyl indication of 2'-O-alkyl nucleosides and their analogues. The methods are especially modified nucleosides and their analogues for the preparation of 2'-O-alkyl nucleosides incleosides and nucleoside surrogates that are precursors for the preparation of ancleoside surrogates that are precursors for the preparation of aligomeric compounds useful as therapeutics, diagnostics and research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alkylation of alcohols, amines, or thiols, useful for preparing nucleosides that are precursors for preparation of oligomeric compounds beneficial as therapeutics, involves use of cyclic sulfate intermediates.
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100:0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
     /*tag= a
/mod_base= OTHER
/not== "2'-methoxyethoxy thymidine"
                                                                                                                                                                                                                                                                                                                  /mod_base= OTHER
/note= "2'-methoxyethoxy thymidine"
                                                                                                                                                                                                                                              note= "2'-methoxyethoxy thymidine"
                                                                                                                        /mod_base= OTHER
/note= "2'-methoxyethoxy thymidine'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jung ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cook PD,
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/mod_base= OTHER
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Best Local Similarity 100:
Matches 19; Conservative
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                                                                                                       *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ISIS-) ISIS PHARM INC
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                                                                           modified base
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                                                                                                                                                                                                                                                                                                                                                                                             JS6277982-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                           21-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of a chimeric oligonucleotide having some 2, dimethylaminopropyl modifications. This was compared with oligonucleotides with methyl, thioethyl (see ABA91949) and methoxyethoxy (see ABA91950) modifications for resistance to snake venom phosphodiesterase. The assay revealed the nuclease resistance of the modified oligomers. The invention provides methods for the alkylation of alcohols, amines, thiols and their derivatives by cyclic sulfate intermediates. In particular, methods for the alkylation of the 2', 3' or 5'-O-alkyl sulfate modified compounds are disclosed. Displacement of nucleosides and their analogues with cyclic sulfates to form the 2', 3' or 5'-O-alkyl sulfate modified compounds are disclosed. Displacement of nucleosides and their analogues. The provides 2', 3' or 5'-O-alkyl sulfate with a nucleophile compounds are especially useful for the preparation of 2', 0-alkyl nucleotides, nucleosides and nucleoside surrogates that are precursors of for the preparation of oligomeric compounds useful as therapeutics,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alkylation of alcohols, amines, or thiols, useful for preparing nucleosides that are precursors for preparation of oligomeric compounds beneficial as therapeutics, involves use of cyclic sulfate intermediates.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cook PD, Jung ME, Kawasaki AM;
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Pred. No. 2e+02;
                                                  /mod_base= OTHER
/note= "2'-dimethylaminopropyl thymidine"
                                                                                                                                            /mod_base= OTHER
/note= "2'-dimethylaminopropyl thymidine"
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                                                                                                                        *tag= d
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Best Local Similarity 100.0
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Manoharan M,
                              •tag=
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modified_base
                                                                                                  modified base
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Kawasaki AM;

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Gaps

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Tailing reaction related exemplary primer biotin-dT18U SEQ ID NO:1.

01-JUL-2002 (first entry)

Location/Qualifiers 16

Key modified_base

Synthetic

LHX SX X X X B X L X X X X X L

ઠે 용 ABL51520;

/*tag= a /mod_base= OTHER /note= "biotinylated"

/*tag=

/*tag=

Location/Qualifiers

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The present invention describes a method for detecting a nucleic acid probe, which comprises using chain extending enzymes to elongate probes. The method comprises: (a) treating the sample with a chain terminating reagent to prevent polynucleotide chain growth from the nucleic acid in the sample; (b) contacting the sample with the probe containing a terminus capable of elongation by a chain extending enzyme, where the probe hybridises to the nucleic acid in the sample; (c) contacting the sample with a chain extending enzyme and its substrates, which elongates the probe; and (d) detecting the elongated hybridised probe. Also described is a method comprising: (a) treating nucleic acid molecules or modified nucleic acid chains unextendable by a non-template-dependent enzyme; (b) hybridising the treated molecules with a nucleic acid probe that includes an extendable terminus, under conditions where hybridis form; and (c) treating any hybrids formed with a non-template dependent chain elongating enzyme and its substrates, where any hybridised probe is extended. The method is useful for identifying and detecting nucleic acids, particularly DNA hybridisation probes. The present sequence represents a tailing reaction exemplary primer, which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying and detecting nucleic acids, particularly DNA hybridization probes, involves employing chain extending enzymes (e.g. telomerase) to elongate probes to render them readily detectable.
               Tailing reaction; tailed primer; primer; probe; identification; detection; linear amplification scheme; chain extending enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 1.1%; Score 19; DB 1; Length 19; Local Similarity 100.0%; Pred. No. 2e+02; No. 2e+02; No. By; Conservative 0; Mismatches 0; Indels
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25-MAY-2000; 2000US-00580358.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rullis RH, Streifel JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TULL/) TULLIS R H. (STRE/) STREIFEL J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-361176/39.
                                                                                                                                                                                                                                                                                    US2002031776-A1
                                                       telomerase; ss
                                                                                                                                                modified_base
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                                                                                          Synthetic
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Alkylating 2' position of 2',3'-dihydroxy sugar molety of nucleoside used for preparation of 2'-O-alkylated compounds comprises dissolving nucleoside in aprotic solvent, cooling, treating with base, warming, cooling and reacting with ester.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a novel method of selective alkylation of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside. The method involves dissolving the nucleoside in at least one aprotic solvent, cooling, treating with base, warming, cooling and reacting with a reactive ester. The method is useful for the preparation of 2'-0-alkyl nucleotides, nucleosides and nucleoside surrogates used for preparation of oligometic compounds having improved hybridisation affinity and nuclear resistance, which are useful as therapeutics, diagnostics and research reagents. The present sequence is a modified oligonucleotide used to illustrate the method of the invention
                                                                                            Dihydroxy sugar moiety, 2'-O-alkyl nucleotide, hybridisation affinity, nuclear resistance, alkylation, therapeutic, diagnostic, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dihydroxy sugar moiety, 2'-O-alkyl nucleotide, hybridisation affinity, nuclear resistance, alkylation; therapeutic; diagnostic; ss.
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                                                             Oligonucleotide #3 used to illustrate the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 19; DB 1; Length 19;
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                          /note= "2'-methoxyethoxy (MOE) residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Cook PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
1.1%; Score 19; DB
Best Local Similarity 100.0%; Pred. No. 2e-
Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       Manoharan M,
                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                           15. 18
/*tag= a
/mod_base= OTHER
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AAD42002 standard; DNA; 19
                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                     (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-546338/58.
                                                                                                                                                                             Key
modified base
                                                                                                                                                                                                                                                                                                                                         08-JAN-1999;
                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                                                                                       08-JAN-1999;
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                               04-NOV-2002
                                                                                                                                                                                                                                                                                                         11-JUN-2002
AAD42000;
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Prakash TP

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Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used for preparation of 2'-O-alkylated compounds comprises dissolving nucleoside in aprotic solvent, cooling, treating with base, warming,
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18. .19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dihydroxy sugar moiety, 2'-O-alkyl nucleotide, hybridisation affinity;
nuclear resistance, alkylation, therapeutic, diagnostic, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide #13 used to illustrate the method of the invention.
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100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
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/note= "Phosphorothioate backbone"
                                                                                                                                                                          Cook PD,
                                                                                                                                                                          Manoharan M,
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                                                                                                                                                                                                                                                                                                                  cooling and reacting with ester.
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                                                       99US-00227782.
                                                                                              99US-00227782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19; Conservative
                                                                                                                                                                          Fraser AS,
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                                                                                                                                     (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                               WPI; 2002-546338/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                       08-JAN-1999;
                                                                                              18-JAN-1999;
                                                                                                                                                                            Kawasaki AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-NOV-2002
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    11-JUN-2002.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                   Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used for preparation of 2'-O-alkylated compounds comprises dissolving nucleoside in aprotic solvent, cooling, treating with base, warming,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a novel method of selective alkylation of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside. The method involves dissolving the nucleoside in at least one aprotic solvent, cooling, treating with base, warming, cooling and reacting with a reactive ester. The method is useful for the preparation of 2'-o-alkyl nucleotides, nucleosides and nucleoside surrogates used for preparation of ollogomeric compounds having improved hybridisation affinity and nuclear resistance, which are useful as therapeutics, diagnostics and research reagents. The present sequence is a modified oligonucleotide used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dihydroxy sugar moiety; 2'-0-alkyl nucleotide; hybridisation affinity; nuclear resistance; alkylation; therapeutic; diagnostic; ss.
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                                                                                            /mod_base= OTHER
/note= "5-methyl, 2'-methoxyethyl residues"
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100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                         Cook PD,
                                                                                                                                                                                                                                                                                                                                                         Manoharan M,
                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 46; Col 33; 24pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cooling and reacting with ester.
                                                                                                                                                                                                                                      99US-00227782
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                                                                            /*tag= a
                                                                                                                                                                                                                                                                                                                                                         Kawasaki AM, Fraser AS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
nes 19; Conservative
                                                                                                                                                                                                                                                                                                                  (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-546338/58.
                                       Key
modified_base
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                                                                                                                                                                                                                                      08-JAN-1999;
Unidentified
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                                                                                                                                                      US6403779-B1
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Matches
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Gaps

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99US-00227782.

38-JAN-1999;

11-JUN-2002

/*tag= a /mod_base= OTHER /not== "5-methyl, 2'-dimethylaminooxyethyl residue"

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WPI; 2002-546338/58
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modified_base
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                                                                                                                                                                                                                       Matches
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                                                                                Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used for preparation of 2'-O-alkylated compounds comprises dissolving nucleoside in aprotic solvent, cooling, treating with base, warming,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
                                                                                                                                                      The present invention relates to a novel method of selective alkylation of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside. The method involves dissolving the nucleoside in at least one aprotic solvent, cooling, treating with base, warming, cooling and reacting with a reactive ester. The method is useful for the preparation of 2'-0-alkyl nucleotides, nucleosides and nucleoside surrogates used for preparation of oligomeric compounds having improved hybridisation affinity and nuclear resistance, which are useful as therapeutics, diagnostics and research reagents. The present sequence is a modified oligonucleotide used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity; nuclear resistance; alkylation; therapeutic; diagnostic; ss.
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide #23 used to illustrate the method of the invention.
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/note= "2'-0-methyleneiminooxyethyl thymidine"
                                         Prakash TP;
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                                                                                                                                                                                                                                                                                             1.1%; Score 19; DB 1; Length 19;
100.0%; Pred. No. 2e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                          Seguence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
                                         Cook PD,
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                                         Manoharan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Manoharan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                     Example 46; Col 35; 24pp; English.
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                                                                                                                  cooling and reacting with ester.
                                                                                                                                                                                                                                                                                                                                                           19 AAAAAAAAAAAAAA 1
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99US-00227782
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                                        Fraser AS,
                                                                                                                                                                                                                                                                                                                   19; Conservative
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                   (ISIS-) ISIS PHARM INC
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                                                            WPI; 2002-546338/58
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Matches 19; Conserv
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modified_base
08-JAN-1999;
                                        Камавакі АМ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
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                                                                                                                                                                                                                                                                                              Query Match
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Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
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/note= "5-methy1, 2'-dimethylaminooxyethyl residues"
for preparation of 2'-O-alkylated compounds comprises dissolving nucleoside in aprotic solvent, cooling, treating with base, warming, cooling and reacting with ester.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.1%; Score 19; DB 1; Length 19;
100.0%; Pred. No. 2e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Manoharan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                Example 46; Col 41; 24pp; English.
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ID AAD42001 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
nes 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fraser AS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16. .19
/*tag=
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Gaps

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nucleoside used
solvent, cooling, treating with base, warming, cooling and reacting with a reactive ester. The method is useful for the preparation of 2'-O-alkyl nucleotides, nucleosides and nucleoside surrogates used for preparation of oligomeric compounds having improved hybridisation affinity and nuclear resistance, which are useful as therapeutics, diagnostics and research reagents. The present sequence is a modified oligonucleotide used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a novel method of selective alkylation of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside. The method involves dissolving the nucleoside in at least one aprotic solvent, cooling, treating with base, warming, cooling and reacting with a reactive ester. The method is useful for the preparation of 2'-0-alkyl nucleotides, nucleosides and nucleoside surrogates used for preparation of oligomeric compounds having improved hybridisation affinity and nuclear resistance, which are useful as therapeutics, disgnostics and research reagents. The present sequence is a modified oligonucleotide used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "2'-dimethylaminooxyethyl thymidine (T-2'DMAOE)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cy sugar moiety, 2'-0-alkyl nucleotide, hybridisation affinity,
resistance, alkylation, therapeutic, diagnostic, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside for preparation of 2'.0-alkylated compounds comprises dissolving nucleoside in aprotic solvent, cooling, treating with base, warming, cooling and reacting with ester.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide #14 used to illustrate the method of the invention.
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                                                                                                                                                                                    Length 19;
                                                                                                                                                                                  1.1%; Score 19; DB 1; Length 19;
100.0%; Pred. No. 2e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cook PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fraser AS, Manoharan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 46; Col 37; 24pp; English.
                                                                                                                                                                                                                                                           1736 AAAAAAAAAAAAAAAA 1754
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nod_base= OTHER
                                                                                                                                                                                                                                                                                           AAAAAAAAAAAAAAA 1
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                                                                                                                                                                                                                                                                                                                                                                                   AAD42011 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-NOV-2002 (first entry)
                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-546338/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dihydroxy sugar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SISI (-SISI)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS6403779-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                       AAD42011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nuclear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a novel method of selective alkylation of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside. The method involves dissolving the nucleoside in at least one aprofic solvent, cooling treating with base, warming, cooling and reacting with a reactive ester. The method is useful for the preparation of 2'-o-alkyl nucleotides, nucleosides and nucleoside surrogates used for preparation of olygomeric compounds having improved hybridisation affinity and nuclear resistance, which are useful as therapeutics, diagnostics and research reagents. The present sequence is a modified oligonucleotide used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                       Dihydroxy sugar moiety; 2'-0-alkyl nucleotide; hybridisation affinity;
nuclear resistance; alkylation; therapeutic; diagnostic; ss.
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                             Oligonucleotide #8 used to illustrate the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "5-methyl, 2'-methoxyethyl residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.1%; Score 19; DB 1; Length 19;
100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
         Length 19;
                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cook PD,
       Score 19; DB 1;
Pred. No. 2e+02;
1.1%; Scot. No. 2010.0%; Pred. No. 2010.0%; Pred. No. 2010.00; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Manoharan M,
                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 46; Col 33; 24pp; English.
                                                                  1736 AAAAAAAAAAAAAAAA 1754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1736 AAAAAAAAAAAAAAAA 1754
                                                                                                                                                                                                                                                                                                                                                                                                              base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 AAAAAAAAAAAAAAA 1
                                                                                                                                                                      BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-00227782.
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                                                                                            1005/c
AAD42005 standard; DNA; 19
                                                                                                                                                                                                                                (first entry)
                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fraser AS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                              pom/
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-546338/58.
                  1 Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                   Key
modified_base
                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kawasaki AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          US6403779-B1
                                                                                                                                                                                                                                04-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JUN-2002
                                                                                                                                                                                                  AAD42005;
       Query Match
Best Local
                        Best Loc
Matches
                                                                                                                                                     AAD42005/
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                                                                                                                                                                                                                                                                                                                                                                                                           Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used for preparation of 2'-O-alkylated compounds comprises dissolving nucleoside in aprotic solvent, cooling, treating with base, warming,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a novel method of selective alkylation of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside. The method involves dissolving the nucleoside in at least one aprofic solvent, cooling treating with base, warming, cooling and reacting with a reactive ester. The method is useful for the preparation of 2'-0-alkyl nucleotides, nucleosides and nucleoside surrogates used for preparation of oligometic compounds having improved hybridisation affinity and nuclear resistance, which are useful as therapeutics, diagnostics and research reagents. The present sequence is a modified oligonucleotide used to illustrate the method of the invention
                                                                                                                       Dihydroxy sugar moiety; 2'-0-alkyl nucleotide; hybridisation affinity; nuclear resistance; alkylation; therapeutic; diagnostic; ss.
                                                                                                 Oligonucleotide #6 used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                 Prakash TP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.1%; Score 19; DB 1; Length 19; 100.0%; Pred. No. 2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                /mod_base= OTHER
/note= "5-methyl, 2'-0-propyl residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                Cook PD,
                                                                                                                                                                                                                                                                                                                                                                Manoharan M,
                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 46; Col 33; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              cooling and reacting with ester.
                                                                                                                                                                                                                                                                                               99US-00227782.
                                                                                                                                                                                                                                                                                                                    99US-00227782
                                AAD42003 standard; DNA; 19
                                                                           04-NOV-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                           (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-546338/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                               Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                Kawasaki AM,
                                                                                                                                                                                                                                                                                               08-JAN-1999;
                                                                                                                                                                                                                                                                                                                    08-JAN-1999;
                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                  US6403779-B1
                                                                                                                                                                                                                                                                        11-JUN-2002
                                                     AAD42003;
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Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used for preparation of 2'-0-alkylated compounds comprises dissolving nucleoside in aprotic solvent, cooling, treating with base, warming, cooling and reacting with ester.

Example 46; Col 31; 24pp; English.

Prakash TP

Cook PD,

Manoharan M,

Fraser AS, PHARM INC

Kawasaki AM,

SISI (-SISI)

WPI; 2002-546338/58.

99US-00227782. 99US-00227782.

08-JAN-1999; 08-JAN-1999;

11-JUN-2002

US6403779-B1

/mod_base= OTHER /note= "5-methyl, 2'-aminooxyethoxy (2'-AOE) residues"

Location/Qualifiers 15. .18 /*tag= a

Key modified_base

Unidentified

Dihydroxy sugar moiety, 2'-O-alkyl nucleotide, hybridisation affinity; nuclear resistance, alkylation, therapeutic, diagnostic, ss.

Oligonucleotide #1 used to illustrate the method of the invention

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The present invention relates to a novel method of selective alkylation of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside. The method involves dissolving the nucleoside in at least one aprotic solvent, cooling treating with base, warming, cooling and reacting with a reactive ester. The method is useful for the preparation of 2'-0-alkyl nucleotides, nucleosides and nucleoside surrogates used for preparation of oligometric compounds having improved hybridisation affinity and nuclear resistance, which are useful as therapeutics, diagnostics and research reagents. The present sequence is a modified oligonucleotide used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cy sugar moiety, 2'-0-alkyl nucleotide, hybridisation affinity,
resistance, alkylation, therapeutic, diagnostic, 88.
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide #2 used to illustrate the method of the invention.
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                                                                                                                                                                                                                                                                                     Score 19; DB 1; Length 19;
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                         1.1%; Scor.
100.0%; Pred. No. c.
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 15. .18
                                                                                                                                                                                                                                                                                                                                                                              1736 AAAAAAAAAAAAAAA 1754
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                                                                                                                                                                                                                                                                                                                                                                                                                            19 AAAAAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                     19; Conservative
                                                                                                                                                                                                                                                                                                                Similarity
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modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jnidentified
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                                                                                                                                                                                                                                                                                            Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 383
                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD41999/
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Gaps

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1736 AAAAAAAAAAAAAAA 1754

19; Conservative

Matches

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AAAAAAAAAAAAAAA 1

19

ВР

AAD41998 standard; DNA; 19

(first entry)

04-NOV-2002

AAD41998; RESULT 382
AAD41998/C
ID AAD419
XX
AC AAD419
XX

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Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used for preparation of 2'-O-alkylated compounds comprises dissolving nucleoside in aprotic solvent, cooling, treating with base, warming, cooling and reacting with ester.
                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a novel method of selective alkylation of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside. The method involves dissolving the nucleoside in at least one aprotic solvent, cooling treating with base, warming, cooling and reacting with a reactive ester. The method is useful for the preparation of 2'-0-alkyl nucleotides, nucleosides and nucleoside surrogates used for preparation of oligomeric compounds having improved hybridisation affinity and nuclear resistance, which are useful as therapeutics, diagnostics and research reagents. The present sequence is a modified oligonucleotide used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide; 2'-O-(2-(methylthio)ethyl)-5-methyluridine; antisense; DNA-RNA hybrid; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "2'-0-(2-methylthio)ethyl)-5-methyluridine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mod_base= OTHER
/note= "2'-0-(2-methylthio)ethyl)-5-methyluridine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mod_base= OTHER
/note= "2'-0-(2-methylthio)ethyl)-5-methyluridine'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide with 2'-O-(2-(methylthio)ethyl)-5-methyluridine.
                                                                                                                           Manoharan M, Cook PD, Prakash TP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.1%; Score 19; DB 1; Length 19; Best Local Similarity 100.0%; Pred. No. 2e+02; Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                             Example 46; Col 35; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1736 AAAAAAAAAAAAAAAA 1754
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  99US-00227782.
                                         99US-00227782.
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                                                                                                                           Fraser AS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *tag=
                                                                                  (ISIS-) ISIS PHARM INC
                                                                                                                                                                  WPI; 2002-546338/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
modified_base
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08-JAN-1999;
                                                                                                                           Kawasaki AM,
                                         08-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABZ58336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABZ58336/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                           Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used for preparation of 2'-O-alkylated compounds comprises dissolving nucleoside in aprotic solvent, cooling, treating with base, warming,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a novel method of selective alkylation of 2.7, 3. dipydroxy sugar moieties of a nucleoside.

The method involves dissolving the nucleoside in at least one aprotic solvent, cooling, treating with base, warming, cooling and reacting with ar acactive ester. The method is useful for the preparation of 2. -O-alkyl nucleotides, nucleosides and nucleoside surrogates used for preparation of oligomeric compounds having improved hybridisation affinity and nuclear resistance, which are useful as therapeutics, diagnostics and research reagents. The present sequence is a modified oligonucleotide used to illustrate the method of the invention
                     /mod_base= OTHER
/note= "5-methyl, 2'-dimethylaminooxyethoxy (2'-DMAOE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dihydroxy sugar moiety, 2'-O-alkyl nucleotide; hybridisation affinity, nuclear resistance; alkylation; therapeutic; diagnostic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide #12 used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                               Prakash TP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.1%; Score 19; DB 1; Length 19; Best Local Similarity 100.0%; Pred. No. 2e+02; Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                               Cook PD,
                                                                                                                                                                                                                                                                                                               Manoharan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 46; Col 31; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1736 AAAAAAAAAAAAAAAA 1754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15..18
/*tag= a
/mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cooling and reacting with ester.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAAAAAAAAAAAAAA
                                                                                                                                                                                      99US-00227782
                                                                                                                                                                                                                             99US-00227782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD42009 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-NOV-2002 (first entry)
  /*tag= a
                                                              residues"
                                                                                                                                                                                                                                                                                                               Fraser AS,
                                                                                                                                                                                                                                                                      (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-546338/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
modified_base
                                                                                                                                                                                                                             38-JAN-1999;
                                                                                                                                                                                                                                                                                                               Камавакі АМ,
                                                                                                      US6403779-B1
                                                                                                                                                                                      08-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
                                                                                                                                             11-JUN-2002
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RESULT 384 AAD42009/ AAD42009

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Gaps

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/mod_base= OTHER /note= "2'-0-(2-methylthio)ethyl)-5-methyluridine"

ש

/*tag=

modified base

/note= "2'-dimethylaminooxyethyl thymidine (T-2'DMAOE)"

US6403779-B1

11-JUN-2002

WO2003004603-A2

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Gaps

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Sequence 19 BP; 0 A; 0 C; 0 G; 15 T; 4 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
                                                                                                                                              Example 27; Page 72; 122pp; English.
                                                                                                                                                                                                                                                                                                      1736 AAAAAAAAAAAAAAA 1754
                                                                                                                                                                                                                                                                                                                                                                                                                                     restriction enzyme; ss
                                                                                                                                                                                                                                                                                                                       AAAAAAAAAAAAAAA 1
                       01-JUL-2002; 2002WO-US020940
                                       03-JUL-2001; 2001US-0302683P.
28-JAN-2002; 2002US-00058740.
                                                                                                                                                                                                                                                                                                                                                              AAQ75569 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                              Local Similarity 100.
es 19; Conservative
                                                                               Prakash TP, Manoharan M;
                                                               (ISIS-) ISIS PHARM INC
                                                                                               WPI; 2003-239204/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-018287/03.
                                                                                                                                                                                                                                                                                                                                                                                                                            Analysis; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JP06303997-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                              04-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1994.
        16-JAN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                      aggregate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                      19
                                                                                                                                                                                                                                                                                                                                                                              AAQ75569,
                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                       therapy
                                                                                                                                                                                                                                                                                                                                              RESULT 386
                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                     AAQ75569/
XX AAQ7
XX AAQ7
XX AAQ7
XX AAA1
XX AAA1
XX SYNC
XX SYNC
XX SYNC
XX SYNC
XX BOD 01-N
XX I6-A
XX I6-A
XX I6-A
XX WPI;
XX WPI;
XX WPI;
XX WPI;
XX WPI;
XX WPI;
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lene expression; reverse transcription; primer; cDNA;
restriction enzyme; ss.
                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                                                                                                                                                                    Query Match 1.1%; Score 19; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 2.1e+02; Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.1%; Score 19; DB 1; Length 20; 100.0%; Pred. No. 2.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                          Sequence 20 BP; 0 A; 0 C; 1 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 5; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                    1734 ACAAAAAAAAAAAAAAA 1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1734 ACAAAAAAAAAAAAAAA 1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ75570/c
ID AAQ75570 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                    19 АСАААААААААААААА
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93JP-00112515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 ACAAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1995-018287/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP06303997-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aggregate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ75570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   **********
                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                               원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is an example of an oligonucleotide of the invention containing 2'.-O'.(T-(methylthio)ethyl)-5-methyluridine (2'.-O-(MTE)-5-methyluridine) modifications. In examples of the invention, 2'.-O-MTE was incorporated into oligonucleotides and evaluated for antisense properties in comparison with the known 2'.-O-(2-methoxyethyl) (2'.-O-MOE) modification. The 2'.-O-MTE modification disponucleotides exhibited similar binding affinity to target RNA as their 2'.-O-MOE equivalent while binding to human serum albumin was improved. The modification can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modulate the pharmacokinetics of oligonucleotides, e.g. in antisense
                                                                                                                                                                                                                                                                                                                               Increasing binding of oligomeric compound to proteins useful in preparation of antisense therapeutics, involves use of modified oligomeric compound having oligonucleotide group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression; reverse transcription; primer; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.1%; Score 19; DB 1; Length 19;
100.0%; Pred. No. 2e+02;
ive 0; Mismatches 0; Indels
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Gaps

Disclosure; Page 5; 11pp; Japanese

93JP-00112515 93JP-00112515

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AAT04915-T04922 are oligonucleotide primers and probes used for the amplification and sequencing of mammalian stem cell factor (SCF). Non-naturally occurring SCF and C-terminally truncated polypeptides, having amino acid sequences sufficiently duplicative of naturally occurring SCF, stimulate growth of primitive progenitors such as haematopoietic progenitor cells, neural stem cells and primordial germ stem cells. The progenitor cells, neural stem cells and primordial germ stem cells. The progenitor cells, neural stem cells and primordial germ stem cells. The reprides can be used in a composition for treating leucopenia, anaemia or thrombocytopenia, for enhancing engraftment of bone marrow during transplantation or for bone marrow recovery after chemotherapy or radiation-induced bone marrow aplasia or myelouspression. They can also be used for treating neoplasia, nerve damage, infartility, intestinal damage or myeloproliferative disorders. Antibodies may be raised against the peptides for use in detection or neutralisation of SCF in serum. SCF may be useful for the treatment of AIDS and severe combined immunodeficiency (SCID) states alone or in combination with other factors immunodeficiency (SCID) states alone or in combination with other factors
                                                                                                                                                                                                                                                                            New stem cell factor polypeptide(s) - for stimulating the growth of primitive progenitor cells, esp. for treating disorders involving blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphorothioate; sulphurisation; heterocycle; automated synthesis; antisense; EDITH; Beaucage reagent; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/note= "phosphorothioate internucleotide linkages"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                  Martin FH;
                                                                                                                                                                                                     Bosselman RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                          Example 3; Fig 12C; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1735 CAAAAAAAAAAAAAAA 1753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phosphorothioate oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 CAAAAAAAAAAAAAA 1
                                      89US-00422383.
90US-00537198.
90US-00573616.
90WO-US005548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV07752 standard; DNA; 20 BP
    95EP-00105391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97WO-US007118.
                                                                                                                       90US-00589701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                  Sugge SV,
                                                                                                                                                                                                                                       VPI; 1995-346090/45
                                                                                                                                                              (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-APR-1997;
04-OCT-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9741130-A2
                                                             11-JUN-1990;
                                                                                                  28-SEP-1990;
01-OCT-1990;
                                         16-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-NOV-1997.
                                                                                24-AUG-1990
                                                                                                                                                                                                     Sebo KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV07752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Analysis of cDNA and gene expression - by amplification of mRNA followed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
transplant; neoplasia; myelosuppression; bone marrow; ss.
                                                                                                                                                                                                Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                              Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.1%; Score 19; DB 1; Le
100.0%; Pred. No. 2.1e+02;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             by digestion with restriction enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 5; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1734 ACAAAAAAAAAAAAAA 1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 ACAAAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT04917 standard; cDNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                             93JP-00112515
                                                                                                                                                                                                                                                                                                                                                                                                                    93JP-00112515
                                         , AAQ75567 standard; DNA; 20
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                                                                                                                  04-AUG-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
ses 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-018287/03
                                                                                                                                                                                                                                                                                                                                                                               16-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                    16-APR-1993;
                                                                                                                                                                                                                                                                                                 JP06303997-A
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15-MAY-1996
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                                                                                                                                                                                                                                                            Synthetic.
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                                                                                AAQ75567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT04917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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(AMGE-) AMGEN
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25-NOV-1992;
21-DEC-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-JUN-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH41331;
                                                     factor
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 392
AAH41331/c
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                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                           containing compounds. It comprises contacting the phosphorus-containing compound which a 1.2,4-dithiazolidine-2,5-dione compound or a 3-bubstiuted-1.2,4-dithiazolin-5-one compound. The method is especially useful for incorporation of phosphorothioate linkages into biologically important molecules such as DNA, RNA and phosphosphides. Molecules containing such linkages are useful e.g. as antisense compounds for protein interactions, or as reagents for studying DNA-protein or RNA-protein interactions, or as catalytic RNA. The present sequence represents an oligonucleotide with phosphorothioate linkages prepared by the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stem cell factor; SCF; haematopoietic progenitor cell; blood forming; primitive progenitor cell; haematopoietic disorder; syngeneic; altologous bone marrow transplant; gene therapy; transfection; haematopoietic stem cell; acute blood loss; neoplasia;
                                                                                                       compounds, e.g.
compound with a di:sulphide-
                                                                                                                                                                    present invention provides a method for sulphurising phosphorus aining compounds. It comprises contacting the phosphorus-contain
                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                   1.1%; Score 19; DB 1; Length 20;
100.0%; Pred. No. 2.1e+02;
tive 0; Mismatches 0; Indels
                                                             Chen L, Hammer RP;
                                                                                                                                                                                                                                                                                               Sequence 20 BP; 1 A; 0 C; 0 G; 0 T; 19 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stem cell factor universal oligonucleotide 220-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zsebo KM, Suggs SV, Bosselmann RA, Martin FH;
                                                                                                     Sulphurisation of phosphorus-containing oligo:nucleotide(8) - by contacting the
                                                                                                                           containing five-membered heterocycle.
                                        (LOUU ) UNIV LOUISIANA STATE & AGRIC.
                                                             Barany G, Musier-Forsyth K, Xu Q,
                                                                                                                                                                                                                                                                                                                                                              1736 AAAAAAAAAAAAAAA 1754
                                                                                                                                               Example 7; Page 30; 51pp; English
                                                                                                                                                                                                                                                                                                                                                                                  19 AAAAAAAAAAAAAAA 1
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90US-00573616.
90WO-US005548.
90US-00589701.
         96US-00641920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99EP-00122861.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89US-00422383
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA13752 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                         Conservative
                             (MINU ) UNIV MINNESOTA
                                                                                  WPI; 1997-549671/50.
                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INC.
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         30-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JUN-1990;
24-AUG-1990;
28-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-OCT-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-1989
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                                                                                                                                                                                                                                                                                                                                         19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer; 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA13752;
                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 391
                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                    The
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administration to a subject. The method comprises: (a) obtaining the cells hematopoietic progenitor cells from a donor; and (b) expanding the cells by adding to the cells a haematopoietically effective dose of a polypeptide product having at least part of the primary structural confirmation and one or more of the biological properties of naturally occurring stem cell factor (SCF). The method is useful for stimulating primative progenitor cells including early haematopoietic progenitor cells which are capable of maturing to erythroid, megakaryocyte, cells which are capable of maturing to erythroid, megakaryocyte, cells which are capable of maturing to erythroid, megakaryocyte, cells which are capable of maturing to erythroid, and lymphoid lineages. Cr for expanding early haematopoietic disorders. The method is useful for treating haematopoietic progenitors in syngeneic, allogeneic cr for expanding early haematopoietic progenitors in syngeneic, allogeneic cr autologous bone marrow transplant. SCF is useful for enhancing the efficiency of gene therapy based on transfecting haematopoietic stem cells. SCF is useful for combating the myeloside capable capable of an as a boost to the immune system for fighting after acute blood loss and as a boost to the immune system for fighting necessaria (cancer). The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                A method has been developed of making haematopoietic cells suitable for
                                                                            Production of hematopoietic cells suitable for administration to a subject using progenitor cells and expanding the cells using stem cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oligonucleotide which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
gene therapy; PCR primer; mutagenesis; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.1%; Score 19; up .

Best Local Similarity 100.0%; Pred. No. 2.19

Best Local Similarity 0; Mismatches
                                                                                                                                                                                                                                               Example 3; Fig 12C; 123pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 садададададададада 1
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90US-00589701.
92US-00982255.
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WPI; 2000-259135/23.
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Zsebo KM,

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29-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                              Zsebo KM, Bosselman RA,
                                                                                                             Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                      WPI; 2001-298941/31
        WPI; 2001-366062/38
                             into cell in vitro.
                                                                                                                                                                                                                                                                         ZSEBO K M.
                                                                                                                                                                                                      PCR primer; ss
                                                                                                                                                                                                                                                    11-JUN-1990;
24-AUG-1990;
01-OCT-1990;
                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                      US6207417-B1
                                                                                                                                                                                                                                       07-JUN-1995;
                                                                                                                                                                                                                                                                 21-DEC-1993;
                                                                                                                                                                                                                                               16-OCT-1989
                                                                                                                                                                                                                               27-MAR-2001
                                                                                        invention
                                                                                                                                                               AAS04111;
                                                                                                         Query Match
                                                                                                                                                                                                                                                                            (BOSS/) (SUGG/) (MART/)
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                                                                                                                                              RESULT 393
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The present sequence for universal PCR primer 220-3 is 1 of 8 universal oligonucleotides (AAS04110-AAS04117) used in the isolation of the human SCF (stem cell factor) CDNA sequence. The present invention relates to novel stem cell factors (AAU02453, AAU02460, AAU02461) and the polynucleotides encoding them. SCF stimulate primitive progenitor cells including early haematopoietic progenitor cells. The invention also describes SCF peptides (AAV02462-AAV02481) and the oligonucleotides (CAS04081-AAS04117) used in the isolation of human and rat SCF sequences. The polynucleotide encoding SCF is useful for producing SCF and useful in CCT and the sells of the second s
disorders involving blood cells, e.g. leukemia, splenomegaly, Hodgkin's disease, Kala azar, anemia and septicemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated non-human mammalian stem cell factor polypeptide stimulating growth of early hematopoietic progenitor cells, useful for treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar, sarcoidosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; rat; mammal; stem cell factor; SCF; cell growth stimulation; gene therapy; haemstopoletic disorder; aplastic anaemia; leukaemia; neurological damage; intestinal damage; infertility; AIDS; SCID; severe combined immunodeficiency; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.1%; Score 19; DB 1; Length 20;
100.0%; Pred. No. 2.1e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalian stem cell factor PCR primer SEQ ID NO: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Martin FH;
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                                                                                     Example 3; Fig 12C; 209pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1735 CAAAAAAAAAAAAAAA 1753
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90US-00537198.
90US-00573616.
90US-00589701.
92US-00982255.
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AAF89091 standard; DNA; 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zsebo KM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 394
AAF89091/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                           The present invention describes a method for enhancing (E) the efficiency of transfer of a polynucleotide (I) into a target mammalian cell (II) in vitro. comprising exposing (II) that expresses a stem cell factor (SCF) receptor to a biologically active SCF, its analogue or fragment, which induces cell proliferation, and introducing (I) to (II) in vitro. Exposure of SCF to (II) results in increased uptake of (I) into the cell. The method is useful for enhancing the efficiency of the transfer of a polynucleotide into a target mammalian cell in vitro. The method is useful in gene therapy techniques. AAH41301 to AAH41364 and AAB98351 to AAB98390 represent sequences used in the exemplification of the present
                                                                                                            Enhancing efficiency of transfer of polynucleotide into a target mammalian cell in vitro, involves exposing cell that expresses a stem cell factor receptor to stem cell factor, and introducing polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, stem cell factor; SCF, early haematopoietic progenitor cell;
blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human SCF (stem cell factor) cDNA universal PCR primer 220-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.1%; Score 19; DB 1; Length 20;
100.0%; Pred. No. 2.1e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
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        Martin FH
  Suggs SV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Suggs SV,
                                                                                                                                                                                                                                                         Example 3; Fig 12C; 210pp; English.
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90US-00573616.
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93US-00172329
     Bosselman RA,
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SUGGS S V.
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10-MAY-2001.
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ID AAS057

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AC AAS057

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DT 07-SEP
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                The present invention provides the protein and coding sequences of mammalian stem cell factors (SCFs). These are capable of stimulating the growth of early haemacopoietic progenitor cells, neural stem cells and primordial garm stem cells. The sequences are useful in the treatment of leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological and intestinal damage, infertility, AIDS and severe combined immunodeficiency (SCID). The present sequence is primer used to amplify an SCF in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                    reverse phase triplex forming oligonucleotide, RP-TFO, protected nucleic acid sequence, PNAS; single nucleotide polymorphism; SNP; short tandem repeat; cancer; Factor V Leiden SNP; ss.
                                                                                                                                                       Gaps
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                                                                                                                                  1.1%; Score 19; DB 1; Length 20; 100.0%; Pred. No. 2.1e+02; tive 0; Mismatches 0; Indels
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|label= OTHER
'note= "A is aminopurine substituted"
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                                                                                                                Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                  Aminopurine substituted region of an RP-TFO.
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Example 3; Fig 12C; 209pp; English.
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label= OTHER
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/label= OTHER
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/label= OTHER
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/label= OTHER
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'label= OTHER
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                                                                                                                                                                                                                                          AAS05714 standard; DNA; 20
                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                           Local Similarity 100.
nes 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                           Synthetic
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                                                                                                                                   Query Match
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Matches
                                                                                                                                                                                                                       RESULT 395
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The sequence is a second reverse phase triplex forming oligonucleotide, RP-TFO (3' to the SNP) used to analyse Factor V Leiden SNP using the method of the invention. The invention relates to analysing target nucleic acid sequences comprising restricting isolated DNA, hybridising at least one triplex forming oligonucleotide (TFO), adding a 3' to 5' exonuclease to form a protected nucleic acid sequence (PNAS) tail structure, hybridising the captured structure with a single nucleotide polymorphisms (SNP) identification probe and determining the SNP score. The methods can be used for analysing target nucleic acid sequences, especially genomic DNA sequences, to determine if they contain SNPs or short tandem repeats (STRS). The methods can be used to detect SNPs for use in population genetics, drug development, forensics, cancer, genetic disease research, genomic analysis, diagnostics and therapeutics in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Analyzing target nucleic acid sequences, useful for population genetics, drug development and diagnosing cancer, comprises hybridizing triple forming oligonucleotide and probe to target sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "A is aminopurine substituted"
                                                          'note= "A is aminopurine substituted"
                                                                                                                                                                                                                                                                                                               'note= "A is aminopurine substituted'
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                                                                                                                                                                                      or
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/label= OTHER
/note= "Other= Hypoxanthine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page 66; 141pp; English.
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label= OTHER
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/label= OTHER
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03-NOV-1999; 99US-0163416P.
21-DEC-1999; 99US-017348P.
07-JUL-2000; 2000US-0216579P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-NOV-2000; 2000WO-US030534
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/label= (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
wes 19; Conserv
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                                                                                        modified base
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/note= "Other= Hypoxanthine or Inosine"

Location/Qualifiers

/*tag= a /label= OTHER

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The sequence is a second reverse phase triplex forming oligonucleotide, RP-TFO (3' to the SNP) used to analyse Factor V Leiden SNP using the method of the invention. The invention relates to analysing target nucleic acid sequences comprising restricting isolated DNA, hybridising at least one triplex forming oligonucleotide (TFO), adding a 3' to 5' exonuclease to form a protected nucleic acid sequence (PNAS) tail structure, hybridising the captured structure with a single nucleotide polymorphisms (SNP) identification probe and determining the SNP score. The methods can be used for analysing target nucleic acid sequences, especially genomic DNA sequences, to determine if they contain SNPs or short tandem repeats (STRS). The methods can be used to detect SNPs for use in population genetics, dryd development, forensics, cancer, genetic disease research, genomic analysis, diagnostics and therapeutics in
                                          reverse phase triplex forming oligonucleotide; RP-TFO; protected nucleic acid sequence; PNAS; single nucleotide polymorphism; SNP; short tandem repeat; cancer; Factor V Leiden SNP; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 1 Other;
              8-aminopurine substituted region of an RP-TFO.
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99US-0163416P.
99US-0171348P.
                                                                                                                                                                                                                                                                                     03-NOV-2000; 2000WO-US030534.
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                                                                                                                                   Key
modified_base
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                                                                                                                                                                                                                                                                                                                                  03-NOV-1999;
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                                                                                                     Synthetic
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AAH23889/C
ID AAH238
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AC AAH238
AC AAH238
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The present sequence for universal PCR primer 220-3 is 1 of 8 universal oligonucleotides (AAH23888-AAH23895) used in the isolation of the human SCF (stem cell factor) CDNA sequence. The present invention relates to novel stem cell factors (AAB73561-AAB73568, AAB73571-AAB73576) and the colymucleotides encoding them. SCF stimulate primitive progenitor cells olymucleotides encoding them. SCF stimulate primitive progenitor cells olymucleotides (AAB73578-AAB73597) and the oligonucleotides (AAB73389-AAB73897) and the oligonucleotides (CAB73889-AAB73897) used in the isolation of human and rat SCF sequences. The polymucleotide encoding SCF is useful for producing SCF and useful in the isolation of human, and rat SCF sequences. The polymucleotide encoding SCF is useful for producing SCF and useful in such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia, congestiva splenomegaly, Kala azar, sarcoidosis, military tuberculosis, disseminated fungus disease, Fulminating septicaemia, malaria, vitamin bypopigmentation disorders such as piebaldism and vitiligo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New stem cell factor polypeptides and their analogs which stimulate growth of early hematopoietic progenitors, useful for treating aplastic anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's
                                    Human, stem cell factor; SCF; early haematopoietic progenitor cell; blood disorder; leukaemia, Hodgkin's disease; lymphoma; splenomegaly; anaemia, Kala azar; septicaemia; malaria; hypopigmentation disorder;
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Human SCF (stem cell factor) cDNA universal PCR primer 220-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Martin FH;
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90US-00537198.
90US-00573616.
90US-00589701.
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ses 19; Conservative
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                                                                                                PCR primer; 88
                                                                                                                                      Homo sapiens
                                                                                                                                                                        JS6204363-B1
                                                                                                                                                                                                                                                    25-NOV-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
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    à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Analyzing target nucleic acid sequences, useful for population genetics, drug development and diagnosing cancer, comprises hybridizing triple forming oligonucleotide and probe to target sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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1.1%; Score 19; DB 1; Length 20; 95.0%; Pred. No. 2.1e+02;

0; Mismatches

1; Indels

Human; stem cell factor; SCF; early haematopoietic progenitor cell;

07-AUG-2001 (first entry)

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The present sequence for universal PCR primer 220-3 is 1 of 8 universal oligonucleotides (AASO4218) used in the isolation of the human SCF (stem cell factor) CDNA sequence. The present invention relates to novel stem cell factors (AANO2761-AANO2767, AANO2777-AANO2775, AANO2797) and the polynucleotides encoding them. SCF stimulate primitive progenitor cells including early hematopoiettic progenitor cells. The invention also describes SCF peptides (AANO2777-AANO2794) and the oligonucleotides (AASO4182-AASO410) used in the isolation of human and rat SCF sequences. The polynucleotide encoding SCF is useful for producing SCF and useful in gene therapy. It is useful for treating disorders involving blood cells such as myelodibrosis, metastatic carcinoma, acute leukaemia, multiple such as myelodibrosis, metastatic carcinoma, acute leukaemia, multiple congestive splenomegally, Kala axar, sarcoidosis, military tuberculosis, disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12
blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly; anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated DNA sequence, encoding polypeptide product useful for stimulating growth of early hematopoietic progenitor cells.
                                                                                                                                                                                                                                                                                                                                                                 Martin FH;
                                                                                                                                                                                                                                                                                                                                                                     Suggs SV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Fig 12C; 167pp; English
                                                                                                                                                                                                                                    90US-00537198.
90US-00573616.
90US-00589701.
92US-00982255.
                                                                                                                                                                                 93US-00172329
                                                                                                                                                                                                                     89US-00422383
                                                                                                                                                                                                                                                                                                                                                                   Zsebo KM, Bosselman RA,
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-281051/29
                                                                                                                                                                                                                                                                                                                               (AMGE-) AMGEN INC.
                                     PCR primer; 88
                                                                         Homo sapiens
                                                                                                                                                                               21-DEC-1993;
                                                                                                           US6218148-B1
                                                                                                                                                                                                                                                                          01-OCT-1990;
25-NOV-1992;
                                                                                                                                             17-APR-2001
                                                                                                                                                                                                                     16-OCT-1989;
                                                                                                                                                                                                                                      11-JUN-1990;
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and folic acid deficiency, pyridoxine deficiency, and hypopigmentation disorders such as piebaldism and vitiligo
                                                                                                                        Gaps
                                                                                                                      ;
                                                                                    Score 19; DB 1; Length 20;
Pred. No. 2.1e+02;
                                                                                                                  0; Indels
                                                    Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
                                                                         1.1%; Scor.
100.0%; Pred. No. 2...
                                                                                                    Local Similarity 100.
hes 19; Conservative
                                                                                        Query Match
                                                                                                                        Matches
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1735 CAAAAAAAAAAAAAAAA 1753
                         19 САААААААААААААААА 1
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Human stem cell factor (SCF) cDNA universal PCR primer 220-3.
              ВР
             AAS10447 standard; DNA; 20
                                         24-OCT-2001 (first entry)
                           AAS10447;
RESULT 399
       AAS10447/
```

Human; stem cell factor; SCF; haematopoietic progenitor cell; blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency; hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.

Homo sapiens

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anaemia; myelosuppression; prove damage; myeloproliferative disorder; infertility; neoplasia; myelofibrosis; myelosolerosis; osteopetrosis; metastatic carcinoma; acute leukaemia; multiple myeloma; sarcoidosis; Hodgxin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease; Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar; Di Guglialmo syndrome, congestive splenomegaly; splenic pancytopaemia; diseaminated fungus disease; Pulminating septicaemia; piebaldism; AIDS; acquired immune deficiency syndrome; malaria; military tuberculosis;
                                                                                                                                                                                                                                                                                                                     Rat; stem cell factor; SCF protein; leucopaenia; thrombocytopaenia;
                                                                                                                                                                                                                                                                           Rat SCF 5' cDNA amplifying PCR primer, 220-3.
                                                                                                                                 464/c
AAD35464 standard; DNA; 20 BP.
                                        19 Садададададададада
                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                     25-JUL-2002
                                                                                                                                                                                             AAD35464;
                                                                                                        RESULT 400
                                                                                                                            AAD35464,
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                                     셤
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Gaps

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0; Indels

1.1%; Score 19; DB 1; Length 20; 00.0%; Pred. No. 2.1e+02;

100.0%; Prea. ....

19; Conservative

Matches

Local Similarity

1735 CAAAAAAAAAAAAAAAA 1753

Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

The present sequence for universal PCR primer 220-3 is 1 of 19 PCR primers (AAS10415-AAS10453) used to amplify various portions of the human SCF cONR sequence. The sequence is described in an invention relating to novel stem cell factors, the polynuclectides encoding them and methods for producing the stem cell factors. The methods involve increasing the number of early haematopoietic progenitor cells in human peripheral blood by administering a haematopoietic progenitor cells in human peripheral blood by administering a haematopoietic progenitor cells in human peripheral including myelofibrosis, myelosclerosis, osteopetrosis, metastatic acriniona, acute leukaemia, multiple myeloma, Hodgkin's disease, including myelofibrosis, multiple myeloma, fodgkin's disease, hamana, malatiple myeloma, doucher's disease, hiemann-pick disease, refractory anaemia, malaria, vitamin B12 and folic acid deficiency, hypopigmentation disorders i.e. piebaldism and viral induced disorders, including AIDS

Increasing the number of early hematopoietic progenitor cells in the peripheral blood useful for the treatment of blood disorders including Hodgkin's disease comprises the administration of human stem cell factor.

Example 3; Fig 12C; 210pp; English

Suggs SV, Martin FH;

Zsebo KM, Bosselman RA,

MARTIN F H.

(BOSS/) E (SUGG/) S (MART/) N ZSEB/)

WPI; 2001-407312/43.

ZSEBO K M. BOSSELMAN R A. SUGGS S V.

90US-00537198. 90US-00573616. 90US-00589701. 91US-00684535. 92US-00982255.

10-APR-1991; 25-NOV-1992; 21-DEC-1993;

95US-00449653

24-MAY-1995; 19-JUN-2001

11-JUN-1990 24-AUG-1990; 01-OCT-1990;

US6248319-B1

Stem cell factor; SCF; blood-forming system; blood cell disorder; haematopoietic system; metastatic carcinoma; acute leukaemia; multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo; refractory erythroblastic anaemia; miliary tuberculosis; cytostatic; disseminated fungus disease; haematopoietic; tuberculostatic; antifungal; antimalarial; dermatological; ss.

E. SCF universal oligonucleotide 220-3.

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δ
                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to novel non-naturally-occurring stem cell factor (SCF) polypeptides having an amino acid sequence sufficiently duplicative of that of naturally-occurring SCF to allow possession of haematopoietic biological activity of naturally occurring SCF. Sequences of the invention are useful for treating leucopaenia, thrombocytopaenia, anaemia and for enhancing bone marrow recovery in treatment of radiation, engraftment of bone marrow during transplantation in mammals and chemical or chemotherapeutic induced bone marrow aplasia or myelosuppression. They are also useful for treating acquired immune deficiency in a human, nerve anaema, neoplasia, infertility, myeloproliferative disorder, intestinal damage in a mammal. SCF sequences are useful for preparing biologically active polymer polypeptide adduct, for enhancing transfection of early haematopoietic progenitor cells with a gene, and transfer of a gene into a mammal. They are useful for treating myelofibrosis, myelosclerosis, ofecopeirosis, metastatic actioned, acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease, carnermer of a promeania, pick disease, carnermer are promeanly. Rala asar, sarcoides, primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   syndrome, congestive splenomegal, Kala azar, sarcoidosis, primary splenic pancytopaenia, disseminated fungus disease, malaria, military tuberculosis, Pulminating septicaemia, pyridoxine deficiency, vitamin B12 and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation disorders such as piebbaldism, AIDS (acquired immune deficiency syndrome) and vitiligo. The present sequence is a PCR primer which is used for amplifying the 5 end of rat SCF CDNA. This sequence is used in the
                                                                                                                                                                                                                                                                                                                                                         Novel non-naturally-occurring stem cell factor polypeptide, useful for treating leucopenia, thrombocytopenia, anemia and for enhancing engraftment of bone marrow during transplantation in a mammal.
pyridoxine deficiency, vitamin B12 deficiency; folic acid deficiency; Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 19; DB 1; Le
Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                Sugge SV, Martin FH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.1%; Scc. No. 2. 100.0%; Pred. No. 2. 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Fig 12C; 217pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exemplification of the invention
                                                                                                                                                        98US-00005243
                                                                                                                                                                                     95US-00449653
                                                                                                                                                                                                                                                                                              Zsebo KM, Bosselman RA,
                                                                                                                                                                                                                  (ZSEB/) ZSEBO K M.
(BOSS/) BOSSELMAN R A.
(SUGG/) SUGGS S V.
(MART/) MARTIN F H.
                                                                                                                                                                                                                                                                                                                           WPI; 2002-350789/38
                                                                                           US2002018763-A1.
                                                                                                                                                                                     24-MAY-1995;
                                                                                                                                                        12-JAN-1998;
                                                                                                                          14-FEB-2002
                                 primer; 88
                                                             Rattue ep.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Production of a human stem cell factor (SCF) polypeptide for treating disorders involving blood cells, such as leukemia, comprises culturing mammalian cells comprising non-human SCF promoter DNA linked to DNA encoding the human SCF.

3xample 3; Fig 12C; 120pp; English.

Martin FH;

Bosselman RA,

Suggs SV,

Zsebo KM,

(AMGE-) AMGEN INC.

04-OCT-1990

WPI; 2002-684093/74.

89US-00422383. 90US-00537198. 90US-00573616. 90US-00588701. 90EP-00310899. 95EP-00105391.

24-AUG-1990; 28-SEP-1990; 01-OCT-1990; 04-OCT-1990;

11-JUN-1990

04-OCT-1990; 2002EP-00008587

3P1241258-A2

Synthetic.

18-SEP-2002

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The present invention relates to novel stem cell factors (SCFs), polynucleotide sequences encoding the SCFs, and methods of producing them. SCFs are involved in the blood-forming (haematopoietic) system in mammals, particularly humans. The method of the invention is useful for the production of human SCF. The stem cell factors are useful to treat disorders involving blood cells e.g. metastatic carcinoma, acute retukaemia, multiple myeloma, Hodgkin's disease, lymphoma, refractory erythroblastic anaemia, miliary tuberculosis, disseminated fungus disease, malaria, and vitiligo. The present sequence representing a universal oligonucleotide for SCF DNA is used in the examples of the
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; antisense; lung dysfunction; nasal airway dysfunction;
                                                                                                                                                                                                                                                                                                                                                                             1.1%; Score 19; DB 1; Length 20;
100.0%; Pred. No. 2.1e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1735 CAAAAAAAAAAAAAAA 1753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAAAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human oligonucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AB288880 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
nes 19; Conservative
                                                                                                                                                                                                                                                                             present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABZ88880;
                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 402
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Gaps ö

0; Indels

1735 CAAAAAAAAAAAAAAAA 1753

Local Similarion hes 19; Conservative

Matches

19 CAAAAAAAAAAAAAAA 1

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ABS73848 standard; DNA; 20

05-DEC-2002 (first entry)

ABS73848; ABS73848/C ID ABS738 XX AC ABS738 XX DT 05-DEC

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the intitation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypebtide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory, antiallergic, antiaethmatic, hypotensive, composition of the invention case in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or the amily and is useful for treating or preventing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing levels of adenosine or reducing bronchodilation, increasing levels of abiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung allergies, or a respiratory disease or condition.

Creceptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung allergies, or a respiratory disease or condition.

Creceptor, producing bronchodilation, increasing levels of ubiquinone or lung inflammation, but was obtained in electronic format directly from WIPO cat fip.wipo.int/pub/published_pct_sequences Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchodilation; lung allergy; lung inflammation; respiratory disease; ds. antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; Katz E, Pabalan J, Aguilar D; Disclosure; SEQ ID NO 4122; 872pp; English. Li Y, Sandrasagra A, Ka Tang L, Shahabuddin S; 23-APR-2002; 2002WO-US013135. 24-APR-2001; 2001US-0286137P. (EPIG-) EPIGENESIS PHARM INC. WPI; 2003-229219/22 Li Y, WO200285308-A2 Homo sapiens. 31-OCT-2002. ubiquinone Miller S, Nyce JW, 

ö Score 19; DB 1; Length 20; Pred. No. 2.1e+02; 0; Indels Sequence 20 BP; 19 A; 0 C; 0 G; 1 T; 0 U; 0 Other; / Matcn Local Similarity 100.0%; Pred. No. 4.1. Query Match Matches

8 셤

ABZ89179 standard; DNA; 20 ABZ89179
TD ABZ8
XX
AC ABZ8
XX
XX
DT 17-C
XX

ABZ89179;

BP

(first entry) 17-OCT-2003

Human oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction;

antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; inflammation; respiratory disease; ds lund 

Homo sapiens.

WO200285308-A2

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P

(EPIG-) EPIGENESIS PHARM INC.

Katz E, Pabalan J, Aguilar D; Tang L, Shahabuddin S; Li Y, Sandrasagra A, Miller S, Nyce JW,

WPI; 2003-229219/22

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

Disclosure; SEQ ID NO 4421; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' end 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition of the invention has antiinflammatory, and cytostatic activity. The composition may have a immunosuppressive, and cytostatic activity. The composition may have a cuse in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antisinflammatory steroid in a subject, for reducing levels of adenosine ceptor, producing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject, a tissue, or treating bronchoconstriction, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO

Sequence 20 BP; 19 A; 0 C; 0 G; 1 T; 0 U; 0 Other;

ftp.wipo.int/pub/published_pct_sequences

Gaps ö 1.1%; Score 19; DB 1; Length 20; [00.0%; Pred. No. 2.1e+02; 0; Indels 0; Mismatches Local Similarity 100.0%; 19; Conservative Query Match Matches

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Gaps

ABZ99050 standard; DNA; 20 ABZ99050; ABZ99050/ EXEXEXEX EXE

RESULT 404

BP.

Human PDE4C oligonucleotide sequence. (first entry) 17-0CT-2003

Human; antisense; lung dysfunction; nasal airway dysfunction;

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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end ganomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antinflammatory steroid and ubiquinone. A composition of the invention has antinflammatory, and cytostatic, antiaschmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an arbject, for reducing levels of adenosine receptor, producing bronchodilation, increasing levels of biquinone or lung surfactent in a subject or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed or specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
antinflammatory steroid, ubiquinone, antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 14292; 872pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                      Katz E,
                                                                                                                                                                                                                                                                                                                                                                                                    Li Y, Sandrasagra A, K.
Tang L, Shahabuddin S;
                                                                                                                                                                                                                                                                 23-APR-2002; 2002WO-US013135.
                                                                                                                                                                                                                                                                                                               24-APR-2001; 2001US-0286137P.
                                                                                                                                                                                                                                                                                                                                                        (EPIG-) EPIGENESIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-229219/22.
                                                                                                                                                                              WO200285308-A2.
                                                                                                                                       Ното варіепв.
                                                                                                                                                                                                                          31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ubiquinone.
                                                                                                                                                                                                                                                                                                                                                                                                                      Miller S,
                                                                                                                                                                                                                                                                                                                                                                                                    Š
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Length 20; Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other; Score 19; DB 1; Le Pred. No. 2.1e+02; 1.1%; Scot. 100.0%; Pred. No. 2... 0; Mismatches Query Match Best Local Similarity 100. Matches 19; Conservative

8 셤

ABZ89678 standard; DNA; 20 ABZ89678 RESULT 405 

Human oligonucleotide sequence

17-OCT-2003 (first entry)

Human; antisense; lung dysfunction; nasal airway dysfunction;

antinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds. 

Homo sapiens

WO200285308-A2

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC.

ä

Pabalan J, Aguilar

ä Aguilar Pabalan J, Katz E, Li Y, Sandrasagra A, K Tang L, Shahabuddin S; Ľ Miller S, Avce JW.

WPI; 2003-229219/22

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

Disclosure; SEQ ID NO 4920; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5, or 3 end genomic flanking regions, 5 and 3 intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or masal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depteting levels of or antiinflammatory steroid in a subject, for reducing levels of adenosine receptor, producing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject stissue, or treating bronchoconstriction, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 20 BP; 19 A; 0 C; 0 G; 0 T; 0 U; 1 Other;

Gaps ö Length 20; 1; Indels 1.1%; Score 19; DB 1; 95.0%; Pred. No. 2.1e+02; tive 0; Mismatches 1. Local Similarity 95.0 nes 19; Conservative Similarity Query Match Matches

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Gaps

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0; Indels

Human oligonucleotide sequence. ВР ABZ87681 standard; DNA; 20 (first entry) 17-OCT-2003 ABZ87681; 

RESULT 406

ABZ87681/

Human; antisense; lung dysfunction; nasal airway dysfunction;

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Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                            Disclosure; SEQ ID NO 2923; 872pp; English.
                         lung inflammation; respiratory disease; ds
                                                                                                              Li Y, Sandrasagra A, Ka
Tang L, Shahabuddin S;
                                                                                                                                                                                                                                                                                                                                                               1736 AAAAAAAAAAAAAAAAA 1754
                                                                                                                                                                                                                                                                                                                                                                           AAAAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human oligonucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                          ABZ89677 standard; DNA; 20 BP
                                                                         23-APR-2002; 2002WO-US013135.
                                                                                      24-APR-2001; 2001US-0286137P.
                                                                                                  (EPIG-) EPIGENESIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                  17-OCT-2003 (first entry)
                                                                                                                                 WPI; 2003-229219/22
                                                 WO200285308-A2
                                     Homo sapiens.
                                                             31-OCT-2002
                                                                                                                                                                ubiquinone
                                                                                                                     Miller S,
                                                                                                                                                                                                                                                                                                                                                                                                                      ABZ89677;
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                                                                                                               Nyce JW,
                                                                                                                                                                                                                                                                                                                                      Query Match
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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the intiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intran-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a cuse in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing levels of adenosine creceptor, producing bronchodilation, increasing levels of adenosine creceptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung allergies, or a respiratory disease or condition. Once: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO cut fig. wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pharmaceutical composition for treating ailments associated with impaired
                        antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pabalan J, Aguilar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.1%; Score 19; DB 1; Length 20; Best Local Similarity 95.0%; Pred. No. 2.1e+02; Matches 19; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 4919; 872pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Katz E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li Y, Sandrasagra A, K
Tang L, Shahabuddin S;
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                                                                                                                                                                                                                                                                                                                                                                                                         24-APR-2001; 2001US-0286137P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EPIG-) EPIGENESIS PHARM INC.
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                                                                                                                                                                                                                                 WO200285308-A2
                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonuclectide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nuclectides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory steroid and ubiquinone. A composition may have a untiinflammatory and cytostatic activity. The composition may have a use nathisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an infilammatory steroid in a subject, for reducing levels of adenosine receptor, producing bronchodilation, increasing levels of adenosine receptor, ung surfactant in a subject's tissue, or treating bronchoconstriction, lung surfactant in a subject's tissue, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO.

I they wipo.int/pub/published_pot_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                           antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Katz E, Pabalan J, Aguilar D;
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Stem cell factor; SCF; haematopoietic activity; infertility;

Human; antisense; lung dysfunction; nasal airway dysfunction;

Stem cell factor (SCF) related DNA #31.

(first entry)

29-JAN-2004

Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.

Reverse transcription primer used in cDNA analysis technique.

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New non-natural stem cell factor, useful for treating e.g. leucopenia or immune deficiency, also related nucleic acid and antibodies.
intestinal damage; myeloproliferative disorder; leucopenia; thrombocytopenia; anaemia; bone marrow transplant; immune deficiency; neoplasia; nerve damage; osteoporosis; metastatic carcinoma; leukaemia; miliary tuberculosis; haematopoletic proganitor cell; ss.
                                                                                                                                                                                                                                                   Martin FH;
                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 32; 217pp; English
                                                                                                                                                                                                                                                  Suggs SV,
                                                                                                               89US-00422383.
90US-00537198.
90US-00573616.
90US-00689701.
91US-00684535.
                                                                                                                                                                   93US-00172329.
95US-00449653.
98US-00005893.
                                                                                               98US-00224683
                                                                                                                                                                                                                                                  Zsebo KM, Bosselman RA,
                                                                                                                                                                                                       ZSEBO K M.
BOSSELMAN R A.
                                                                                                                                                                                                                                                                  WPI; 2003-851459/79.
                                                                                                                                                                                                                        SUGGS S V.
                                                             JS2002031491-A1
                                                                                                                                          01-OCT-1990;
10-APR-1991;
25-NOV-1992;
                                                                                               31-DEC-1998;
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                                                                              14-MAR-2002
                                                                                                                 16-OCT-1989
                                                                                                                          11-JUN-1990
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                                                                                                                                                                             24-MAY-1995
                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention
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The invention relates to stem cell factor (SCF) polypeptides with haematopoietic activity and the polymucleotides encoding them. The polypeptides are used for treating infertility, intestinal damage, myeloproliferative disorders, leucopenia, thrombocytopenia or anaemia, for improving engraftment of bone marrow transplants, for enhancing bone marrow recovery after radiotherapy or chemotherapy and in treatment of immune deficiency, neoplasia, nerve damage, osteoporosis, metastatic carcinoma, leukaemia and miliary tuberculosis. The SCF polypeptides are also used to expand haematopoitetic progenitor cells for transplantation and to prepare such cells for transfection with a gene. The SCF polypeptides and also as probes for mapping of the SCF gene, for identifying SCF-related diseases and as a marker for neighbouring genes. Antibodies raised against the polypeptides are useful in diagnosis and to remove SCF from blood. This sequence represents SCF related DNA of the

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/ Match 1.1%; Score 19; DB 1; Length 21; Local Similarity 100.0%; Pred. No. 2.2e+02; les 19; Conservative 0; Mismatches 0; Indels

Query Match

Matches

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BP

AAQ75639 standard; DNA; 21

RESULT 410

AAQ75639/

Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

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A method for the analysis of cDNA comprises (a) preparing an aggregate double-stranded cDNAs by using an aggregate of mRNAs and a plural type labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily

expression - by amplification of mRNA followed

by digestion with restriction enzymes. Disclosure; Page 6; 11pp; Japanese.

gene

Analysis of cDNA and

WPI; 1995-018287/03

(NITE ) NIPPON TELEGRAPH & TELEPHONE CORP

93JP-00112515 93JP-00112515

.6-APR-1993; 16-APR-1993;

JP06303997-A

Synthetic.

01-NOV-1994.

Gaps ö 1.1%; Score 19; DB 1; Length 20; 100.0%; Pred. No. 2.1e+02; tive 0; Mismatches 0; Indels Seguence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other; Conservative Local Similarity les 19; Conserv Query Match Best Loca Matches

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1735 CAAAAAAAAAAAAAAA 1753 19 CAAAAAAAAAAAAAAAA

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AAQ75651 standard; DNA; 21 BP AAQ75651; 409 RESULT 40:
AAQ75651/c
ID AAQ75
XX
AC AAQ75
DT 04-AU

04-AUG-1995 (first entry)

gene expression - by amplification of mRNA followed Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss. Reverse transcription primer used in cDNA analysis technique. (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP Analysis of cDNA and gene expression - by digestion with restriction enzymes. 93JP-00112515. (first entry) WPI; 1995-018287/03 16-APR-1993; JP06303997-A 16-APR-1993; 04-AUG-1995 11-NOV-1994. Synthetic. AAQ75639; THE STATE OF 
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A method for the analysis of cDNA comprises (a) preparing an aggregate of wouble-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GRNESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
                                                                  double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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                                                                                                                                                                                                                                               1.1%; Score 19; DB 1; Length 21; 100.0%; Pred. No. 2.2e+02; tive 0; Mismatches 0; Indels
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Pred. No. 2.2e+02;
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                                                   analysis of cDNA comprises
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                  Disclosure; Page 6; 11pp; Japanese.
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AAQ75650 standard; DNA; 21 BP
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                                                                                                                                                                                                                                                                                    Conservative
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AAQ75650/
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Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
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                                                                                                                                                 expression; reverse transcription; primer; cDNA;
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                                                                                                                  Reverse transcription primer used in cDNA analysis technique.
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                                                                                                                                                               aggregate; restriction enzyme; ss.
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AAQ75649 standard; DNA; 21 BP.
                             AAQ75642 standard; DNA; 21 BP
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Best Local Similarity
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                                                          AAQ75642;
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RESULT 412
AAQ75642/c
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                                                                                               Analysis of cDNA and gene expression – by amplification of mRNA followed by digestion with restriction enzymes.
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                                                                                                                                                       A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of abablled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digesquate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                              1.1%; Score 19; DB 1; Length 21; 100.0%; Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                       Sequence 21 BP; 0 A; 0 C; 1 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       by digestion with restriction enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 6; 11pp; Japanese.
                                                                                                                                  Disclosure; Page 6; 11pp; Japanese.
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 93JP-00112515
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                                                                                                                                                                                                                                                                                                          Local Similarity 100.
nes 19; Conservative
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 16-APR-1993;
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                         16-APR-1993;
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                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reverse transcription primer used in cDNA analysis technique.
                                                 1.1%; Score 19; DB 1; Length 21;
100.0%; Pred. No. 2.2e+02;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 2.2e+02;
ive 0; Mismatches 0; Indels
Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;
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                                                                                                                                                                             1734 ACAAAAAAAAAAAAAA 1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aggregate; restriction enzyme; ss
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Best Local Similarity 100.0
Matches 19; Conservative
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Matches 19; Conservative
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04-DEC-2001

Synthetic

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AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides. They are used in a method for detecting an antigen in a subject. The method involves binding the antigen to a solid support and then reacting it with an immunoreactive ligand (L) bound to an oligo; removing any unreacted L, and then detecting the presence of the oligo. A similar method can be used to detect Abs, in which case the ligand is an oligolable day. The use of an amplifiable oligo as the label allows Ap to be detected at very low levels. An exemplary olgi is AAQ75024 which a synthetic peptide. For LCR using oligo AA275024, oligos 1-4 (see AAQ7507-Q75030) can be used. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                      Solid phase immunoassay using oligo:nucleotide as label - also new conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for diagnosing hepatitis C or E virus infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 23 BP; 19 A; 4 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES
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AAQ75029 standard; RNA; 23 BP.
                                  94WO-US005407.
                                                                                                            93US-00061694.
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(first entry)
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                                                                                                                                                                                                                                                           Fields HA, Khudyakov YE,
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                                      13-MAY-1994;
                                                                                                            13-MAY-1993;
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The adaptor and adaptor; and (j) the ratios of the amplified by using an adaptor by an encourse of the adaptor; and (j) the ratios of the amplified by using an adaptor by an encourse of the adaptor and a sequence-specific adaptor; and (j) the ratios of the amplified by using an adaptor DNAs are measured between the individuals. The method is used for the detection of the amounts of RNA and DNA. The present seem the invention is used in the exemplification of the present invention
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100.0%; Pred. No. 2.3e+02;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Comparative detection of the amounts of RNA and DNA
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                                  Detection; comparative detection; adaptor; ss.
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(first entry)
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Matches 19; Conservative
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WO9426932-A1

Synthetic.

24-NOV-1994.

25-MAR-2003 03-AUG-1995 LCR oligo 2.

AAQ75028;

Query Match

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Gaps

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                               AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides. They are used in a method for detecting an antigen in a subject. The method involves binding the antigen to a solid support and then reacting it with an immunoreactive ligand (L) bound to an oligo; removing any unreacted L, and then detecting the presence of the oligo. A similar method can be used to detect ABs, in which case the ligand is an oligo-labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab to be detected at very low levels. An exemplary olgi is AAQ75024 which can be covalently attached by the 5' terminus to the N- or C-terminal of a synthetic peptide. For LCR using oligo AAZ75024, oligos 1-4 (see AAQ75027-Q75030) can be used. (Updated on 25-MAR-2003 to correct PN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The specification describes a support for immobilizing nucleotides which contributes to the efficient clarification of DNA without damaging the terminal parts of the DNA. The support is a chemically treated modified substrate on which oligonucleotides with restriction enzyme cleavage sites are immobilised. The support is useful for immobilizing nucleic acids such as DNA. The present sequence represents a synthetic oligonucleotide used in the course of the invention
                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                              Length 23;
                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleotide sequence of a synthetic oligonucleotide
                                                                                                                                                                                                                                                                              Sequence 23 BP; 0 A; 0 C; 4 G; 1 T; 18 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 24 BP; 3 A; 0 C; 3 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                            Score 19; DB 1; Le
Pred. No. 2.4e+02;
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                                                                                                                                                                                                                                                                                                           / Match 1.1%; Score 19; DB Local Similarity 100.0%; Pred. No. 2.4 Ne 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Support for immobilizing nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 8; 18pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                 1735 CAAAAAAAAAAAAAAAA 1753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid immobilisation; ss.
                     Page 13; 34pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Takagi K,
                                                                                                                                                                                                                                                                                                                                                                                                                 19 CAAAAAAAAAAAAAAAA 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH43079 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-OCT-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-488794/53
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                     Example;
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Matches
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Carrying out a thermal cycle of polymerase chain reaction (PCR) by using a substrate on which a DNA is immobilized used in medical, biochemical, molecular biological and gene engineering fields.
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                                                                                                                                                                          Polymerase chain reaction; thermal cycle; immobilisation; genetic engineering; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.1%; Score 19; DB 1; Length 24;
100.0%; Pred. No. 2.5e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24 BP; 3 A; 0 C; 3 G; 18 T; 0 U; 0 Other;
                                                                                                                                                       Nucleotide sequence of a PCR primer #8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1735 CAAAAAAAAAAAAAAAAA 1753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example; Page 10; 13pp; Japanese.
                                                                            BP
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ss; biosensor; hybridisation.
                                                                                                                                                                                                                                                                                                 27-DEC-2000; 2000JP-00399573
                                                                                                                                                                                                                                                                                                                          27-DEC-2000; 2000JP-00399573
                                                                           ABQ79878 standard; DNA; 24
                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                (TAKA/) TAKAHASHI K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                              JP2002191369-A.
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                                                                                                                                                                                                                      Synthetic.
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                                                                                                    ABQ79878;
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                                                  RESULT 420
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Query Match 1.1%; Score 19; DB 1; Length 24; Best Local Similarity 100.0%; Pred. No. 2.5e+02; Matches 19; Conservative 0; Mismatches 0; Indels

Gaps

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1.1%; .Score 19; DB 1; Length 25; 100.0%; Pred. No. 2.5e+02; tive 0; Mismatches 0; Indels

ВЪ.

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The invention relates to nucleic acid molecules from regions of the soybean genome which are associated with soybean cyst nematode (SCN) resistance. The nucleic acids are used to transform plants, and produce soybean plants having an rhg1 or an Rhg4 SCN resistant allele.
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                                                                                             invention
                                                                                                                                                                       AA162055;
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The nucleic acids can be used for investigating rhg1 or Rhg4 haplotypes of soybean plants and for introgressing SCN resistance or partial SCN resistance into soybean plants. They can also be used in plant breeding programmes. The invention also relates to proteins encoded by such nucleic acid molecules, as well as antibodies capable of recognising these proteins. The present sequence is a primer used to amplify a region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, macro protein 17.40, nerve system disorder disease, protein metabolic disorder relative disease, PCR primer; ss
                                                                                                                                                          Sequence 25 BP; 12 A; 1 C; 12 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human macro protein 17.49 PCR primer 1 SEQ ID NO:3
                                                                                                                                                                                                                                                                        860 CAGGAAGAGGAAGAGGAGG 878
                                                                                                                                                                                                                                                                                                              1 CAGGAAGAGGAAGAGGAGG 19
                                                                                                                                                                                                                                                                                                                                                                                                          ABQ73254 standard; DNA; 24
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                                                                                                                                                                                                                                      19; Conservative
                                                                                                                    of the soybean genome
                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                      The invention relates to a novel solid support body comprising a crystal resonator on which a surface treatment layer is formed. The biosensor is useful for analysing biological samples e.g., gene, a protein, and a peptide, and for analysing because substances. Preferably, the biosensor is useful for analysing base sequences by carrying out hybridisation. The present sequence is used in the exemplification of the
                                                                                                                                                                      Solid support body comprising crystal resonator on which a surface treatment layer is formed, and a substrate whose surface treatment layer is chemically modified, useful as biosensor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Soybean, antihelmintic, gene therapy, soybean cyst nematode, SCN, SCN resistant allele, plant breeding, 240017 region G3, 318013 region A3, 515002 region G2, PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 19; DB 1; Length 24;
Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24 BP; 3 A; 0 C; 3 G; 18 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Pred. .v..
                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 1; 7pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 CAAAAAAAAAAAAAAA 6
                  2001JP-00374764.
                                                        07-DEC-2001; 2001JP-00374764
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                                                                                            (TOJO ) TOYO KOHAN CO LTD
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Best Local Similarity 100.
Matches 19; Conservative
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                                                                                                                                    WPI; 2003-819164/77
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                  07-DEC-2001;
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                                                                                                                                                                                                                                                                                     New polypeptide-human macro protein 17.49 and polynucleotide for encoding such polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 24 BP; 2 A; 0 C; 4 G; 17 T; 0 U; 1 Other;
                                                                                                                         (BODE-) BODE GENE DEV CO LTD SHANGHAI.
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                                                            21-AUG-2000; 2000CN-00119647.
21-AUG-2000; 2000CN-00119647.
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RESULT 424

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Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
                                                                                                                                                Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
                                                                                                                                                                                                                              A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type clabelled reverse transcription primers (GENESED files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A method for the analysis of cDNA comprises (a) preparing an aggregate double-stranded cDNAs by using an aggregate of mRNAs and a plural type labelled reverse transcription primers (GBNBSEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                               method can be used to analyse gene expression rapidly and easily
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                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           1.0%; Score 18.4; DB 1; Length 95.0%; Pred. No. 2.5e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 2 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
                                                                                    (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP
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                                                                                                                                                                                                   Disclosure, Page 5; 11pp; Japanese.
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Best Local Similarity 95.0'
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16-APR-1993;
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                                                       16-APR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a method for identifying a set of extendible primers which can be used in the identification, typing and classification of genes. This can then be used to predict protein sequence and structure, in organ donation to match the organ with the receiver, and to identify bacteria in a sample. The method can be used to type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying extendible primers for use in identification, or classification of a nucleic acid of an organism, allele or gene such as class 1/2 HLA comprises identifying all possible nucleotide sequences of
                                                                                                                                                DNA sequence analysis, sequencing, protein sequence, protein structure, gene typing, organ donation, bacteria identification; 16s rRNA, HLA, human leukocyte antigen; PCR primer; 8s.
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                                                                                                                                                                                                                                                                                                                                                                             (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
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HLA DPAl gene PCR primer #13
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RESULT 425

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Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
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Reverse transcription primer used in cDNA analysis technique
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                                                                                          aggregate; restriction enzyme; ss
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Best Local Similarity
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                                                           Sequence 20 BP; 1 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
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1.0%; Score 18.4; DB 1;
Best Local Similarity 95.0%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 1;
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nes 19; Conservative
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AAQ75560/C
ID AAQ7555
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Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.

93JP-00112515.

16-APR-1993;

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JP06303997-A.

Synthetic.

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Reverse transcription primer used in cDNA analysis technique.

(first entry)

04-AUG-1995

AAQ75561;

AAQ75561 standard; DNA; 20 BP

RESULT 431

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
                                                      A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
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                                                                          double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GRNESGO files AAQ75547-075798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of CDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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Pred. No. 2.5e+02;
0; Mismatches 1; Indels
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                    Disclosure, Page 5, 11pp; Japanese
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Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
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ID AAQ75601 standard; DNA; 20 BP.
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Analysis of cDNA and gene expression - by amplification of mRNA followed
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Best Local Similarity 95.0-
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Pred. No. 2.5e+02;
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Pred. No. 2.5e+02;
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                  Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;
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AAQ75600 standard; DNA; 20
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Best Local Similarity 95.0
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AAQ75583/c
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Disclosure, Page 5; 11pp; Japanese.
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AAQ75599/
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           transcription; primer; cDNA;
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by digestion with restriction enzymes.
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          Analysis; gene expression; reverse
aggregate; restriction enzyme; ss.
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of ababelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 3 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-018287/03.
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L6-APR-1993;
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                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-11.

(first entry)

(revised)

25-MAR-2003 15-MAY-1996

AAT04918;

Stem cell factor; progenitor; haematopoiesis; SCF; anaemia; thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft; transplant; neoplasia; myelosuppression; bone marrow; ss.

EP676470-A1 11-0CT-1995

Synthetic.

**Page 214** 

us10008789-3.rng

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maplification and sequencing of manualian stem cell factor (SCP). Non-
naturally occuring SCF and C-terminally truncated polypeptides, having
amino acid sequences sufficiently duplicative of naturally occuring SCF,
comming acid sequences sufficiently duplicative of naturally occuring SCF,
comming acid sequences sufficiently duplicative of naturally occuring SCF,
comming acid sequences sufficiently duplicative and naturally occuring SCF,
composition for treating leucopenia, anaemia or
thrombocytopenia, for enhancing engraftment of bone marrow during
transplantation or for bone marrow recovery after chemotherapy or
cadistion-induced bone marrow aplasia or myelosuppression. They can also
be used for treating neoplasia, nerve damage, infertility, intestinal
damage or myeloproliferative disorders. Antibodies may be raised against
the peptides for use in detection or neutralisation of SCF in serum. SCF
cmay be useful for the treatment of AIDS and severe combined
immunodeficiency (SCID) states alone or in combination with other factors
such as IL-7. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New stem cell factor polypeptide(s) - for stimulating the growth of primitive progenitor cells, esp. for treating disorders involving blood
                                                                                                                                                                                                                                                                                                                                    Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT04915-T04922 are oligonucleotide primers and probes used for the
                                                                                                                                                                                                                                                                                                                                                                                                         Stem cell factor; progenitor; haematopoiesis; SCP; anaemia;
thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
transplant; neoplasia; myelosuppression; bone marrow; ss.
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                                                                         AAT04916 standard; cDNA; 20 BP
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90US-00537198.
90US-00573616.
90WO-US005548.
90US-00589701.
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                                                                                                                                                                                                                            (revised)
(first entry)
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                                                                                                                                                                                                                        25-MAR-2003
15-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                  AAT04916;
RESULT 436
AAT04916/C
XX
XX
AAT04916/C
DT 25-MP
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AAT04915-T04922 are oligonucleotide primers and probes used for the amplification and sequencing of mammalian stem cell factor (SCF). Non-naturally occuring SCF and C-terminally truncated polypeptides, having amino acid sequences sufficiently duplicative of naturally occuring SCF, etimulate growth of primitive progenitors such as haematopoietic progenitor cells, neural stem cells and primordial germ stem cells. The progenitor cells, neural stem cells and primordial germ stem cells. The peptides can be used in a composition for treating leucopenia, anaemia or thrombocytopenia, for enhancing engraftment of bone marrow during transplantation or for bone marrow recovery after chemotherapy or calation-induced bone marrow aplasia or myelosuppression. They can also be used for treating neoplasia, nerve damage, infertility, intestinal damage or myeloproliferative disorders. Antibodies may be raised against the peptides for use in detection or neutralisation of SCF in serum. SCF may be useful for the treatment of AIDS and severe combined immunodeficiency (SCID) states alone or in combination with other factors such as IL-7. (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New stem cell factor polypeptide(8) - for stimulating the growth of primitive progenitor cells, esp. for treating disorders involving blood
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95.0%; Pred. No. 2.5e+02;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bosselman RA, Martin FH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Fig 12C; 127pp; English.
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90US-00573616.
90WO-US005548.
90US-00589701.
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Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zsebo KM, Suggs SV,
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Gaps

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1.0%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 2.5e+02; tive 0; Mismatches 1; Indels

1735 CAAAAAAAAAAAAAAAA 1754

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Local Similarity 95.0 tes 19; Conservative

Query Match Matches CTAAAAAAAAAAAAAA 1

20

AAT04918 standard; cDNA; 20 BP

RESULT 439 AAT04918/C ID AAT04 Stem cell factor; SCF; haematopoietic progenitor cell; blood forming; prinhitive progenitor cell; haematopoietic disorder; syngeneic; allogeneic; autologous bon marrow transplant; gene therapy; transfection; haematopoietic stem cell; acute blood loss; neoplassa;

Stem cell factor universal oligonucleotide 220-11.

(first entry)

# 27-JUL-2000

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Amethod has been developed of making haematopoietic cells suitable for administration to a subject. The method comprises: (a) obtaining commissing the cells has a manatopoietic progenitor cells from a donor; and (b) expanding the cells by adding to the cells a haematopoietically effective dose of a polypeptide product having at least part of the primary structural confirmation and one or more of the biological properties of naturally confirmation and one or more of the biological properties of naturally confirmation and one or more of the biological properties of naturally confirmation and one or more of the biological properties of naturally confirmation and one or more of the biological properties of naturally confirmation are capable of maturing to erythroid, megakaryocyte, cells which are capable of maturing to erythroid, megakaryocyte, cells which are capable of maturing to erythroid, megakaryocyte, cells which are capable of maturing to erythroid, megakaryocyte, cells which are capable of maturing to erythroid, megakaryocyte, cells which are manatopoietic disorders. The method is useful for expanding early haematopoietic progenitors in syngeneic, allogeneic for expanding early haematopoietic progenitors in syngeneic, allogeneic confinency of gene therapy based on transfecting haematopoietic recovery cefficiency of gene therapy based on transfecting haematopoietic recovery after acute blood loss and as a boost to the immune system for fighting neoplasia (caneer). The present sequence represents a universal configuration hamber in weaple from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Production of hematopoietic cells suitable for administration to a subject using progenitor cells and expanding the cells using stem cell
                                                               Stem cell factor; SCF; haematopoietic progenitor cell; blood forming; primitive progenitor cell; haematopoietic disorder; syngeneic; allogeneic; autologous bone marrow transplant; gene therapy; transfection; haematopoietic stem cell; acute blood loss; neoplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
                     Stem cell factor universal oligonucleotide 220-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bosselmann RA, Martin FH;
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90WO-US005548.
90US-00589701.
90EP-00310899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMGE-) AMGEN INC.
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11-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-OCT-1990;
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                                                                                                                                                          cancer; ss.
                                                                                                                                                                                                  Synthetic.
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Production of hematopoietic cells suitable for administration to a subject using progenitor cells and expanding the cells using stem cell

Example 3; Fig 12C; 123pp; English.

Bosselmann RA, Martin FH;

Suggs SV,

Zsebo KM,

(AMGE-) AMGEN INC.

90US-00537198. 90US-00573616. 90WO-US005548. 90US-00589701.

24-AUG-1990 04-OCT-1990

01-OCT-1990

99EP-00122861.

04-OCT-1990;

16-0CT-1989 11-JUN-1990

3P992579-A1

cancer; 88. Synthetic. 12-APR-2000

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A method has been developed of making haematopoietic cells suitable for administration to a subject. The method comprises: (a) obtaining haematopoietic progenitor cells from a donor; and (b) expanding the cells by adding to the cells a haematopoietically effective dose of a polypeptide product having at least part of the primary structural confirmation and one or more of the biological properties of naturally occurring stem cell factor (SCF). The method is useful for stimulating primitive progenitor cells including early haematopoietic progenitor cells which are capable of maturing to erythroid, megakaryocyte, granulocyte, lymphocyte and macrophage cells. SCF results in absolute increases in haematopoietic cells of both myeloid and lymphoid lineages. SCF is useful for treating haematopoietic disorders. The method is useful for expanding early haematopoietic progenitors in syngeneic, allogeneic or autologous bone marrow transplant. SCF is useful for enhancing the cells. SCF is useful for combating the myelosuppressive effects of anti-HIV drugs such as AZT and for enhancing haematopoietic recovery after acute blood loss and as a boost to the immune system for fighting after acute blood loss and as a boost to the immune system for fighting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oligonucleotide which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a universal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18.4; DB 1; Length 20;
Pred. No. 2.5e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
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hes 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neoplasia (cancer).
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Gaps

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AAH41332 standard; DNA; 20 BP.

RESULT 442

AAA13754 standard; DNA; 20 BP

RESULT 441

AAA13754;

SXS

19; Conservative

Matches

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20

Local Similarity

Query Match

AAH41332/

AAH41332;

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Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                       Suggs SV,
                                                                                                                                                                                                                           Example 3; Fig 12C; 210pp; English.
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                                                                                                       89US-00422383.
90US-00537198.
90US-00573616.
90US-0058250.
93US-00172329.
95US-00449653.
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                (first entry)
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                                                                                                                                                                        Bosselman RA,
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nes 19; Conservative
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                                                                                                                                                                                                                into cell in vitro.
                                                                                                                                                           (AMGE-) AMGEN INC.
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                                                                                                                        01-OCT-1990;
25-NOV-1992;
21-DEC-1993;
24-MAY-1995;
                21-AUG-2001
                                                                    US6207454-B1
                                                                                            31-DEC-1998;
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24-AUG-1990;
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                                                                                                                                                                       Zsebo KM,
                                                         Synthetic.
                                                                                                                                                                                                                                                                                                  invention
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The present invention describes a method for enhancing (E) the efficiency of transfer of a polynucleotide (I) into a target mammalian cell (II) in vitro, comprising exposing (II) that expresses a stem cell factor (SCF) receptor to a biologically active SCF, its analogue or fragment, which induces cell proliferation, and introducing (I) to (II) in vitro. Exposure of SCF to (II) results in increased uptake of (I) into the cell. The method is useful for enhancing the efficiency of the transfer of a polynucleotide into a target mammalian cell in vitro. The method is useful in gene therapy techniques. Advisible to Advisible and AAB989351 to AAB98190 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enhancing efficiency of transfer of polynucleotide into a target mammalian cell in vitro, involves exposing cell that expresses a stem cell factor receptor to stem cell factor, and introducing polynucleotide into cell in vitro.
SCF; stem cell factor receptor; blood cell disorder; primer; mutagenesis; probe; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, stem cell factor, SCF; early haematopoietic progenitor cell,
blood disorder, leukaemia, Hodgkin's disease, lymphoma, splenomegaly,
anaemia, Kala azar, septicemia, malaria, hypopigmentation disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human SCF (stem cell factor) cDNA universal PCR primer 220-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18.4; DB 1; Length 20;
Pred. No. 2.5e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Martin FH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suggs SV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Fig 12C; 210pp; English.
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                                                                                                                                                                                                                         89US-00422383.
90US-00537198.
90US-00573616.
90US-0088255.
93US-00172329.
95US-00449653.
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                                                                                                                                                                                      98US-00224681.
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[1 Similarity 95.0%;
19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bosselman RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-366062/38.
                                                                                                                                                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC.
Stem cell factor;
gene therapy; PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR primer; ss.
                                                                                                       US6207454-B1
                                                                                                                                                                                      31-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-AUG-2001
                                                                                                                                                                                                                               16-OCT-1989
                                                                                                                                                                                                                                                     11-JUN-11990
                                                                                                                                                                                                                                                                      24-AUG-1990
01-OCT-1990
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                                                                                                                                                                                                                                                                                                                                  21-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                             12-JAN-1998
                                                                                                                                                27-MAR-2001
                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zsebo KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS04112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a method for enhancing (E) the efficiency of transfer of a polynucleotide (I) into a target mammalian cell (II) in vitro, comprising exposing (II) that expresses a stem cell factor (SCP) receptor to a biologically active SCF, its analogue or fragment, which induces cell proliferation, and introducing (I) to (II) in vitro. Exposure of SCF to (II) results in increased uptake of (I) into the cell. The method is useful for enhancing the efficiency of the transfer of a polynucleotide into a target mammalian cell in vitro. The method is useful in gene therapy techniques. Advision to Advision of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enhancing efficiency of transfer of polynucleotide into a target mammalian cell in vitro, involves exposing cell that expresses a stem cell factor receptor to stem cell factor, and introducing polynucleotide
                                                                                                                                           Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
gene therapy; PCR primer; mutagenesis; probe; ss.
                                                                                                     Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 2.5e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Martin FH;
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Gaps ö

(ZSEB/) (BOSS/) (MART/)

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The present sequence for universal PCR primer 220-11 is 1 of 8 universal oligonucleotides (AAS04110-AAS04117) used in the isolation of the human SCF (#term cell factor) CDNA sequence. The present invention relates to novel stem cell factors (AAU02453-AAU02469, AAU02461) and the polynucleotides encoding them. SCF stimulate primitive progenitor cells to polynucleotides encoding them. SCF stimulate primitive progenitor cells including early haematopoietic progenitor cells. The invention also including early haematopoietic progenitor cells. The invention also cascribes SCF peptides (AAU02462-AAU02481) and the oligonucleotides (AAS04081-AAS04117) used in the isolation of human and rat SCF sequences. The polynucleotide encoding SCF is useful for producing SCF and useful in gene therapy. It is useful for treating disorders involving blood cells cuch as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia, congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis, congestive splenomegaly, Rala azar, sarcoidosis, military tuberculosis, and folic acid deficiency, pyridoxine deficiency, and hypopigmentation condition as piebaldism and vitiligo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids encoding stem cell factor useful for treating disorders involving blood cells, e.g. leukemia, splenomegaly, Hodgkin's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; rat; mammal; stem cell factor; SCF; cell growth stimulation; gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia; neurological damage; intestinal damage; infertility; AIDS; SCID; severe combined immunodeficiency; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.0%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 2.5e+02; tive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Martin FH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease, Kala azar, anemia and septicemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sugge SV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Fig 12C; 209pp; English.
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90US-00537198.
90US-00573616.
90US-00589701.
93US-00172329.
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                                                                                                        95US-00482918
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BOSSELMAN R A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MART/) MARTIN F H.
                                                                                                     07-JUN-1995;
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01-OCT-1990;
              27-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                             ZSEB/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encoding stem cell factor useful for treating blood cells, e.g. leukemia, splenomegaly, Hodgkin's anemia and septicemia.
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blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Suggs SV, Martin FH,
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90US-00537198.
90US-00573616.
90US-00589701.
93US-00172329.
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                                                                                                                                  95US-00482918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           zsebo KM, Bosselman RA,
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Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             ZSEBO K M.
BOSSELMAN R A.
SUGGS S V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids
disorders involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease, Kala azar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-298941/31
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US6207417-B1
                                                                                                                                  07-JUN-1995;
                                                                                                                                                                                                                                                                    24-AUG-1990;
01-OCT-1990;
                                                                                                                                                                                                                                                                                                                                            21-DEC-1993;
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                                                                    27-MAR-2001
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Gaps

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US6207802-B1

Mammalia.

Homo sapiens US6207417-B1

AAS04113;

RESULT 445

Query Match

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The present invention provides the protein and coding sequences of mammalian stem cell factors (SCFS). These are capable of stimulating the growth of early haematopoietic progenitor cells, neural stem cells and primordial germ stem cells. The sequences are useful in the treatment of leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological and intestinal damage, infertility, AIDS and severe combined immunodeficiency (SCID). The present sequence is primer used to amplify an SCF in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention is directed to BAP28 polypeptides, BAP28 polynucleotide sequences and regulatory region located at the 3' and 5' ends of the BAP28 coding region. The BAP28 polypeptides can be expressed by standard
                                                                                                           Novel isolated non-human mammalian stem cell factor polypeptide stimulating growth of early hematopoietic progenitor cells, useful for treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BAP28; prostate; tumour; cancer; diagnostic; genetic analysis; PCTA-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New BAP28 polynucleotides and polypeptides overexpressed in prostate cancer cells for diagnosing prostate tumors, e.g. by hybridization or polymerase chain reaction assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 1.0%; Score 18.4; DB 1; Length 20; Local Similarity 95.0%; Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BAP28 gene fragment amplifying primer BAP28polyTcourt.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
                                       Martin FH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                   Suggs SV,
                                                                                                                                                                                                          Example 3; Fig 12C; 209pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1735 CAAAAAAAAAAAAAAAAA 1754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example; Page 347; 349pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 CGAAAAAAAAAAAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JUN-1999; 99US-0141323P.
18-JAN-2000; 2000US-0176880P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF83959 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19; Conservative
                                       Bosselman RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bougueleret L,
                                                                          WPI; 2001-353108/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-367032/38
 (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR primer; 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200100669-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-AUG-2001
                                                                                                                                                                        sarcoidosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-JAN-2001
                                       Zsebo KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences of mammalian stem cell factors (SCF8). These are capable of stimulating the growth of early haematopoietic progenitor cells, neural stem cells and primordial garm stem cells. The sequences are useful in the treatment of leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological and intestinal damage, infertility, AIDS and severe combined immunodeficiency (SCID). The present sequence is primer used to amplify an SCF in the exemplification of the invention
                                                                                                                                                                                                                                                                                                  Novel isolated non-human mammalian stem cell factor polypeptide stimulating growth of early hematopoietic progenitor cells, useful for treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy, haematopoietic disorder, aplastic anaemia; leukaemia; neurological damage; intestinal damage; infertility; AIDS; SCID; severe combined immunodeficiency; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18.4; DB 1; Length 20;
Pred. No. 2.5e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalian stem cell factor PCR primer SEQ ID NO: 34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                             Martin FH;
                                                                                                                                                                                                                           Suggs SV,
                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Fig 12C; 209pp; English
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                                                                      89US-00422383.
90US-00537198.
90US-00573616.
90US-00589701.
92US-00982255.
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                                                                                                                                                                                                                           Zsebo KM, Bosselman RA,
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                                                                                                                                                                                                                                                               WPI; 2001-353108/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                      (AMGE-) AMGEN
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24-AUG-1990;
01-OCT-1990;
25-NOV-1992;
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                                     09-NOV-1994;
                                                                                                                             01-OCT-1990;
25-NOV-1992;
                                                                                            11-JUN-1990;
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                                                                          16-OCT-1989
                                                                                                                                                                                                                                                                                                                                                               sarcoidosis
27-MAR-2001
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           found to be over expressed in prostate tumour cells, therefore levels of BAP28 expression and/or activity may be assayed (e.g. by polymerase chain reaction (PCR)) to diagnose patient suffering from or susceptible to prostate cancer. Antibodies appecific for the BAP28 polypeptides are useful as diagnostic reagents. Biallelic markers of the BAP28 gene are the BAP28 gene and PCTA-1 gene (the coding strand of PCTA-1 gene is on the opposite of the coding strand of BAP28)
 recombinant methodology. BAP28 polynucleotides and polypeptides have been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               growth of early hematopoietic progenitors, useful for treating aplastic anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; stem cell factor; SCF; early haematopoietic progenitor cell; blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly; anaemia; Kala azar; septicaemia; malaria; hypopigmentation disorder; PCR primer; ss.
                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                               Human SCF (stem cell factor) cDNA universal PCR primer 220-11.
                                                                                                                                                                   1.0%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 2.5e+02; tive 0; Mismatches 1; Indels
                                                                                                                                        Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Martin FH;
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90US-00537198.
90US-00573616.
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91US-00684535.
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                                                                                                                                                                                                                                                                                                                                                                                   07-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zsebo KM, Bosselman RA,
                                                                                                                                                                   Query Match
Best Local Similarity 95.0
Matches 19; Conservative
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24-AUG-1990;
01-OCT-1990;
10-APR-1991;
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oligonuclectides (AAH23888-AAH22895) used in the isolation of the human SCF (stem cell factor) CDNA sequence. The present invention relates to novel stem cell factors (AAB73568, AAB73568, AAB73568, AB73571-AAB73575) and the polymuclectides encoding them. SCF stimulate primitive progenitor cells including early haematopoietic progenitor cells. The invention also describes SCF peptides (AAB73578-AAB73597) and the oligonuclectides (AAH23897) used the oligonuclectides (AAH23897) used in the isolation of human and rat SCF sequences. The polymuclectide encoding SCF is useful for producing SCF and useful in gene therapy. It is useful for treating disorders involving blood cells

present sequence for universal PCR primer 220-11 is 1 of 8 universal

Example 3; Fig 12C; 166pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New stem cell factor polypeptides and their analogs which stimulate growth of early hematopoietic progenitors, useful for treating aplastic anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's
such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia, congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis, disseminated fungus disease, Fulminating septicaemia, malaria, vitamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, stem cell factor; SCF; early haematopoietic progenitor cell;
blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
anaemia; Kala azar; septicaemia; malaria; hypopigmentation disorder;
                                                                                                                                                                                                           Gaps
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                                                                                                                                                                  / Match 1.0%; Score 18.4; DB 1; Length 20; Local Similarity 95.0%; Pred. No. 2.5e+02; ne 19; Conservative 0; Mismatches 1; Indels
                                                                           B12 and folic acid deficiency, pyridoxine deficiency, and
hypopigmentation disorders such as piebaldism and vitiligo
                                                                                                                                 Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
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90US-00537198.
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91US-00684535.
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                                                                                                                                                                      Query Match
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The present sequence for universal PCR primer 220-7 is 1 of 8 universal coligonucleotides (AASO4211-AASO4218) used in the isolation of the human SC SCF (Gerem cell factor) cDNA sequence. The present invention relates to novel stem cell factors (AAU02761-AAU02767, AAU02775, AAU02775, AAU02777) and the polynucleotides encoding them. SCF stimulate primitive progenitor cells including early haematopoietic progenitor cells. The invention also describes SCF peptides (AAU02777-AAU02794) and the oligonucleotides (AASO4182-AASO4210) used in the isolation of human and rat SCF sequences. The polynucleotide encoding SCF is useful for producing SCF and useful in gene therapy. It is useful for treating disorders involving blood cells such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia, congestive splenomeaply, Kala azar, sarcoidosis, military tuberculosis, disseminated fungus disease, Pulminating septicemia, malaria, vitamin B12 and folic acid deficiency, pyridoxine deficiency, and hypopigmentation congestive such as piebaldism and vitiligo
disseminated fungus disease, Fulminating septicaemia, malaria, vitamin B12 and folic acid deficiency, pyridoxine deficiency, and hypopigmentation disorders such as piebaldism and vitiligo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; stem cell factor; SCF; early haematopoietic progenitor cell; blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly; anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human SCF (stem cell factor) cDNA universal PCR primer 220-7.
                                                                                                                                                                                                Length 20;
                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                  Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                Score 18.4; DB 1;
Pred. No. 2.5e+02;
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                                                                                                                                                                                                                                                                 0; Mismatches
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90US-00573616.
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                                                                                                                                                                                                                               Best Local Similarity 95.0
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1990,
25-NOV-1992,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS04213;
                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 45

AAS04213/
AAS04
8,83333
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Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

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The present sequence for universal PCR primer 220-11 is 1 of 8 universal oligonucleotides (AAS04211-AAS04218) used in the isolation of the human SCF (stem cell factor) CDNA sequence. The present invention relates to novel stem cell factors (AAU02761-AAU02767, AAU02770-AAU02797) and the polynucleotides encoding them. SCF stimulate primitive progenitor cells including early haematopoietic progenitor cells. The invention also describes SCF peptides (AAU02777-AAU02794) and the oligonucleotides.

CAAS04182-AAS04210) used in the isolation of human and rat SCF sequences. The polynucleotide encoding SCF is useful for producing SCF and useful in SCF is useful for producing SCF and useful in setul for treating disorders involving blood cells cuch as myelofibrosis, methodstatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia, congestive splenomegaly, Kala azar, sarcoidosis; military tuberculosis, and seminated fungus disease, Pulminating septicemia, malaria, vitamin B12 and folic acid deficiency, pyridoxine deficiency, and hypopigmentation and vitiligo
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                                                                                                                                                                                                                                                                                                                                                Human, stem cell factor; SCF; early haematopoietic progenitor cell; blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly; anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                    ;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated DNA sequence, encoding polypeptide product useful for stimulating growth of early hematopoietic progenitor cells.
                                                                                                                                                                                                                                                                                                             Human SCF (stem cell factor) cDNA universal PCR primer 220-11.
1.0%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 2.5e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.0%; Score 18.4; DB 1; Length 20; Best Local Similarity 95.0%; Pred. No. 2.5e+02; Matches 19; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Martin FH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Suggs SV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Fig 12C; 167pp; English
                                                                      1735 CAAAAAAAAAAAAAAA 1754
                                                                                                          20 CTAAAAAAAAAAAAAA 1
                                                                                                                                                                                                     BP
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90US-00537198.
90US-00573616.
90US-00589701.
92US-00982255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93US-00172329
                                                                                                                                                                                                 AAS04214 standard; DNA; 20
                                                                                                                                                                                                                                                                           (first entry)
                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bosselman RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-281051/29.
                  Local Similarity
nes 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                         PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US6218148-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-DEC-1993;
                                                                                                                                                                                                                                                                         29-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-AUG-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-NOV-1992
 Query Match
Best Local Si
Matches 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zsebo KM,
                                                                                                                                                                                                                                       AAS04214;
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Page 221

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RESULT 454
                                                                        AAS10448/
                                                                                                                 The present sequence for universal PCR primer 220-11 is 1 of 19 PCR primers (AAS10435-AAS10453) used to amplify various portions of the human SCF cDNA sequence. The sequence is described in an invention relating to novel stem cell factors, the polynucleotides encoding them and methods number of early haematopoietic progenitor cells in human peripheral blood by administering a haematopoietic progenitor cells in human peripheral blood by administering a haematopoietic progenitor cells in human peripheral blood polypeptide. The methods are useful for the treatment of blood disorders, including myelofibrosis, myelosclerosis, osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease, carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease, malaria, vitemin B12 and folic acid deficiency, hypopigmentation disorders i.e. piebaldism and viral induced disorders, including AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Increasing the number of early hematopoietic progenitor cells in the peripheral blood useful for the treatment of blood disorders including Hodgkin's disease comprises the administration of human stem cell factor.
                                                                                                                                                                                                                                                                                                                                            Human, stem cell factor; SCF; haematopoietic progenitor cell;
blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.
                                                                                                                                                                                                                                                                                                 Human stem cell factor (SCF) cDNA universal PCR primer 220-11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suggs SV, Martin FH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Fig 12C; 210pp; English.
1735 CAAAAAAAAAAAAAAAAAA 1754
                                           CGAAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90US-00537198.
90US-00573616.
90US-00589701.
91US-00684535.
92US-00982255.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89US-00422383
                                                                                                                                                          AAS10449 standard; DNA; 20
                                                                                                                                                                                                                                                   24-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zsebo KM, Bosselman RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZSEBO K M.
BOSSELMAN R A.
SUGGS S V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-407312/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MARTIN F H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6248319-B1.
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24-AUG-1990;
01-OCT-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUN-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-APR-1991
25-NOV-1992
                                                                                                                                                                                                        AAS10449;
                                           20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BOSS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MART/)
                                                                                                                                  AAS10449/(
XX
AAC
AAS10
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AAC
AAS10
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XX
AAC
AAS10
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Human
XX
Human
XX
Human
XX
Homo
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The present sequence for universal PCR primer 220-7 is 1 of 19 PCR primers (AAS10435-AAS10453) used to amplify various portions of the human SCF cDNA sequence. The sequence is described in an invantion relating to movel stem cell factors, the polymucleotides encoding them and methods for producing the stem cell factors. The methods involve increasing the number of early haematopoietic progenitor cells in human peripheral blood by administering a haematopoietically effective human stem cell factor by administering are useful for the treatment of blood disorders, including myelofibrosis, myelosclerosis, osteoperrosis, metsatatic carcinoma, acute lenkaemia, multiphe myeloma, Hodgkin's disease, refractory anaemia, lymphoma, Gaucher's disease, Niemann-Pick disease, refractory anaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Increasing the number of early hematopoietic progenitor cells in the peripheral blood useful for the treatment of blood disorders including Hodgkin's disease comprises the administration of human stem cell factor.
                                                                                                                                                                                                                            Human, stem cell factor, SCF, haematopoietic progenitor cell;
blood disorder, Hodgkin's disease, vitamin B12; folic acid deficiency;
hypopigmentation disorder, viral disorder; AIDS; PCR primer, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   malaria, vitamin B12 and folic acid deficiency, hypopigmentation
disorders i.e. piebaldism and viral induced disorders, including AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                         Human stem cell factor (SCF) cDNA universal PCR primer 220-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.0%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 2.5e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Martin FH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Suggs SV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Fig 12C; 210pp; English.
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AAS10448 standard; DNA; 20 BP
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90US-00537198.
90US-00573616.
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91US-00684535.
92US-00982255.
93US-00172329.
                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bosselman RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZSEBO K M.
BOSSELMAN R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-407312/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SUGG/) SUGGS S V. (MART/) MARTIN F H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-APR-1991;
25-NOV-1992;
21-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                        JS6248319-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-MAY-1995;
                                                                                                                24-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUN-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         zsebo KM,
                                                        AAS10448;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ZSEB/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (/SSOE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Gaps ö

1735 CAAAAAAAAAAAAAAAAA 1754

CGAAAAAAAAAAAAAA 1

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Rat; stem cell factor; SCF protein; leucopaenia; thrombocytopaenia; anaemia; myelosuppression; nerve damage; myeloproliferative disorder; infertility; neoplasia; myelofibrosis; myeloproliferative disorder; metastatic carcinoma; acute leukaemia; multiple myeloma; sarcoidosis; Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease; Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar; bl Guglielmo syndrome; congestive splenomegaly; splenic pancytopaenia; disseminated fungus disease; Fulminating septicaemia; piebaldism; AlDS; acquired immune deficiency syndrome; malaria; militery tuberculosis; pyridoxine deficiency; vitamin Bl2 deficiency; folic acid deficiency; blamond Blackfan anaemia; hypopigmentation disorder; vitiligo; PCR;
                                                                         Rat SCF 5' cDNA amplifying PCR primer, 220-7.
          AAD35465 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                        98US-00005243
                                                                                                                                                                                                                                                                                                                              95US-00449653
                                                     25-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                  (ZSEB/) ZSEBO K M.
(BOSS/) BOSSELMAN R A.
                                                                                                                                                                                                                                                                                                                                                                       (SUGG/) SUGGS S V.
(MART/) MARTIN F H.
                                                                                                                                                                                                                                                             US2002018763-A1
                                                                                                                                                                                                                                                                                                        12-JAN-1998;
                                                                                                                                                                                                                                                                                                                            24-MAY-1995;
                                                                                                                                                                                                                                                                                   14-FEB-2002.
                                                                                                                                                                                                                     primer; ss
                                                                                                                                                                                                                                         Rattus sp.
                               AAD35465;
AAD35465/c
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Suggs SV, Martin FH; Zsebo KM, Bosselman RA,

WPI; 2002-350789/38.

Novel non-naturally-occurring stem cell factor polypeptide, useful for treating leucopenia, thrombocytopenia, anemia and for enhancing engraftment of bone marrow during transplantation in a mammal.

98US-00005243. 95US-00449653

US2002018763-A1.

Rattus sp.

(ZSEB/) ZSEBO K M. (BOSS/) BOSSELMAN R A. (SUGG/) SUGGS S V.

24-MAY-1995; 12-JAN-1998; 14-FEB-2002.

MART/) MARTIN F H.

Example 3; Fig 12C; 217pp; English.

The present invention relates to novel non-naturally-occurring stem cell factor (SCF) polypeptides having an amino acid sequence sufficiently challed to the control of that of naturally-occurring SCF to allow possession of haemale activity of naturally occurring SCF. Sequences of the invention are useful for treating leucopaenia, thrombocytopaenia, anaemia and for enhancing bone marrow recovery in treatment of radiation, engraftment of bone marrow during transplantation in mammals and chemical or chemocherapeutic induced bone marrow aplasia or myelosuppression. They are also useful for treating acquired immune deficiency in a human, nerve damage, neoplasia, infertility, myeloproliferative disorder, intestinal chamage in a mammal. SCF sequences are useful for proparing biologically active polymer polypeptide adduct, for enhancing transfection of early active polymer polypeptide adduct, for enhancing transfection of early active polymer polypeptide adduct, for enhancing transfection of early active polymer polypeptide adduct, for enhancing transfection of early active polymer polypeptide adduct, for enhancing transfection of serior mammal. They are useful for treating myelofitheses, myelosase, costeopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma, costeopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma, costeopetrosis, metastatic splenomegaly, Kala azar, sarcoidosis, primary tuberculosis, Pulminating septicaemia, pyridoxine deficiency, vitamin Bl2 and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation and vitiligo. The present sequence is a PCR primer which is used for amplifying the 5' end of rat SCF cDNA. This sequence is used in the cost amplifying the struction of the invention

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                                                                                                                                                                                                                                                                                  anaemia; myelosuppression; nerve damage; myeloproliferative disorder; infertility; neoplasia; myelofibrosis; myelosclerosis; osteopetrosis; metastatic carcinoma; acute ludwaemia; multiple myeloma; sarcoidosis; hodgxin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease; Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar; Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopaenia; diseaminated fungus disease; Pulminating septicaemia; piebaldism; AIDS; acquired immune deficiency syndrome; malaria; military tuberculosis; pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency; Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo; PCR;
                                                   Gaps
                                                                                                                                                                                                                                                                  Rat; stem cell factor; SCF protein; leucopaenia; thrombocytopaenia;
                                                  ö
                      Score 18.4; DB 1; Length 20;
Pred. No. 2.5e+02;
0; Mismatches 1; Indels
Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                              Rat SCF 5' cDNA amplifying PCR primer, 220-11.
                                                                           1735 CAAAAAAAAAAAAAAAAA 1754
                                                                                                     20 CTAAAAAAAAAAAAAA 1
                         Query Match
Best Local Similarity 95.0%;
Matches 19; Conservative
                                                                                                                                                                   AAD35466 standard; DNA; 20
                                                                                                                                                                                                                      25-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                  primer; ss
                                                                                                                                                                                             AAD35466;
                                                                                                                                             RESULT 456
                                                                                                                                                          AAD35466,
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Novel non-naturally-occurring stem cell factor polypeptide, useful for treating leucopenia, thrombocytopenia, anemia and for enhancing engraftment of bone marrow during transplantation in a mammal. Suggs SV, Martin FH; Zsebo KM, Bosselman RA, WPI; 2002-350789/38.

Example 3; Fig 12C; 217pp; English.

The present invention relates to novel non-naturally-occurring stem cell factor (SCF) polypeptides having an amino acid sequence sufficiently duplicative of that of naturally-occurring SCF to allow possession of haemacopoietic biological activity of naturally occurring SCF. Sequences of the invention are useful for treating leucopaenia, thrombocytopaenia, anaemia and for enhancing bone marrow recovery in treatment of radiation, engraftment of bone marrow during transplantation in mammals and chemical or chemotherapeutic induced bone marrow aplasia or myelosuppression. They are also useful for treating acquired immume deficiency in a human, nerve damage, neoplasia, infertility, myeloproliferative disorder, intestinal damage in a mammal. SCF sequences are useful for preparing biologically active polymer polypeptide adduct, for enhancing transfection of early haemacopoietic progenitor cells with a gene, and transfer of a gene into a mammal. They are useful for treating myelofibrosis, myelosclerosis,

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osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease, Letterer-Siwe disease, refractory erythroblastic anaemia, Di Guglielmo syndrome, congestive splenomegaly, Kala azar, sarcoidosis, primary splenic pancytopaenia, disseminated fungus disease, malaria, military tuberculosis, Fulminating septicaemia, pyridoxine deficiency, vitamin B12 and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation disorders such as piebaldism, AIDS (acquired immune deficiency syndrome) and vitiligo. The present sequence is a PCR primer which is used for amplifying the 5' end of rat SCF CDNA. This sequence is used in the
                                                                                                                                                                                                                                                                                                                      exemplification of the invention
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Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

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                          Gaps
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1.0%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 2.5e+02; ative 0; Mismatches 1; Indels
                         Conservative
             Similarity
                         19;
Query Match
                Local
                         Matches
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1735 CAAAAAAAAAAAAAAAA 1754

20 CGAAAAAAAAAAAAAAA 엄

ABS73849 standard; DNA; 20 (first entry) 05-DEC-2002 ABS73849 RESULT 457 ABS73849 

ВР

SCF universal oligonucleotide 220-7.

Stem cell factor; SCF; blood-forming system; blood cell disorder; haematopoietic system; metastatic carcinoma; acute leukaemia; multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo; refractory erythroblastic anaemia; miliary tuberculosis; cytostatic; disseminated fungus disease; haematopoietic; tuberculostatic; antifungal; antimalaria; dermatological; ss.

Synthetic.

EP1241258-A2

04-OCT-1990; 2002EP-00008587

900S-00537198. 900S-00573616. 900O-US005548. 90US-00589701. 89US-00422383 28-SEP-1990; 01-OCT-1990; 04-OCT-1990; 04-OCT-1990; 16-0CT-1989 11-JUN-1990 24-AUG-1990

(AMGE-) AMGEN INC.

95EP-00105391

Martin FH; Bosselman RA, Sugga SV, WPI; 2002-684093/74. ₹ Zsebo

Production of a human stem cell factor (SCF) polypeptide for treating disorders involving blood cells, such as leukemia, comprises culturing mammalian cells comprising non-human SCF promoter DNA linked to DNA encoding the human SCF.

Example 3; Fig 12C; 120pp; English.

The present invention relates to novel stem cell factors (SCFS), polymuclectide sequences encoding the SCFS, and methods of producing them. SCFS are involved in the blood-forming (haematopoietic) system in mammals, particularly humans. The method of the invention is useful for

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the production of human SCF. The stem cell factors are useful to treat disorders involving blood cells e.g. metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, refractory erythroblastic anaemia, miliary tuberculosis, disseminated fungus disease, malaria, and vitiligo. The present sequence representing a universal oligonucleotide for SCF DNA is used in the examples of the present invention
                                                                                                                                                                                                                                                                                                                                                              Stem cell factor; SCF; blood-forming system; blood cell disorder; haematopoietic system; metastatic carcinoma; acute leukaemia; multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo; refractory erythroblastic anaemia; miliary tuberculosis; cytostatic; adisseminated fungus disease; haematopoietic; tuberculostatic; antianaemic; antifungal; antimalarial; dermatological; ss.
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                                                                                                    Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                        SCF universal oligonucleotide 220-11.
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90US-00537198.
90US-00573616.
90US-005848.
90US-005899701.
90EP-00310899.
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                                                                                                                                                                                                                                                                ABS73850 standard; DNA; 20
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                                                                                                                                       l Similarity 95.(
19; Conservative
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28-SEP-1990;
01-OCT-1990;
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The present invention relates to novel stem cell factors (SCFB), polynuclectide sequences encoding the SCFB, and methods of producing them. SCFB are involved in the blood-forming (haematopoietic) system in mammals, particularly humans. The method of the invention is useful for the production of human SCF. The stem cell factors are useful to treat disorders involving blood cells e.g. metastatic carcinoma, acute leukaemia, multiple myeloma, Hodgin'n sidisease, lymphoma, refractory erythroblastic anaemia, miliary tuberculosis, disseminated fungus treating culturing to DNA Production of a human stem cell factor (SCF) polypeptide for disorders involving blood cells, such as leukemia, comprises mammalian cells comprising non-human SCF promoter DNA linked sxample 3; Fig 12C; 120pp; English. the human SCF. WPI; 2002-684093/74

Martin FH;

Bosselman RA,

Zsebo KM, Suggs SV,

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disease, malaria, and vitiligo. The present sequence representing a universal oligonucleotide for SCF DNA is used in the examples of the present invention
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Seguence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Gaps .. 0 Length 20; 1; Indels Score 18.4; DB 1; Pred. No. 2.5e+02; 0; Mismatches 1; 1.0%; Local Similarity 95.0 les 19; Conservative Query Match datches

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## 1735 CAAAAAAAAAAAAAAAA 1754 20 CGAAAAAAAAAAAAAAAA 1

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Human oligonucleotide sequence. ABZ89546 standard; DNA; 20 (first entry) 17-0CT-2003 ABZ89546; RESULT 459 ABZ89546 

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antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; Human; antisense; lung dysfunction; nasal airway dysfunction; lung inflammation; respiratory disease; ds.

Ното варіепв.

WO200285308-A2.

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC

Katz E, Pabalan J, Aguilar D; Li Y, Sandrasagra A, Ka Tang L, Shahabuddin S; Nyce JW, I Miller S,

WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone

Disclosure; SEQ ID NO 4788; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonuclectide antieense to the initiation codon, coding region, 5 or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an entitiflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antialergic, antiasthmatic, hypotensive, numbering an expiratory, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing levels of of or reducing sensitivity to adenosine, reducing levels of condition, increasing bronchoconstriction, lung surfactant in a subject states, or a respiratory disease or condition.

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Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                      Sequence 20 BP; 18 A; 0 C; 0 G; 2 T; 0 U; 0 Other;
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                                                                                Score 18.4; DB 1;
Pred. No. 2.5e+02;
0; Mismatches 1
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                                                                                                                                                                    1 TTAAAAAAAAAAAAAAA 20
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Best Local Similarity 95.07
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Human, antisense, lung dysfunction; nasal airway dysfunction; antiinflammatory; antiallergic; antiinflammatory; antiallergic; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds. Human oligonucleotide sequence. 

(first entry)

17-OCT-2003

ABZ89085;

Homo sapiens.

WO200285308-A2.

31-OCT-2002

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC

Katz E, Pabalan J, Aguilar D; Sandrasagra A, Ka L, Shahabuddin S; Li Y, San Tang L, Nyce JW, ] Miller S,

WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid

Disclosure; SEQ ID NO 4327; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 mucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an entinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antialergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depteting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine or ung surfactant in a subject, increasing levels of ubiquinone or lung surfactant in a subject stissue, or a treating bronchoconstriction. Ung inflammation, lung allergies, or a respiratory disease or condition.

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first active agent comprising an oligomuclectide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an untinflammatory steroid and ubiquinone. A composition of the invention has antinflammatory, antiallergic, antisthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antinflammatory steroid in a subject, for reducing or depleting levels of adenosine receptor, producing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject stateshes, or treating bronchoconstriction, lung allergies, or a respiratory disease or condition.
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Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pharmaceutical composition for treating ailments associated with impaired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiathmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodiation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid
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                                                                                                                         1.0%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 2.5e+02; ive 0; Mismatches 1; Indels
                                                                                   Seguence 20 BP; 19 A; 0 C; 1 G; 0 T; 0 U; 0 Other;
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Tang L, Shahabuddin S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human oligonucleotide sequence.
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                                                                                                                                                                       Conservative
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                                                                                                                                               Best Local Similarity
Matches 19; Conserv
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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the instraint acodon, coding region, 5 or 3 end genomic flanking regions, 5 and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antisflammatory steroid and ubjudinone. A composition of the invention has antiinflammatory, antialergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory ing or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing levels of adenosine of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing purchedilation, increasing bronchoconstriction, lung surfactant in a subject's tissue, or treating bronchoconstriction.
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Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodiation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
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                                                                                    Sequence 20 BP; 17 A; 0 C; 0 G; 3 T; 0 U; 0 Other;
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Tang L, Shahabuddin S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human oligonucleotide sequence.
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                                                                                                                                              95.0%;
                                                                                                                                                                                                                                                                                                                                                         ABZ89240 standard; DNA; 20
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tes 19; Conservative
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31-DEC-1998;
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                                                       invention.
                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           haematopoietic activity and the polymucleotides encoding them. The polymeptides are used for treating infertility, intestinal damage, myeloproliferative disorders, leucopenia, thrombocytopenia or anaemia, for improving engraftment of bone marrow transplants, for enhancing bone marrow recovery after radiotherapy or chemotherapy and in treatment of immune deficiency, neoplasia, nerve damage, osteoporosis, metastatic carcinoma, leukaemia and miliary tuberculosis. The SCF polypeptides are also used to expand haematopoietic progenitor cells for transplantation and to prepare such cells for transfection with a gene. The SCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New non-natural stem cell factor, useful for treating e.g. leucopenia or immune deficiency, also related nucleic acid and antibodies.
                                                                                                                                                                                                                                                                   Stem cell factor; SCF; haematopoietic activity; infertility; intestinal damage; myeloproliferative disorder; leucopenia; thrombocytopenia; anaemia; bone marrow transplant; immune deficiency; neoplasia; nerve damage; osteoporosis; metastatic carcinoma; leukaemia; miliary tuberculosis; haematopoietic progenitor cell; ss.
Note: The sequence data for this patent is not represented in the printe specification, but was obtained in electronic format directly from WIPO
                                                                                      Gaps
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                                                               Length 20;
                                                                                   1; Indels
                                          Sequence 20 BP; 18 A; 1 C; 0 G; 1 T; 0 U; 0 Other;
                                                              Score 18.4; DB 1;
Pred. No. 2.5e+02;
0; Mismatches 1;
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                     at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                 Stem cell factor (SCF) related DNA #33.
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                                                                                                          1735 CAAAAAAAAAAAAAAAA 1754
                                                                                                                             1 CTAAAAAAAAAAAAAA 20
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90US-00573616.
90US-00589701.
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92US-00982255.
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98US-00005893
                                                                                                                                                                                   ADE52462 standard; DNA; 20
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                                                                        Local Similarity 95.0
nes 19, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BOSSELMAN R A.
SUGGS S V.
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01-OCT-1990;
10-APR-1991;
25-NOV-1992;
21-DEC-1993;
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polynucleotides can be used for recombinant expression of the polypeptides and also as probes for mapping of the SCF gene, for flatentifying SCF-related diseases and as a marker for neighbouring genes. Antibodies raised against the polypeptides are useful in diagnosis and to remove SCF from blood. This sequence represents SCF related DNA of the
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                                                                                                                                                                                                                                                                                                   1.0%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 2.5e+02; ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stem cell factor (SCF) related DNA #32.
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90US-00573616.
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93US-00172329.
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BOSSELMAN R A.
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(SUGG/) SUGGS S V.
(MART/) MARTIN F H.
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us10008789-3.rng

BP

(first entry)

93JP-00112515. 93JP-00112515.

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Analysis; gene expression; reverse transcription; primer; cDNA;
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                                                                                                                                                                                                                                                                                                       aggregate; restriction enzyme; ss.
                                                             AAQ75630 standard; DNA; 21
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        RESULT, 466
AAQ75630/c
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carcinoma, leukaemia and miliary tuberculosis. The SCF polypeptides are also used to expand haematopoietic progenitor cells for transplantation and to prepare such cells for transfection with a gene. The SCF polymclectides can be used for recombinant expression of the polymclectides and also as probes for mapping of the SCF gene, for flachtifying SCF-related diseases and as marker for neighbouring genes. Antibodies raised against the polypeptides are useful in diagnosis and to remove SCF from blood. This sequence represents SCF related DNA of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene expression - by amplification of mRNA followed
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                                                                                                                                                                                                                                                                                                                              1.0%; Score 18.4; DB 1; Length 20; 95.0%; Pred. No. 2.5e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                              Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     by digestion with restriction enzymes.
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                                                                                                                                                                                                                              invention.
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                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                               expression - by amplification of mRNA followed
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                                                                                                                                                                                                                                                                                                                                                                                                                 1.0%; Score 18.4; DB 1; Length 21; 95.0%; Pred. No. 2.7e+02;
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(NITE ) NIPPON TELEGRAPH & TELEPHONE CORP
                                                                                                       by digestion with restriction enzymes.
                                                                                                                                              Disclosure; Page 6; 11pp; Japanese.
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                                                                               Analysis of cDNA and gene
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                                          by digestion with restriction enzymes.
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                                                      Disclosure; Page 8; 11pp; Japanese.
                                                                                                                                                              1731 TTTACAAAAAAAAAAAA 1750
                                                                                                                                                                                                                                                               aggregate; restriction enzyme; ss
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Local Similarity 95.0%;
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(first entry)

93JP-00112515. 93JP-00112515

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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                                              Gaps
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    Length 21;
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Score 18.4; DB 1;
Pred. No. 2.7e+02;
0; Mismatches 1;
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AAQ75671 standard; DNA; 21
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    Query Match
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of abelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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Matches 19; Conservative
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Pred. No. 2.7e+02;
0; Mismatches 1; Indels
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    aggregate; restriction enzyme; ss
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Sequence 21 BP; 0 A; 2 C; 0 G; 19 T; 0 U; 0 Other;
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                                                                   Reverse transcription primer used in cDNA analysis technique.
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Matches 19; Conservative
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(NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
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                                                                                                                                                                                                                                                 Disclosure, Page 7; 11pp; Japanese.
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double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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Pred. No. 2.7e+02;
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1.0%; Score 18.4; DB 1; Length 21; 95.0%; Pred. No. 2.7e+02; ive 0; Mismatches 1; Indels
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AAQ75629 standard; DNA; 21
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Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.

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Reverse transcription primer used in cDNA analysis technique.

(first entry)

04-AUG-1995

AAQ75614 standard; DNA; 21 BP.

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double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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Pred. No. 2.7e+02;
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Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.

Disclosure, Page 6; 11pp; Japanese

(NITE ) NIPPON TELEGRAPH & TELEPHONE CORP

WPI; 1995-018287/03.

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

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                             and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
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and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
                                                      Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                                                                          (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
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                                                                                                                                                                          93JP-00112515.
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AAQ75768 standard; DNA; 21
                                    (first entry)
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5617/c AAQ75617 standard; DNA; 21 BP.

RESULT 494

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AAQ75617/ ID AAQ75 XX

WPI; 1995-018287/03

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Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
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                                                                                                                                     Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
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                Analysis of cDNA and gene expression - by digestion with restriction enzymes.
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                                         Disclosure; Page 9; 11pp; Japanese.
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
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ID AAQ75774 standard; DNA; 21 BP.
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AAQ75662 standard; DNA; 21 BP.
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                                                                                                                                                                                                                                                double-stranded cDNAs by using an aggregate of mENAS and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mENAS as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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Analysis of cDNA and gene expression - by amplification of mRNA followed
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transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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nes 19; Conservative
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RESULT 499

AAQ75613

Query Match

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Best Loca Matches

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                                                                                                                                                              restriction enzyme; ss.
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Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
                  Analysis of cDNA and gene expression - by amplification of mRNA followed
                                                                                                                       A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of abelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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                                          by digestion with restriction enzymes.
                                                                                   Disclosure; Page 9; 11pp; Japanese.
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AAQ75711 standard; DNA; 21
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Matches 19; Conservative
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                                                                                                       Analysis; gene expression; reverse transcription; primer; cDNA;
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                                                               Reverse transcription primer used in cDNA analysis technique.
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Pred. No. 2.7e+02;
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Human; variant thrombospondin 1; variant thrombospondin 4; SNP; polymorphism; vascular disease; coronary artery disease; forensics; myocardial infarction; atherosclerosis; stroke; venous thromboembolism; pulmonary embolism; paternity test; ds.

duman gene single nucleotide polymorphism #477,

(first entry)

06-JUN-2001

AAF95716;

ВЪ

AAF95716 standard; DNA; 21

RESULT 505

AAF95716/

/*tag= a /standard_name= "single nucleotide polymorphism"

WO200118250-A2

15-MAR-2001.

Location/Qualifiers replace(11,T)

Key Variation

Homo sapiens

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cell viability; loss of heterozygosity; precancerous condition; ASI; allele specific inhibitor; somatic cell; diagnosis; prevention; atheroscierotic plaque; premalignant metaplastic lesion; endometriosis; dysplastic lesion; benign tumour; polycystic kidney disease; transplant; graft versus host disease; malignant cell removal; bone marrow; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human polymorphic sites described in the method of the invention
                                                                                                                                             Polymorphism; human; inhibitor; cancer; treatment;
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1734 ACAAAAAAAAAAAAAA 1753
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                   20 ACTAAAAAAAAAAAAAAA
                                                                                                                           Human polymorphic region 752.
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                                                                 AAZ26563 standard; DNA; 21
                                                                                                      30-NOV-1999 (first entry)
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Best Local Similarity
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Mccarthy JJ;

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genes. The sequences at a number of polymorphic sites are also provided in the specification. In particular, the method can be used in the diagnosis of atherosclerosis, myocardial infarction, coronary heart disease, stroke, peripheral vascular diseases, venous thromboembolism and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also correlations to diseases. The present sequence is an aphencype the human gene SNPS shown in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a method of diagnosing a vascular disease in an individual, involving determining the sequence at various polymorphic sites within the human thrombospondin 1 and thrombospondin 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids comprising single nucleotide polymorphisms, useful in applications such as forensics, paternity testing, medicine, genetic analysis and phenotype correlations to diseases such as diabetes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.0%; Score 18.4; DB 1; Length 21; 95.0%; Pred. No. 2.7e+02; tive 0; Mismatches 1; Indels
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26-JUL-2000; 2000US-0220947P.
16-AUG-2000; 2000US-0225724P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-SEP-2000; 2000WO-US024503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-226749/23
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ES,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel method for identifying an inhibitor potentially useful for treatment of cancer, where the inhibitor is active on a gene vital for cell growth or viability, and where the gene is updect to loss of heteroxygosity (LOH) in a cancer. The inhibitor is used for preventing the development of cancer in a patient having a pecific inhibitor (ASI) targeted to an allele of a first allele specific inhibitor (ASI) targeted to an allele of a first essential gene present in cells of the patient are heteroxygous for the first gene, the inhibitor is active on at least one but less than all allelic forms of the gene present in a population and targets only one allelic forms present in the normal somatic cells, and the first gene. The products and methods can be normal somatic cells, and the first gene. The products and methods can be cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic centers, atherosclerotic plaques, premalignant metaplastic or dysplastic cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying target genes for allele-specific drugs - used for diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic plaque, dysplastic lesions, endometriosis or graft versus host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  graft versus host disease. The method can also be used to remove
malignant cells from bone marrow transplants. AA225812-226825 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1734 ACAAAAAAAAAAAAAAA 1753
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AAF24290 standard; DNA; 21 BP

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AAF24290;

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The invention discloses a method for identifying a candidate polymorphic repeat within a coding sequence (expressed sequence tag, EST), which comprises detecting tandem repeats in a target coding sequence, scoring the repeats for polymorphic probability and generating a dataset confidate polymorphic probability and generating a dataset correlating the repeats with polymorphic probability to identify a candidate polymorphic repeat. The computational methods (polymorphic marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are useful for identifying and detecting candidate polymorphic repeats in human genes, which can be used to understand, treat or eliminate genetic diseases, predispositions or adverse drug-treatment reactions. Examples of diseases linked to nucleotide repeats are Machado-Joseph, Haw River syndrome, Huntington's disease, fragile-X syndrome, Eredreich's ataxis, myotonic dystrophy, hyperandrogensemia, spinal and bulbar atrophy and spinocereballar ataxia. The sequences presented in ABX79676-ABX80022 are the polymorphic repeats identified for a search of human ESTs
                                                                                                                                                                                              Identifying a candidate polymorphic repeat within a coding sequence, funderstanding or treating genetic disease, comprises detecting tandem repeats in a target coding sequence and scoring the repeats for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               b
"n = 5-(aminomethyl)-1,3-benzenedimethanol"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino modified oligodeoxyribonucleotide; oligonucleotide;
achiral linker reagent; 5-(aminomethyl)-1,3-benzenedimethanol;
N-fluresceinyl-(5-aminomethyl)-1,3-benzenedimethanol;
hybridisation probe; PCT primer; nucleic acid sequencing;
affinity matrix; cloning recombinant DNA; in-vitro mutagenesis; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5-(aminomethyl)-1,3-benzenedimethanol"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18.4; DB 1; Length 21;
Pred. No. 2.7e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21 BP; 1 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
                                                                                                          Fondon JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino modified oligodeoxyribonucleotide.
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                                                                                                                                                                                                                                                                                                           Example; Col 495; 588pp; English.
                                                                                                        Minna JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 AAAAAAATAAAAAAA 2
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                    99US-00475947.
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/note= "n =
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                                                            (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 95.0
nes 19; Conservative
                                                                                                                                                                                                                                                                    polymorphic probability.
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                                                                                                          Garner HR, Wren JD,
                                                                                                                                                  WPI; 2003-208818/20
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                    31-DEC-1999;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides a method for analysing a nucleic acid strand to determine the degree of complementarity between two sequences. This involves the measurement of an electric current along the annealed strands compared to a standard. This is useful in the analysis of genetic polymorphisms and variation between genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Determining complementarity of nucleotide fragment for gene analysis, by comparing flow of electric current from or to electroconductive substrate through DNA fragment, with reference obtained from its complement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat; polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                    nucleic acid; gene analysis; polymorphism; variation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ogawa M, Takagi M, Takenaka S, Yamashita K;
                                                                                                        Complementary nucleic acid detection method related sequence #5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18.4; DB 1; Length 21;
Pred. No. 2.7e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21 BP; 1 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 12; 28pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                           (FUJF ) FUJI PHOTO FILM CO LTD
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                                                                                                                                                                                                                                                                                                                                                       07-JUN-2000; 2000EP-00112235.
                                                                                                                                                                                                                                                                                                                                                                                                   99JP-00159339
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Local Similarity 95.0%;
hes 19; Conservative
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                                                                                                                                                                           DNA chip; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-140003/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Makino Y, Abe Y,
                                                                                                                                                      Complementary
                                                                                                                                                                                                                                                                 EP1065278-A2
                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1999;
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                                                                                                                                                                                                                     Unidentified
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                                                              03-APR-2001
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ABX79794;

ABX79794/c
ABX7977XX
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The present line present in the present line anti-free and can be used in vaccines. (I) or an anti-body binding (I) can be used for suppressing the immune system for reducing rejection of tissue or organ transplants and grafts and for treating T-cell specific arthritis, multiple sclerosis, diabetes mellitus, inflammatory bowel disease and crohn's disease. The anti-bodies can also be used for treating immunologic renal diseases. The anti-bodies can also be used for treating diseases, chronic lymphocytic leukaemia, secondary glomerulonephritis or vasculitis associated with lupus, polyarteritis, scleroderma, HIV-related diseases, amyloidosis and haemolytic uraemic syndrome. (I) and the anti-bodies can also be used for renal or urological neoplasms and multiple myelomas, asthma, bronchitis, emphysema and other chronic airway diseases. Human zcytor19 is located to chromosome light or renal in which is chromosome light from the present sequence represents a PCR primer which is
                                                                                                                                                                                                                                                                          Novel Zyctor19 polypeptides and polynucleotides useful for stimulating immune responses in animals for producing antibodies, and for treating autoimmune diseases, leukemia and asthma.
                                                                                                                                                                                                                                                                                                                                                             3xample 2; Page 187; 200pp; English.
                                             28-NOV-2001; 2001WO-US044808.
                                                                                       28-NOV-2000; 2000US-0253561P.
07-FEB-2001; 2001US-0267211P.
                                                                                                                                                  (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                   WPI; 2002-527700/56.
                                                                                                                                                                                            Presnell SR,
      36-JUN-2002.
    Achiral linker reagents have been developed for the incorporation of multiple amino groups into oligonucleotides. The present sequence represents a modified oligodeoxyribonucleotide. The achiral linker reagents can be used for incorporation of multiple primary amino groups or reporter groups into oligonucleotides. They are compatible with conventional DNA synthesis following the phosphoramidite methodology, and can be incorporated in good yields. They linker reagents may be used for labelling of oligonucleotides. They may also be used for preparation of oligonucleotides, e.g. for use as hybridisation probes, for use as primers in the polymerase chain reaction or in nucleic acid sequencing binding proteins or other biomolecules, for production of affinity matrices for detection of nucleic acid sequences, for cloning recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                          New achiral linker reagents - useful for incorporation of multiple amino gps. or reporter gps. into oligo:nucleotide(s).
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                                                                                                                                                                                                         Behrens C, Petersen KH, Egholm M, Nielsen J, Dahl O;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.0%; Score 18.4; DB 1; Best Local Similarity 86.4%; Pred. No. 2.8e+02; Matches 19; Conservative 0; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 20; 42pp; English
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  96WO-DK000330
                                           95DK-00000863
                                                                                   BEHRENS C.
PETERSEN K H.
                                                                                                                                                                                                                                                    WPI; 1997-145615/13
                                                                                                                        EGHOLM M.
NIELSEN J.
                                                                                                                                                                    DAHL O.
26-JUL-1996;
                                         27-JUL-1995;
                                                                                                    (PETE/)
(EGHO/)
(NIEL/)
                                                                                   (BEHR/)
                                                                                                                                                                    (DAHL/)
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present invention describes an isolated human zcytor19 protein (I)

Grant FJ;

Whitmore TE,

Novak JE,

Xu W,

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0
                                             ch 1.0%; Score 18.4; DB 1; Length 22; Il Similarity 95.0%; Pred. No. 2.8e+02; 19; Conservative 0; Mismatches 1; Indels
                        Seguence 22 BP; 1 A; 13 C; 1 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                            21 GAGGAGGAAGAGGAGGCGAG 2
                                                                                                                                                                               AAA29753 standard; DNA; 23 BP
                                                                                                                                                                                                                                                    Synthetic oligonucleotide #1.
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used in an example from
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AAA29753/
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22 AAAAAAAANNAAAAAAAA 1
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Human zcytor19 PCR primer ZC37681 SEQ ID NO:27. 084/c ABQ73084 standard; DNA; 22 BP 25-SEP-2002 (first entry) ABQ73084; ABQ73084 

Human; zcytor19; cytokine receptor; immunosuppressive; cytostatic; antitheumatic; antiarthritic; neuroprotective; antiinflammatory; antidabetic; nephrotropic; dermatological; anti-HIV; haemostatic; vaccine; immune system; T-cell specific leukaemia; lymphoma; lupus; autoimmune disease; rheumatorid arthritis; multiple sclerosis; HIV; diabetes mellitus; inflammatory bowel disease; crohn's disease; asthma; immunologic renal disease; chronicsphritis; vasculitis; polyarteritis; eccondary glomerulonephritis; cleukaemia; bronchitis; secondary glomerulonephritis; clerodera; amtlippe myeloma; haemolytic uraemic syndrome; renal neoplaem; urological neoplaem; emphysema; chronic airway disease; chromosome 1; chromosome 1936.11; PCR primer; ss

sapiens. Synthetic

WO200244209-A2

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The invention relates to human phosphatase 79 (AAB71700), nucleic acids encoding it (AAH24264), and a method for the recombinant production of human phosphatase 79. The present invention additionally discloses an agonist of phosphatase 79 for therapeutic use, and an antibody which specifically binds to human phosphatase 79. Human phosphatase 79, and cucleotides which encode it may be used for treating a variety of diseases, such as malignant tummors, blood diseases, HIV (human conditions. The protein may also be used to screen for modulators of its activity or for peptide fingerprinting identification. The polynucleotide cat be used as a primer for nucleic acid amplification reaction or as a primer for nucleic acid amplification reaction or as a microarrays. Sequences AAH224265 represent reverse transcription-cept (RT-PCR) primers used in an exemplification of the invention to
                                                                                                                     Human phosphatase 79 and encoded polynucleotide, applicable in diagnosis and treatment of malignant tumor, hemopathy, HIV infection, immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human polypeptide FD 17 for diagnosing and treating malignant tumor, hemopathy, human immunodeficiency virus (HIV) infection, immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; FD 17; cytostatic; virucidal; immunomodulatory; haemostatic; antiinflammatory; gene therapy; malignant tumour; haemopathy; human immunodeficiency virus infection; HIV infection; immunological disease; inflammation; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.0%; Score 18.4; DB 1; Length 24; 95.0%; Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 24 BP; 2 A; 0 C; 0 G; 22 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
                (BIOR-) BIOROAD GENE DEV LTD SHANGHAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human FD 17 PCR primer 2 SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1736 AAAAAAAAAAAAAAAA 1755
                                                                                                                                                        diseases and various inflammation.
                                                                                                                                                                                             Example 3; Page 12; 38pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 AAAAAAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH44623 standard; DNA; 24 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 95.0
Matches 19; Conservative
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                                                                                      WPI; 2001-355903/37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH44623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mao Y,
                                                   Mao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 512
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                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a method for destabilising non-specific duplex formation, between an oligonucleotide and a target nucleic acid (NA), comprising incubating the target NA with a modified oligonucleotide (I) comprising a homopolymeric sequence having a modification which decreases or abrogates H-bonding between the modified oligonucleotide and the non-specific target NA. The modified oligonucleotide is used to improve discrimination between the targeted homopolymeric sequence and a non-homopolymeric target sequence. It is used to increase the proportion of full length cDNA clones for a library, to reduce mispriming during sequencing, 5, or 3, RACE (rapid amplification of cDNA ends) or DNA synthesis or to generate bons fide genetic markers. The present sequence represents an oligonucleotide which is used in the exemplification of the
                                                                                                                                                                                                                                                                              Novel method of stabilizing duplex formation, or destabilizing non-specific duplex formation using primer containing modified nucleotide analogs, useful for preventing mispriming during PCR, RACE, DNA synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phosphatase 79; human; BAC clone CTB-54D4-encoded protein homologue; recombinant production; malignant tumour; cancer; blood disease; HIV infection; human immunodeficiency virus; immuno disorder; inflammatory condition; eytostatic; anti-HIV; antinflammatory; immunomodulator; reverse transcription-PCR; RT-PCR primer; se.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.0%; Score 18.4; DB 1; Length 23; 86.4%; Pred. No. 2.8e+02; ative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 23 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human phosphatase 79 RT-PCR primer, SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1734 ACAAAAAAAAAAAAAAAAA 1755
                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 25; 46pp; English
/note= "inosine"
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                                                                                                       99WO-CA000933
                                                                                                                                          98CA-02246623
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                                                                                                                                                                                                              Das M;
                                                                                                                                                                         (UYMC-) UNIV MCGILL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention
                                   WO200020630-A1
                                                                                                                                                                                                                                                                                                                                         or sequencing.
                                                                                                                                                                                                            Pelletier J,
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                                                                                                                                          07-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                     06-OCT-1999;
                                                                      13-APR-2000
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diseases and inflammations.

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The present invention describes the human FD 17 protein (I). (I) has actostatic, virucidal, immunomodulatory, antinflammatory and haemostatic activities. The polynucleotide encoding (I) can be used in gene therapy. (I) and the polynucleotide encoding it are applicable in the diagnosis and treatment of malignant tumour, haemopathy, human immunodeficiency virus (HIV) infection, immunological diseases and various inflammations. The present sequence represents a PCR primer for human FD 17, which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to the isolation of human transcriptional activation subunit 14, and the polymucleotide encoding it. Also described is the process for preparing the protein by DNA recombination and the application of the polypeptide and polymucleotide in treating various diseases such as malignant neoplasms, haematopathy, human immunodeficiency virus (HIV) infection, immunological diseases, and various inflammations. Antagonists against the polypeptide can also be used in treating such diseases. The present sequence for reverse transcriptase (RT)-PCR primer #2 is used with RT-PCR primer #1 (ABK13714) for isolating cDNA encoding human transcriptional activation subunit 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human transcriptional activation subunit 14 and encoding polynucleotide, used in diagnosis and treatment of malignant tumors, hemopathy, human immunodeficiency virus infection, immunological diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, transcriptional activation subunit 14; malignant neoplasm; haematopathy; cytostatic, HIV infection; human immunodeficiency virus; immunological disease; inflammation; virucide; immunomodulatory; antiinflammatory; reverse transcriptase-PCR; RT-PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RT-PCR primer #2 for human transcriptional activation subunit 14 cDNA
                                                                                                                                                                                                                                                                                                               Query Match 1.0%; Score 18.4; DB 1; Length 24; Best Local Similarity 95.0%; Pred. No. 2.9e+02; Matches 19; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                          Sequence 24 BP; 0 A; 2 C; 1.G; 21 T; 0 U; 0 Other;
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                                         Example 2; Page 11; 36pp; Chinese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polypeptide-laminin B210.67, useful for treating diseases such as embryo development teratogenesis.
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                  RT-PCR primer #1 for cDNA encoding polypeptide-laminin B210.67.
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                                                                                                                                                                                                                                                                                            Polypeptide-laminin B210.67; embryo development teratogenesis; cytostatic; reverse transcriptase-PCR; RT-PCR; primer; 88.
                        1.0%; Score 18.4; DB 1; Length 24; 95.0%; Pred. No. 2.9e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.0%; Score 18.4; DB 1; Length 24; 95.0%; Pred. No. 2.9e+02; [ve 0; Mismatches 1; Indels
SQ Sequence 24 BP; 0 A; 2 C; 2 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 24 BP; 19 A; 2 C; 0 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Page 18 (disclosure); 33pp; Chinese.
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                                                                                  1735 CAAAAAAAAAAAAAAAA 1754
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                                                                                                                                                                                  ABK12409 standard; DNA; 24 BP
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19; Conservative
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                                                        19; Conservative
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                                           Best Local Similarity
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                                                                                                                                                                                                                                        18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-APR-1999
                                                                                                                                                                                                                                                                                                                                        Unidentified
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                             Query Match
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                                                       Matches
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(-)-limonene-6-hydroxylase primer 3.B.

24-FEB-2000.

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The invention relates to nucleotide sequences encoding spearmint (-)-
limonene-6-hydroxylase (L6H) and peppermint (-)-limonene-3- hydroxylase
(L3H). Host cells containing a vector comprising the nucleotide sequences
can be used for the recombinant production of limonen hydroxylases or of
primary enzyme products. The primary enzyme products are trans-carveol in
the case of (-)-L6H or trans-isopiperitenol in the case of (-)-L3H, which
are of subsequent use, to obtain enhanced expression of limonen
hydroxylase in plants to attain enhanced trans- carveol or trans-
isopiperitenol production as a predator or pathogen defense mechanism,
attractant or environmental signal. The limonene hydroxylase cDNAs also
provide a useful tool for isolating other monoterpene hydroxylase genes
cand for examining the developmental regulation of monoterpene
blosynthesis. Sequences AAXO6564-73 represent primers for the PCR
maplification of (-)-limonene-6-hydroxylase cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated limonene hydroxylase nucleic acids - which encode limonene-6-hydroxylase and limonene-3-hydroxylase, which can be used to produce trans-carveol and trans-isopiperitenol.
              (-)-limonene-6-hydroxylase; (-)-limonene-3-hydroxylase; L3H; L6H; spear mint; peppermint; enzyme; limonene hydroxylase; trans-carveol; trans-isopiperitenol; pathogen defense mechanism; attractant; environmental signal; monoterpene hydroxylase; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gibberellic acid, copalyl diphosphate synthase; 3beta-hydroxylase; 2-oxidase; phytoene synthase; C-20 oxidase; 2beta.3beta-hydroxylase; seed germination; seedling growth; gibberellin biosynthetic pathway; transgenic plant; hypocotyl; epicotyl; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.0%; Score 18.2; DB 1; Length 19; 04.7%; Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer HOOK for cDNA encoding a C-20 oxidase polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
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1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                     Karp F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-00881784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JUL-2000 (first entry)
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nes 18, Conservative
                                                                                                                                                                                                                                                                                                                                                                   Croteau RB, Lupien SL,
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-105618/09.
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                                                                                                                                  Mentha spicata.
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                                                                                                                                                                      WO9859042-A1
                                                                                                                                                                                                                                                 15-JUN-1998;
                                                                                                                                                                                                                                                                                         24-JUN-1997;
                                                                                                                                                                                                            30-DEC-1998.
                                                                                                              Synthetic
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XX
AC AAZ9
XX
AC AAZ9
DE Prim
XW Gibb
KW 2-0x
KW 2-0x
KW Seec
KW trar
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The present primer was used to reverse transcribe cDNA encoding a C-20 oxidase. The amplifie fragment is used in the method of the invention. The specification describes methods for the inhibition and control of gibberellic acid levels. Gibberellic acid levels may be inhibited or controlled by use of a chimeric expression construct expressing a RNA or protein which suppresses the gibberellin biosynthetic pathway sequence, diverts substrate from the pathway, or degrades pathway substrates or products. The methods uses copalyl diphosphate synthase, 3beta- hydroxylase, plytroene synthase, C-20 oxidase, and a choracylase, plytroene synthase, C-20 oxidase, and a choracylase polynucleotides to achieve this. The method is used to control seed germination and seedling growth especially to regulate gene products of gibberellin biosynthetic pathway and restoration of normal seed germination, in transgenic plants. The plants produced are gibberellin deficient, and have shortened hypocotyl and/or epicotyl phenotypes compared to normal plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fatty lesion development, atherosclerosis, Alzheimer's disease; nervous system disorder; parkinson's disease; immune system disorder; ischaemia; lymphopaemia; leukocyte adhesion deficiency syndrome; haemoglobinuria; anaemia; hyperproliferative disorder; Gaucher's disease; coagulation disorder; blood platelet disorder; autoimmune disorder; Garderis; ships herpes simplex; Addison's disease; rheumatoid arthritis; Garave's disease; gene therapy; antiarteriosclerotic; immunostimulant; cardiovascular; antiviral; primer; ss.
                                                                                                                                                                                                                                                                                   Obtaining transgenic plant useful for controlling seed germination and seedling growth comprises transgene comprising a sequence expressing altered levels of an essential hormone.
                                                                                                                                                                                        Logusch SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3' sequencing primer #1 to identify and characterise polynucleotides
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                                                                                                                                                                                        Kishore GM, Logusch EW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                              Example 17; Page 262; 267pp; English.
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                                                                                                                                                                                    Heck GR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 BAAAAAAAAAAAAAA 1
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AAD15201 standard; DNA; 19 BP
                                                     99WO-US018066.
                                                                                         98US-0096111P.
                                                                                                                                                                                                            Ream JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.78;
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hes 18, Conservative
                                                                                                                                                                                        Elich TD,
                                                                                                                                                (MONS ) MONSANTO CO.
                                                                                                                                                                                                                                               WPI; 2000-224351/19.
                                                                                                                                                                                                            Rao S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40200154651-A2
                                                     10-AUG-1999;
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                                                                                         10-AUG-1998;
07-JUN-1999;
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                                                                                                                                                                                        Brown SM,
Piller KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD15201;
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1735 CAAAAAAAAAAAAAAAAA 1753
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                    Sutcliffe JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 94.7
hes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lupien SL,
                                                        WPI; 2001-300499/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mentha spicata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L5-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-FEB-2001
         Thomas EA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                   The present invention relates to an isolated nucleic acid regulated by fatty lesion development, which comprises any of 55 polynucleotide or sequences from Orycotolagus cuniculus. The polynucleotide, polypetide or antibody is useful for preventing, treating, modulating or ameliorating a medical condition, particularly atherosclerosis. The invention is used as a marker or detector of nervous system disorder or disease (e.g. Parkinson's disease, ischaemia, dementia). The invention may also be useful for treating deficiencies or disorders of the immune system (e.g. lymphopaenia, leukocyte adhesion deficiency syntheticome or haemoglobinuria, anaemia), hyperproliferative disorders (e.g. Gaucher's disease), infectious disease (e.g. herpes simplex), coagulation disorders, blood platelet disorders and autoimmune disorders (Addison's disease, theumatoid arthritis, dermatitis, Grave's disease). The polynucleotide sequence is also used in gene therapy. The present sequence is a 3' sequencing primer used in the identification and characterisation of polynucleotides up-regulated by fatty lesion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse; human; total gene expression analysis; TOGA; DST; EST; digital sequence tag; expressed sequence tag; neuroleptic; antimanic; central nervous system; antidepressant; gene therapy; disgnosis; neuropsychiatric disorder; schizophrenia; bipolar disorder; addiction-related behaviour; chromosome identification; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse total gene expression analysis (TOGA) 3' sequencing primer SEQ:92.
                                                                                                                                                                                New polynucleotides regulated by fatty lesion development and their encoded polypeptides, useful for preventing, treating or ameliorating atherosclerosis, as well as for immune or hyperproliferative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                            Hasel KW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18.2; DB 1; Length 19; Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
                                                                                                            Glass JR, Sutcliffe JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
                                                                         (DIGI-) DIGITAL GENE TECHNOLOGIES INC
                                                                                                                                                                                                                                                       Example 1; Page 79; 188pp; English.
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25-JAN-2001; 2001WO-US002439
                                     25-JAN-2000; 2000US-0177963P
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nes 18; Conservative
                                                                                                           Sartani A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR primer; probe; ss
                                                                                                                                              WPI; 2001-514526/56
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                                                                                                            Leonardi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          development
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Matches

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RESULT 518 AAH21968/c

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The present invention describes isolated metalogues. Carlo molecules. (1) have neuroleptic, antimatic and antidepressant activities, and can be used in gene therapy. (1), polypeptides (11) comprising (1), are useful for preventing, treating, modulating or ameliorating a medical condition such as a neuropsychiatric disorder. (1) are useful as diagnostic agents for diagnosing a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition such as neuropsychiatric disorder e.g. schizophrenia, a bipolar disorder or addiction-related behaviour. (1) are useful for detecting the presence of a nucleic acid encoding a protein in a mammalian tissue presence of a nucleic acid encoding a protein in a mammalian tissue cample. (1) can be used as probes and primers, for chromosome cidentification, to control gene expression through triple helix formation or antisense DNA or RNA, in gene therapy to treat the above mentioned alternative to restriction fragment length polymorphism (RFLP) and as an alternative to restriction fragment length polymorphism (RFLP) and as molecular weight markers for forensic purposes. (1) is also useful as molecular weight markers on Southern gels, diagnostic probes for the subtract-out known sequences in the process of discovering novel content support, to raise anti-DNA antibodism using DNA immunisation technique, and as an antigen to elicit an immune response. AAH21877 to AAH218877 to AAH218877 to AAH218877 to AAH218877 to AAH218877 to AAH218877 to AAH218874 habs98084 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                           New neuroleptic-regulated polynucleotides expressed in the central nervous system for diagnosing and treating neuropsychiatric disorders such as schizophrenia, bipolar disorder and addiction-related behavior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neuroleptic-regulated nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
Hasel KW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.0%; Score 18.2; DB 1; Length 19; 94.7%; Pred. No. 2.6e+02; ve 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spearmint (-)-limonene-6-hydroxylase PCR primer SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spearmint; peppermint; (-)-limonene-6-hydroxylase;
Pribyl TM, Hilbush B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention describes isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UNIW ) UNIV WASHINGTON STATE RES FOUND.
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activated macrophage. The polynucleotides of the invention,

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The present invention provides the protein and coding sequences of the peppermint and spearmint (-)-limonene-3-hydroxylase and the spearmint (-)-limonene-6-hydroxylase. Provided are a number of probes and PCR primers which were used to isolate the sequences. These are useful in the production of transgenic plants with altered flavour and aroma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse; microglia; macrophage; regulatory gene; digital sequence tag; DST;
                                     Novel isolated limonene hydroxylase encoding nucleic acid molecule, useful for altering production of limonene-6-hydroxylase or limonene-3-hydroxylase in suitable host cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR-based total gene expression analysis; TOGA; infectious disorder; neuroinflammatory pathology; neurodegenerative disease; gene therapy; hyperproliferative disorder; autoimmune; inflammatory disorder; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse microglia and macrophage regulatory gene primer #60.
                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                 Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tobal GM;
                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                           Score 18.2; DB 1;
Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Almazan MT,
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                                                                                         Example 4; Col 55; 57pp; English
                                                                                                                                                                                                                                                                                                       19 DAAAAAAAAAAAAAA 1
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                                                                                                                                                                                                                           1.0%;
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19-JUN-2000; 2000US-0212465P.
                                                                                                                                                                                                                                                                                                                                                                       AAS06525 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                           07-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sutcliffe JG,
                                                                                                                                                                                                                                                     18; Conservative
             WPI; 2001-243405/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-308782/32.
                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-MAY-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                 AAS06525;
                                                                                                                                                                                                                                                    Matches
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The present sequence represents a primer used to isolate novel mouse microglia and macrophage regulatory gene DST (dightal sequence tag) sequences. AASO6401-AASO6590 represent these novel sequences and the primer sequences used to isolate them. The PCR-based total gene primer sequences used to solate them. The PCR-based total gene expression analysis (TOGA) system is used to examine the expression pattern of molecules corresponding to genes that are regulated in unstimulated microglia, activated microglia, unstimulated macrophage and

New regulated genes of microglia and macrophages, useful for diagnosing, preventing or treating neuroinflammatory pathology and neurodegenerative

Example 1; Page 88; 244pp; English

disease.

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Gaps ö

Length 19;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to the cDNA sequences of novel isolated polynucleotides associated with psychoses or other neuropsychiatric disorders. The sequences of the invention may act as blockers of D_{-2} receptors in the meso-limbic dopamine system. The nucleotide sequences of the invention and the polypeptides encoded by them are useful in the manufacture of a medicament useful for preventing, treating, modulating
             polypeptides encoded by the and antibodies that bind to these polypeptides are useful are useful for the diagnosis, prevention, treatment or amelioration of a medical condition, preferably a neuroinflammatory pathology or a neurodegenerative disease such as Alzheimer's disease, senile dementia, Parkinson's disease, obsessive compulsive disorders, eppliapsy, schizophrenia, multiple sclerosis, depression and bipolar manic-depressive used for detecting or treating infectious disorders (e.g. AIDS), hyperproliferative disorders (e.g. ancer), immune diseases (e.g. insulin dependent diabetes mellitus), inflammatory disorders (e.g. arthritis). The polynucleotides can be used inflammatory disorders (e.g. arthritis). The polynucleotides can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Central nervous system; CNS; neuroleptic; mouse; human; psychoses;
neuropsychiatric disorder; psychiatric disorder; Alzheimer's disease;
Pick's disease; Binswanger's disease; senile dementia; encephalopathy;
Parkinson's disease; obsessive compulsive disorder; epilepsy; ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           addiction; multiple sclerosis; depression; manic-depressive disorder;
                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                               DB 1; Length 19;
                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thomas EA, Sutcliffe JG, Pribyl TM, Hilbush BS,
                                                                                                                                                                                                                                                                                         Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                         Score 18.2; DB 1;
Pred. No. 2.6e+02;
1; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNS related 3' sequencing primer.
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                                                                                                                                                                                                                                                                                                                             1.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             19 BAAAAAAAAAAAAAAAA
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18-JAN-2001; 2001US-0263084P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABK71509 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                     for gene therapy
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                                                                                                                                                                                                                                                                                                                                                                   18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK71509;
                                                                                                                                                                                                                                                                                                                                                                     Matches
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antibody that binds the proteins of the invention is useful for preventing, treating, modulating or ameliorating neurological disorders beychoses or other neuropsychiatric disorders in a subject. The sequences are also useful for disorders in a subject. The sequences are also useful for disorder such as psychoses or a subject subject billty to a neurological disorder such as psychoses and other neuropsychiatric disorders in a subject by determining the presence or absence of mutation in the nuclectide sequence of apolipoprotein D or by determining the alteration in the nuclectide sequence of apolipoprotein D or by determining the alteration (increase or decrease) in the expression of apolipoprotein D. The sequences of the invention are useful in treating deficiencies or disorders of the central nervous system by activating or inhibiting the proliferation, and interesting or inhibiting the proliferation, and interesting or inhibiting the proliferation, and interesting or inhibiting the proliferation, and interest or detector of a particular nervous system disease or disorder such as Alzheimer's disease, pick's disease, Binswanger's disease, other senile dementia, entered as disease, obsessive compulaive disorders, epilepsy, encephalopathy, ischaemia, addiction, multiple sclerosis, depression and manic-depressive disorder. The present sequence represents an or particular used in the identification of the cDNA sequences
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Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

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Gaps
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Query Match 1.0%; Score 18.2; DB 1; Length 19; Best Local Similarity 94.7%; Pred. No. 2.6e+02; Matches 18; Conservative 1; Mismatches 0; Indels
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ABQ73231 standard; DNA; 19 BP 27-SEP-2002 (first entry) roda primer; ss ABQ73231; RESULT 522

Rabbit atherosclerosis related TOGA primer SEQ ID NO:26.

Rabbit; Oryctolagus cuniculus; atherosclerosis; intimal hyperplasia;

Oryctolagus cuniculus. Synthetic

WO200242420-A2.

30-MAY-2002

21-NOV-2001; 2001WO-US044072

(DIGI-) DIGITAL GENE TECHNOLOGIES INC. 21-NOV-2000; 2000US-0252216P

Glass JR, Hasel KW; Leonardi A, Sartani A,

WPI; 2002-575233/61.

New polynucleotides related to regulated genes characteristic of atherosclerosis, useful for diagnosing, preventing, treating, modulating or ameliorating atherosclerosis in a mammalian subject.

Disclosure; Page 28; 130pp; English.

complements, and degenerate variants, comprising a sequence selected from those given in ABQ73206 to ABQ73222 (NS), which is a digital sequence tag (DST) corresponding to mRNAs whose expression is regulated by The present invention describes an isolated polynucleotide (I) and its

The present invention relates to a method for preventing, treating, modulating or ameliorating a medical condition. The method involves administering one or more nucleic acid molecules up- or down-regulated in hepatitis B virus (HBV) infection or polypeptides encoded by the nucleic acid molecules or antibodies that bind to the polypeptide. The method is useful for preventing, treating, modulating or amaliorating a medical condition. It is also useful for determining the presence or absence of a mutation in the nucleic acid molecules or detecting an alteration in

Disclosure; Page 28; 125pp; English.

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proliferative lesion development caused by mechanically induced intimal hyperplasia, or by lercanidipine treatment, or by proliferative lesions and reversed by lercanidipine treatment. (I) has antiatherosclerotic activity and can be used in gene therapy. (I) can be used for diagnosing a medical condition (e.g. atherosclerosis) in a subject which involves determining the presence or absence of a mutation in (I) and diagnosing the medical condition based on the presence or absence of the mutation. (I) is also useful for diagnosing atherosclerosis, or the susceptibility to atherosclerosis in a subject which involves detecting an alteration (an increase or decrease) in amount of expression of (I). (I) is also useful for diagnosing or monitoring the effects of treating a subject with dihydrospridine calcium antagonist e.g., lercanidipine. (I) can also be used for preventing, treating, modulating, or ameliorating a medical condition such as atherosclerosis in a mammalian subject. The present
                                                                                                                                                                                                                                                  conditions but as atheroscierosis in a mammalian subject. The present exequence represents a TOGA primer which is used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Preventing and treating hepatitis viral infection in a mammal, comprises administering nucleic acid molecules that up· or down-regulate in hepatitis B virus infection or polypeptides encoded by the nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR primer #4 used for direct sequencing of TOGA generated PCR products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis B virus; HBV infection; chronic hepatitis; toxicity; virucide; acute hepatitis; therapeutic; gene therapy; vaccine; infectious disease; TOGA; Total Gene expression Analysis; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                             1.0%; Score 18.2; DB 1; Length 19; 94.7%; Pred. No. 2.6e+02; tive 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                       the present invention
                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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hepatitis viral infection. The method is useful for assessing the stage of hepatitis viral infection (e.g., acute hepatitis versus chronic hepatitis) or assessing the efficacy or toxicity of therapeutic treatment for hepatitis viral infection and a gene expression profile is useful for identifying polypeptides and polynucleotides which are associated with hepatitis viral infection. Sequences of the invention are used in gene therapy and as vaccines. Nucleic acid sequences are useful as a diagnostic markers for HBV infection and for treating infectious diseases. The present DNA sequence is a PCR primer which is used for direct sequencing of TOGA (TOtal Gene expression Analysis) generated PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to control of gibberellin (GA) levels in plants. The method involves producing transgenic plants having a phenotype of reduced seed germination and reduced early seedling growth, then restoring seed germination and early seedling growth by treating plants with an appropriate compound when conditions are favourable. The method is useful to control seed germination and/or early seedling growth in agricultural production so that unfavorable environmental conditions normally reducing agronomic output can be avoided and yields increased. Plants also demonstrate increased uniformity of germination, emergence and seedling vigor, so increasing yields at harvest. The method is especially useful in crop plants such as e.g. canola, soybean, cotton, etc., and is also useful in storage and transport of seeds to reduce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Control of gibberellin levels in plants useful to avoid unfavorable conditions in crops to increase yields, using transgenic plants having reduced seed germination and early seedling growth then treatment to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gibberellin, transgenic plant; seed germination; seedling growth; GA; transgenic; 2beta-1beta hydroxylase; enzyme; pumpkin; PCR; primer; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOOK PCR primer used to isolate pumpkin 2beta-3beta hydroxylase cDNA
  expression of the polypeptide which is useful for the diagnosis of
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                                                                                                                                                                                                                                                         Seguence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                          Score 18.2; DB 1;
Pred. No. 2.6e+02;
1; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD40279 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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ses 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-489107/52
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Piller KJ,
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premature germination which may affect agronomic or food quality of the seeds. The present sequence is a PCR primer used to isolate pumpkin 2beta -3beta hydroxylase cDNA. This primer is used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New chimeric polypeptide comprising a histone acetyltransferase polypeptide segment and a segment comprising a histone deacetylase chromatin-associated protein complex subunit, useful for modulating gene expression in cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Histone acetyltransferase, histone deacetylase, gene expression profile, chromatin-associated protein, gene expression, primer, ss.
                                                                                                                                                           Gaps
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                                                                                                                     1.0%; Score 18.2; DB 1; Length 19; 94.7%; Pred. No. 2.6e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Reverse transcription primer used to produce yeast cDNA.
                                                                                    Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
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                                                                                                                                                                                                                                                                                                                   ABZ68389 standard; DNA; 19
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                                                                                                                                                           18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Okamuro J;
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wes 18; Conserv
                                                                                                                                           Similarity
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                                                      the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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Parkinson's disease, multiple sclerosis; immune disorder; gene therapy; autoimmune disorder; rheumatoid arthritis; hyperproliferative disorder; haemolytic anaemia; graft-versus-host disease; inflammation; infection; epilepsy; Addison's disease; neoplasm; tissue regeneration; chemotaxis; food additive; food preservative; primer; ss.

Atherosclerosis; vaccine; nervous system disorder; Alzheimer's disease;

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Preventing or treating a pathological condition e.g., ataxia
telangiectasia (AT), AT tumors or other cancers comprises administering
polynucleotides.
                                                                         Pathological condition; ataxia telangiectasia; AT; tumour; cancer; cytostatic; vaccine; gene therapy; PCR primer; ss.
                                                                                                                                                                                                                                   Callahan MLA, Pankratz DG, Vibat CRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
                                                        M13 sequencing primer 3' primer SEQ ID NO:84.
                                                                                                                                                                                                                (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                        Example 1; Page 76; 184pp; English.
ACC79402 standard; DNA; 19 BP.
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                                                                                                                                                                                             17-OCT-2001; 2001US-0330206P
                                    (first entry)
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189 18; Conservative
                                                                                                        Enterobacteria phage M13.
                                                                                                                                                                                                                                   Winrow CJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention
                                                                                                                                   WO2003033668-A2.
                                     04-AUG-2003
                                                                                                                                                       24-APR-2003
                                                                                                                                                                                                                                   Barlow C,
Warren AJ;
                                                                                                                  Synthetic
                  ACC79402;
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Matches
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New polypeptide associated with atherosclerosis, useful for treating atherosclerosis, nervous system disorders, immune disorders, hyperproliferative disorders and infectious diseases.

Disclosure; Page 139; 146pp; English

Hasel KW;

Leonardi A, Sartani A, Glass J, Sutcliffe JG,

WPI; 2003-058561/05

(DIGI-) DIGITAL GENE TECHNOLOGIES INC.

15-NOV-2001; 2001WO-US043741

WO200281726-A2 Unidentified.

17-OCT-2002.

15-NOV-2000; 2000US-0248892P 28-NOV-2000; 2000US-0253623P

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The invention relates to polynucleotides and polypeptides associated with atherosclerosis. Polynucleotides of the invention are useful for delivery of genes, DNA vaccines, diagnostic reagents, peptides, proteins or macromolecules. Sequences of the invention are useful for treating nervous system disorders (e.g., Alzheimer's disease, Parkinson's disease, multiple sclerosis, epilepsy), immune disorders (e.g., autoimmune disorders such as rheumatoid arthritis, Addison's disease, haemolytic anaemia, graft-versus-host disease, inflammation), hyperproliferative disorders (e.g., neoplasme) and infectious diseases (e.g., viral, or parasite infection). They are used for regeneration of tissues, to repair, replace or protect damage tissues, for increasing chemotaxis activity of cells, for increasing or decreasing the citerentiation or proliferation of publication of multiple mammalian characteristics, (such as body weight or height), for modulating mammalian metabolism affecting catabolism, consideration of mammal's mental or physical state, or as a food additive or preservative. The invention is useful in gene therapy. The present sequence is a sequencing primer used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a method for preventing or treating a pathological condition (comprising ataxia telangiectasia (AT), AT tumours or other cancers), which comprises administering to a mammalian subject at least one of: (a) a first polynucleotide comprising a sequence having 38-889 bp (consisting of the sequences in ACC79319 to ACC79322 (I)) or a second polynucleotide at least 95% identical to the first polynucleotide (b) a third polynucleotide comprising at least 10-bp sequence that is hybridisable to the first polynucleotide under stringent conditions; or (c) a gene corresponding to any of (1)-(2) or another gene at least 95% identical to the gene. (I) have cytostatic activities, and can be used in vaccines and in gene therapy. The method is useful for preventing or treating e.g., ataxia telangisectasia (AT), AT tumours or other cancers.
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Pred. No. 2.6e+02;
1; Mismatches 0; Indels
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    sequencing primer #1 used to illustrate the method of the invention.

                                                                                                                                                                                                                      Gene expression; drug interaction mechanism; drug screening; primer; genomic mapping; 88.
1735 CAAAAAAAAAAAAAAA 1753
                  AAD50267 standard; DNA; 19 BP
                                                                                                                                                                24-MAR-2003 (first entry)
                                                                                                                                  AAD50267;
                                                                                                                      XXXXXXXXXX
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3' sequencing primer #1 used in the invention.

07-MAR-2003 (first entry)

AAD49149;

RESULT 527

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AAD49149/C
ID AAD491
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AC AAD491
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DT 07-MAR
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Gaps

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0; Indels

Length 19;

Score 18.2; DB 1; Pred. No. 2.6e+02; 1; Mismatches

1.0%;

18; Conservative

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29-SEP-2001; 2001DE-01048236.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003029282-A2
                                                                                 WO200261045-A2
                                                                                                                                                                                                                                                                                                                                                QUAN/) QUAN J
                              Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interaction.
                                                                                                                                              08-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-APR-2003,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADC21495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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1D ADC2

AC ADC2

XX ADC2

XX I8-Di

XX Lumo

KW Tumo

KW POSi

KW POSi

KW PRIM

XX Homo

XX XX Homo

XX XX Homo

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This invention describes a novel tumor-associated oligopeptide that is recognized as an antigen by CD8+ cytotoxic T lymphocytes (CTL) and causes CTL-induced lysis and/or apoptosis of tumor cells, especially multiple myeloma cells. The oligopeptide is derived from human PRD1-BF1 (positive regulatory domain I-binding factor-1) which is able to induce an MHC (major histocompatibility complex) Class I allele variant A2-restricted immune response of CD8+ CTL against tumor cells. The products of the invention have cytostatic activity and can be used in a vaccine. The peptide of the invention, also related retro-inverse and pseudopeptides, cusion proteins (RP), polymucleotides, vectors, host cells and antibodies and T cell receptors specific for PRDI-BF1, particularly tumors. The products of the invention are also useful as diagnostic, therapeutic and products of the invention are also useful as diagnostic, therapeutic and prophylactic agents for detecting, modifying, generating, expanding complyancing activation and functional status of T cells, and for preparation of poly- or mono-clonal or recombinant A2-restricted T cell receptors and their functional equivalents. This sequence represents and PEPPER primer used to amplify the human PRDI-BF1 gene described in the
                                                                                                                                                      New tumor-associated oligopeptide, useful particularly for treating multiple myeloma, is recognized by CD8 cytotoxic T cells, also derivatives and related nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.0%; Score 18.2; DB 1; Length 19; 94.7%; Pred. No. 2.6e+02; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer; DNA analysis; amplification; hybridisation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonuclectide 9 for DNA analysis.
                                                                                                                                                                                                                                                   Disclosure; Page 22; 64pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1735 CAAAAAAAAAAAAAAAA 1753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18; Conservative
                     (IMMU-) IMMUGENICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HITA ) HITACHI LTD.
                                                                                                           WPI; 2003-354724/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JP11196874-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-0CT-1999
                                                                Theobald M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-JUL-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ09197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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AAZ09197/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a novel simplified TOGA (RTM) method for simultaneous sequence-specific identification of multiple mRNA molecules in a RNA population. The method involves characterising each of the sequence-specific polymerase chain reaction (PCR) products by partial sequence and length. The method is useful for determining tissue-specific patterns of gene expression or mechanisms of drug interaction. It is also useful for drug screening, studying physiological processes, genomic mapping or manufacture of diagnostic, prognostic or therapeutic reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                Simplified TOGA method for simultaneous sequence-specific identification of multiple mRNA molecules in mRNA population, useful for determining tissue-specific patterns of gene expression or mechanisms of drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumor; antigen; CD8+ cytotoxic T lymphocyte; CTL; CTL-induced lyais; multiple myeloma cell; human; PRDI-BF1; positive regulatory domain I-binding factor-1; MHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                major histocompatibility complex Class I; cytostatic; vaccine; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.0%; Score 18.2; DB 1; Length 19; 94.7%; Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                    Hasel KWPD, Sutcliffe GJ, Chang HW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                 DIGI-) DIGITAL GENE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 39; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1735 CAAAAAAAAAAAAAAAA 1753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-2002; 2002WO-US002666
                                                                                                                                                                                                      01-FEB-2001; 2001US-00775217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human PRDI-BF1 RT-PCR primer.
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nes 18; Conservative
                                                                                                                                                                                                                                                                                                                    Quan J, Hilbush BS,
Callahan MA;
                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-092784/08
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Gaps

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Analysis of DNA fragment - comprises addition of known common oligonuclectide, amplification of resultant DNA fragment and analysis and labelling of amplified DNA.

WPI; 1999-496652/42.

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                                                       which comprises: (i) addition of a known common oligonucleotide sequence to at least one terminal of each DNA fragment, (ii) amplification of the resultant DNA fragment as a primer using a first common primer containing a complementary nucleotide sequence to the above mentioned known common complementary nucleotide sequence to the above mentioned known common oligonucleotide sequence to the prepared known common oligonucleotide sequence to the prepared known common oligonucleotide sequence optionally having been introduced with complementary nucleotide sequence at a terminal, and a specific primer capable of hybridisation with a DNA fragment containing whole or part of the gene having known sequence, to give amplified DNA, (iii) analysis of the amplified DNA to find the information of the DNA fragment, in which the specific primer is designed to prepare fragments of the common first and second primers and to give short fragment of amplified DNA and (iv) labelling them to make their differentiation. Differentiation of informations of known and unknown gene readily provides information of unknown gene and simultaneous monitoring of signals derived from minor genes Furthermore, labelling of DNAs according to functions of known
                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                             This invention descibes a novel method for the analysis of a DNA fragment
                                                                                                                                                                                                                                                                                                                                  genes can be performed. AAZ09189-Z09201 represent oligonucleotide primers
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                      Score 18.2; DB 1; Length 20;
Pred. No. 2.7e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                             Seguence 20 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence of a microsatellite from clone TGLA60B.
                                                                                                                                                                                                                                                                                                                                               used to illustrate the method of the invention
                Example 5; Page 12; 17pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                            1.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 94.79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JAN-1991;
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02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 531
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clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (T6) n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trail loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ3501-34437. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides. They are used in a method for detecting an antigen in a subject. The method involves blading the antigen to a solid support and then reacting it with an immunoreactive ligand (L) bound to an oligo, removing any unreacted L, and then detecting the presence of the oligo. Removing any method can be used to detect Abs, in which case the ligand is an oligolable led Ag. The use of an amplificable oligo as the label allows Ag or Ab to be detected at very low levels. An exemplary olgi is AAQ75024 which can be covalently attached by the 5'- terminus to the N· or C-terminal of a synthetic peptide. In the example, peptide AR62941 was coupled to oligo AAQ75024 using disuccinimidyl suberate. Serum samples suspected to contain HEV Abs were immobilised on plastic tubes or wells, then incubated for 30-60 mins with the peptide-oligo proruct. The vessels were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Solid phase immunoassay using oligo:nucleotide as label - also new conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for diagnosing hepatitis C or E virus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.0%; Score 18; DB 1; Length 18; Best Local Similarity 100.0%; Pred. No. 2.6e+02; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                     Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic oligo; solid phase immunoassay; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example; Page 12; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AAAAAAAAAAAAAA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-006819/01.
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03-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCR primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ75025;
                                                                                                                                                                                                                                                                                                        field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 532
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and 500

The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50

Table 7; Page 375; 517pp; English.

mapping, and selective breeding.

Polymorphic bovine DNA markers - used in genetic identification, gene

AAV21970 standard; DNA; 18 BP

AAV21970/c

Nuclease resistant antisense oligo NBT 13 targeted against (T)18.

(first entry)

14-JUL-1998

AAV21970;

Nuclease resistant; bacterial infection; antibiotic; target; veterinary medicine; treatment; human; industrial process;

bacterial control; ss.

ETC & OLIGOS THERAPEUTICS INC.

97WO-US012961. 96US-00685575.

23-JUL-1997; 24-JUL-1996;

WO9803533-A1

Synthetic.

29-JAN-1998.

Thompson TL;

Arrow A, Dale RMK, WPI; 1998-120687/11

(OFIG-) OFIGOS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream region of a polyadenylation sequence. They were used to prime cDNA synthesis from snapdragon (Antirkhinum majus) petal and leaf RNA, and were also utilised in the PCR amplification of plant cytochrome P450 aguences (see also AAT94670-73). A cDNA clone (see AAT94657) encoding flavonoid 3' hydroxylase (see AAM9504) was isolated using a differential display approach. This can be used to manipulate the pigmentation of
washed; bound oligo was released with 0.2M glycine and amplified in a separate tube using as primers AAQ75025 and AAQ75026 in 30 cycles of PCR. The amplification product - AAQ75031 - was treated with uracil DNA glycoslase to remove the U18 fragment, and the product captured by immoblised oligo-dr. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Flavonoid 3' hydroxylase; pigmentation; flower colour; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel flavonoid 3'-hydroxylase(s) from flowering plants - and corresponding DNA, used in the manipulation of pigmentation in plants.
                                                                                                                                                                    Gaps
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                                                                                                                                     Length 18;
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                                                                                                    Sequence 18 BP; 0 A; 0 C; 0 G; 0 T; 18 U; 0 Other;
                                                                                                                                   1.0%; Score 18; DB 1; Le
100.0%; Pred. No. 2.6e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                        Anchored poly(T) oligonucleotide polyT-AnchG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 15; Page 59; 234pp; English
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                                                                                                                                                                                                                                                                                                                       AAT94669 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                 Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brugliera F, Holton TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        snapdragon; primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FLOR-) FLORIGENE LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-448691/41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                        AAT94669;
                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chemotherapy or radiation therapy), optionally in combination with, or fused to, antiviral or other antimicrobial oligonucleotides. Apart from therapeutic use, the oligonucleotides can be used to control bacteria in laboratory cultures, foods, beerages and industrial processes. The oligonucleotides are specific for bacteria, without affecting metabolism in mammalian cells. They may also activate RNase H and have a general, non-specific immune-stimulating effect. The oligonucleotides can be administered orally, intranasally, rectally, topically or by injection, optionally coupled to an agent (e.g. carbohydrate or polyamine) that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treating bacterial infections in humans or animals with oligo:nucleotide(s) - resistant to nuclease and targetted to bacterial nucleic acid or proteins, also conjugates of these oligo:nucleotide(s)
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Pred. No. 2.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.0%; Scott No. 2.100.0%; Pred. No. 2.100.0%; Pred. No. 2.100.0%; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 49; Page 87; 163pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enhances cellular uptake
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Best Local Similarity
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Gaps

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1.0%; Score 18; DB 1; Length 18; 100.0%; Pred. No. 2.6e+02; tive 0; Mismatches 0; Indels

Query Match Best Local Similarity 100. Matches 18; Conservative

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18 САААААААААААААА 1

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RESULT 534

Gaps

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Synthetic

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A method has been developed for labelling an oligonucleotide having a repeated sequence of (XY)n (where X and Y consists of a combination of adenine and thymine or uracil or guanine and cytosine, and n is an integer of 1 or more ) at the 3'-terminal side in which the repeated sequence is added and extended using a labelled body of the nucleotide constituting the repeated sequence and a DNA polymerase lacked in 5' to 3' exonuclease activity. The method can be used for detecting a gene. The method can detect a gene in a sensitivity up to ten times higher than prior art methods. The present sequence represents a primer used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Therapeutic composition containing antieense oligonucleotides that include arabinose sugars, particularly for inhibiting viral replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a new composition for selective, sequence-specific inhibition of gene transcription and expression in a host. The composition comprises oligomelectides containing arabinose sugars that can hybridise to either a a single-stranded (ss) RNA to induce RNase H cleavage activity, or to a DNA/DNA or DNA/RNA duplax to form a triple helix, thereby inhibiting DNA replication and/or transcription. The oligoarabinonucleotides are used for antisense inhibition of gene
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/note= "Ribose moiety replaced by beta-D-arabinose"
      Labelling of an oligonucleotide - useful for detecting genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beta-D-arabinose; antisense; inhibition; transcription; expreverse transcription; viral replication; RNase H cleavage;
triple helix formation; ss.
                                                                                                                                                                                                                                                                                                                                                          Score 18; DB 1; Length 18;
Pred. No. 2.6e+02;
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100.0%; Pred. No. ...
0; Mismatches
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                                                   Example 1; Page 7; 10pp; Japanese.
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/*tag=
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modified_base
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A method has been developed for labelling an oligonucleotide having a repeated sequence of (XY)n (where X and Y consists of a combination of adenine and thymine or uracil or guanine and cytosine, and n is an integer of 1 or more ) at the 3'-terminal side in which the repeated sequence is added and extended using a labelled body of the nucleotide constituting the repeated sequence and a DNA polymerase lacked in 5' to 3' exonuclease activity. The method can be used for detecting a gene. The method can detect a gene in a sensitivity up to ten times higher than example from the present invention
                                                                                                           Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Labelling of an oligonucleotide - useful for detecting genes.
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1.0%; Score 18; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 0;
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                                                                    Primer SEQ ID NO:3 from JP11075880.
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                           14-JUN-1999 (first entry)
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               by retroviruses. The compositions are therefore particularly used to inhibit retroviral replication. The oligoarabinonuclectides can also be used, in combination with Rhase H, as reagents for sequence-specific cleavage or RNA mapping, and additionally for the study and control of gene expression in cells. The oligoarabinonuclectides have excellent affinity for RNA, increased resistance to nucleases and show little if any non-specific binding to callular or serum proteins. They target se RNA, but not complementary as DNA, so may be useful for targetting retroviral genomic RNA to inhibit the early stages of viral replication. Oligoarabinonuclectides containing pyrimidine bases form triple helices with significantly higher thermal stability than those produced by normal oligoarabinonuclectides containing beta-57164 represent oligoarabinonuclectides containing beta-57164 represent exemplification of the present invention
   expression or to prevent DNA replication, or reverse transcription of RNA
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                                                                                                                                                                                                                                                                                                                                        Gaps
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/note= "Ribose moiety replaced by beta-D-arabinose"
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modified base
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The invention relates to a new composition for selective, sequence-specific inhibition of gene transcription and expression in a host. The composition comprises oligonucleotides containing arabinose sugars that can hybridise to either a a single-stranded (ss) RNA to induce RNAse H cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple helix, thereby inhibiting DNA replication and/or transcription. The

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expression or to prevent DNA replication, or reverse transcription of RNA by retroviruses. The compositions are therefore particularly used to inhibit retroviral replication. The oligorabinonucleotides can also be used, in combination with RNase H, as reagents for sequence-specific cleavage or RNA mapping, and additionally for the study and control of gene expression in cells. The oligorabinonucleotides have excellent affinity for RNA, increased resistance to nucleases and show little if any non-specific binding to cellular or serum proteins. They target ss RNA, but not complementary ss DNA, so may be useful for targetting retroviral genomic RNA to inhibit the early stages of viral replication. Oligoarabinonucleotides containing pyrimidine bases form triple helices with significantly higher thermal stability than those produced by normal oligoarabinous sequences AZSN160-287164 represent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Therapeutic composition containing antisense oligonucleotides that include arabinose sugars, particularly for inhibiting viral replication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a new composition for selective, sequence-
specific inhibition of gene transcription and expression in a host. The
composition comprises oligonuclectides containing arabinose sugars that
can hybridise to either a a single-stranded (ss) RNA to induce RNase H
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2'-deoxy-2'-fluoro-beta-D-arabinose; antisense; inhibition;
transcription; expression; reverse transcription; viral replication;
RNase H cleavage; triple helix formation; ss.
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/note= "Deoxyribose moiety replaced by 2'-deoxy-2'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arion D;
oligoarabinonucleotides are used for antisense inhibition of gene
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                                                                                                                                                                                                                                                                                                                                            1.0%; Score 18; DB 1; Length 18;
100.0%; Pred. No. 2.6e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                          Sequence 18 BP; 0 A; 0 C; 0 G; 0 T; 18 U; 0 Other;
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                                                                                                                                                                                                                                                                        exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fluoro-beta-D-arabinose"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Deoxyarabinonucleotide SEQ ID NO:7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ87166 standard, DNA, 18 BP
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                                                                                                                                                                                                                                                                                                                                              Query Match 1.0
Best Local Similarity 100.
Matches 18; Conservative
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modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 539
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us10008789-3.rng

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cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple heltx, thereby inhibiting DNA replication and/or transcription. The oligoarabinound-cetides are used for antisense inhibition of gene expression or to prevent DNA replication, or reverse transcription of RNA by retroviruses. The compositions are therefore particularly used to inhibit retroviral replication. The oligoarabinouncleotides can also be used, in combination with RNase H, as reagents for sequence-specific cleavage or RNA mapping, and additionally for the study and control of gene expression in cells. The oligoarabinouncleotides have excellent affinity for RNA, increased nesistance to nucleases and show little if any non-specific binding to cellular or serum proteins. They target is RNA, but not complementary so DNA, so may be useful for targetting retroviral genomic RNA to inhibit the early stages of viral replication. Oligoarabinonucleotides containing pyrimidine bases form triple helices with significantly higher thermal stability than those produced by normal coligoarabinoucleotides. Sequences AAZ87165-Z87169 represent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oligodeoxyarabinonucleotides containing 2'-deoxy-2'fluoro-beta-D-arabinose used in an exemplification of the present invention
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Gaps
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. Match 1.0%; Score 18; DB 1; Length 18; Local Similarity 100.0%; Pred. No. 2.6e+02; les 18; Conservative 0; Mismatches 0; Indels
  Query Match
                                           Matches
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Deoxyarabinonucleotide SEQ ID NO:8. AAZ87167 standard; DNA; 18 08-MAY-2000 (first entry) AAZ87167; RESULT 540 AAZ87167 

transcription, expression, reverse transcription, viral replication, RNase H cleavage, triple helix formation, 88. 2'-deoxy-2'-fluoro-beta-D-arabinose; antisense; inhibition;

Synthetic

/*tag= a
/*tag= a
/note= "Deoxyribose moiety replaced by 2'-deoxy-2'fluoro-beta-D-arabinose" Location/Qualifiers Key modified_base

WO9967378-A1

29-DEC-1999.

99WO-CA000571. 17-JUN-1999; 98CA-02241361. 19-JUN-1998;

(UYMC-) UNIV MCGILL.

Borkow G, Arion D; Noronha AM, Wilds C, Damha MJ, Parniak MA,

27-SEP-2000; 2000WO-US026544. 27-SEP-1999; 99US-0156280P

Rattus norvegicus. WO200123564-A1 Stanton LW, Kapoun AM; WPI; 2001-266159/27.

(SCIO-) SCIOS INC.

WPI; 2000-160584/14.

Therapeutic composition containing antisense oligonucleotides that include arabinose sugars, particularly for inhibiting viral replication.

Example 2; Page 31; 91pp; English.

The invention relates to a new composition for selective, sequence-specific inhibition of gene transcription and expression in a host. The

Novel secreted factor encoded by clone P00108D12 which is differentially expressed in certain disease states, useful in diagnosing and treating cardiac, renal or inflammatory diseases.

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composition comprises oligonucleotides containing arabinose sugars that
can hybridise to either a single-stranded (ss) RNA to induce RNAse H
cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
chalix, thereby inhibiting DNA replication and/or transcription. The
cligoarabinonucleotides are used for antisense inhibition of gene
expression or to prevent DNA replication, or reverse transcription of RNA
cy retroviruses. The compositions are therefore particularly used to
inhibit retroviral replication. The oligoarabinonucleotides can also be
used, in combination with RNAse H, as reagente for sequence specific
cleavage or RNA mapping, and additionally for the study and control of
gene expression in cells. The oligoarabinoucleotides have excellent
cany non-specific binding to cellular or serum proteins. They target ss
RNA, but not complementary ss DNA, so may be useful for targetting
cretroviral genomic RNA to inhibit the early seages of viral replication.
Oligoarabinonucleotides containing pyrimidine bases form triple helices
with significantly higher thermal stability than those produced by normal
coligodeoxyarabinonucleotides containing 2-deoxy-2-fluoro-beta-D-
coligoarabinonucleotides containing 2-deoxy-2-fluoro-beta-D-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide #6 used for the preparation of normalised cDNA libraries.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat; secreted factor; clone P00188_D12; cardiant; antiinflammatory;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.0%; Score 18; DB 1; Length 18;
.00.0%; Pred. No. 2.6e+02;
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Local Similarity 100.0%; Pred. NO. ...
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18; Conservative
                                                                                      Best Local Similarity
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                                                                                                                                                          Unidentified
                                                                                                                                                                    misc_feature
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1.0%; Score 18; DB 1; Length 18; 100.0%; Pred. No. 2.6e+02; ive 0; Mismatches 0; Indels

Scaffold protein; antibody mimic; fibronectin type III domain; randomised loop; randomised beta-sheet; diagnostic purpose; protein designing; ss. /*tag= a /note= "Linked to (PEG)2CCPuromycin" Location/Qualifiers 1736 AAAAAAAAAAAAAA 1753 Oligonucleotide A18-2PEG linker. 18 ААААААААААААА 1 AAD17014 standard; DNA; 18 BP. 28-FEB-2001; 2001WO-US006414. 29-FEB-2000; 2000US-00515260 29-NOV-2001 (first entry) (PHYL-) PHYLOS INC. 07-SEP-2001 

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The present invention relates to an array of proteins (antibody mimics) comprising a fibronectin type III domain having a randomised loop, a randomised beta-sheet, or their combination, and has the capacity to bind to a compound that is not bound by a corresponding naturally-occurring fibronectin, immobilised onto a solid support. The antibody mimics is useful for detecting a compound preferably a protein, in a biological sample. It is also useful to detect one or more different analytes simultaneously in a sample. Hence is useful for diagnostic purposes. It is also useful for the purpose of designing proteins capable of to virtually any compound of interest. The present sequence is an oligonucleotide Al8-2PEG linker used in an exemplification of the
having a randomized loop, a randomized beta-sheet or their combination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.0%; Score 18; DB 1; Length 18;
100.0%; Pred. No. 2.6e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                          Disclosure, Page 25; 67pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1736 AAAAAAAAAAAAAAAA 1753
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Best Local Similarity 100.
Matches 18; Conservative
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#XXXCCCCCCCCCXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                             disease states accreted factor is differentially expressed in certain disease states. Secreted protein, its antibodies, antagonists or compositions comprising them are useful in the diagnosis and treatment of cardiac diseases such as congestive heart failure, myocarditis, cardiac diseases such as congestive heart failure, myocarditis, cardiac arrhythmia, arteriosclerosis, kidney diseases such as acute renal cardiac arrhythmia, arteriosclerosis, kidney diseases such as acute renal failure, renal glucosuria, renal infarction, nephrogenic diabetes calmingue, polycystic failure, nead infarction, nephrogenic diabetes inflammatory diseases such as asthma, autoimmune diabetes, tumour anglogenesis, rheumatoid arthritis, osteoarthritis, toxic shock syndrome, asthma, stroke, neural trauma, psoriasis, cerebral malaria, osteoporosis, crohn's disease, ulcerative colitis, Alzheimer; disease. Secreted protein DNA is useful in antisense-mediated gene inhibition and in gene therapy. An array comprising one or more oligonuclectides complementary to reference RNA or DNA encoding the secreted factor is useful for detecting cardiac, kidney and inflammatory disease. The present DNA containing secreted factor by preparation of a normalised cDNA library containing secreted factor DNAs. The normalised cDNA libraries are used in the identification of differentially expressed con at secreted factor bNAs. The normalised cDNA libraries are used in the identification of differentially expressed con at secreted factor bNAs. The normalised cDNA libraries are used in the identification of differentially expressed con a secreted factor bNAs. The normalised cDNA libraries are used in the identification of differentially expressed con a secreted factor bNAs.
                                                                                                                            patent discloses novel secreted factor protein encoded by clone
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                                 Example 1; Page 42; 71pp; English.
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Gaps ö

> ry encoded sequence tag; BEST; nucleic acid analysis; expression; adaptor; PCR primer; 88. Binary encoded sequence tag method anchored primer #2. BP. 11-AUG-2000; 2000WO-US022164. 99US-0148870P 06-APR-2000; 2000US-00544713 AAF75597 standard; DNA; 18 (first entry) Binary encoded WO200112855-A2. 13-AUG-1999; 10-MAY-2001 22-FEB-2001. Synthetic. AAF75597; RESULT 543 AAF75597/c gene

The present invention describes a method of producing binary sequence tags from nucleic acid fragments in a sample, involving incubating the sample with cleaving reagents, mixing offset adaptors with the sample, incubating with more cleaving reagents and mixing the sample with adaptor—indexers where the adaptors are coupled to binary sequence tags. The method is useful in sequence analysis, including analysis and comparison of gene expression, nucleic acid samples and genomes Producing binary sequence tags, useful for analyzing nucleic acid sequence tags, gene expression or gene-expression patterns, involves generating nucleic acid fragments, which are mixed with offset adaptors Feng L, Latimer DR; Disclosure; Page 100; 101pp; English Lizardi PM, Roth ME, and adaptor-indexers. WPI; 2001-202878/20 Kaufman JC, 

Fibronectin scaffold protein array for obtaining a protein/compound which binds to a compound/protein, comprises a fibronectin type III domain

Kuimelis RG;

Lipovsek D, Wagner RW, WPI; 2001-557782/62.

(UYYA ) UNIV YALE.

BP

(first entry)

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18 AAAAAAAAAAAAAA 1
                                                                 AAF99734 standard; DNA; 18
                                                                                                                    12-JUN-2001
                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Krieg AM,
                                                                                           AAF99734;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to waccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae haemophilus, campylobacter, closeridium, Becherichia coli and/or staphylococus), fungal antigens and/or parastitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or fimmune deficiency. The present sequence can also be used to redirect a Th2 to a Th1 immune response and to activate immune cells. Note: the present sequence may have a phosphorothioate backbone
                                                                                                                                                                                                                                                                            Vaccine, cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic; immunostimulatory; tumour; viral infection; bacterial infection; fungal infection; parasitic infection; cancer; asthma; infectious disease; allergy; immune deficiency; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.
                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.0%; Score 18; DB 1; Length 18; Best Local Similarity 100.0%; Pred. No. 2.6e+02; Matches 18; Conservative 0; Mismatches 0; Indels
                          Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
Sequence 18 BP; 0 A; 0 C; 1 G; 17 T; 0 U; 0 Other;
                         Query Match
1.0%; Score 18; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                      Immunostimulatory nucleic acid #824.
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                                                                             1734 ACAAAAAAAAAAAAAA 1751
                                                                                                      18 ACAAAAAAAAAAAAA 1
                                                                                                                                                                        AAF99708 standard; DNA; 18 BP
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27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
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                                                                                                                                                                                                                           12-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Krieg AM, Schetter C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-273485/28.
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                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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                                                                                                                                             RESULT 544
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The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (r) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, hemophilus, campylobacter, clostridium, Escherichia coll and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a final to a Thl immune response and to activate immune cells. Note: the present sequence may have a phosphorothioate backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                  Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic; immunostimulatory; tumour; viral infection; bacterial infection; fungal infection; parasitic infection; cancer; asthms; infections disease; allergy; immune deficiency; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaccinating against tumors, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match
Local Similarity 100.0%; Pred. NO. 4...
Immunostimulatory nucleic acid #850.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 101; Page 56; 338pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vollmer J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1736 AAAAAAAAAAAAAAAA 1753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-SEP-1999; 99US-0156113P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-SEP-2000; 2000WO-US026383
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(COLE-) COLEY PHARM GMBH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schetter C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-273485/28
                                                                                                                                                                                                                                                                                                                          WO200122972-A2.
                                                                                                                                                                                                                                                                                                                                                                                            05-APR-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db

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RESULT 546

AAF82472/c
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Gaps . 0

1736 AAAAAAAAAAAAAAA 1753 |||||||||||||||||

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RESULT 548
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                                                                                                                                                                                                                                                                                                                                                                                          The present sequence corresponds to polylinker DNA of the phagemid vector pDCR2.1. It was used in the construction of a normalised rat cDNA library, which was used in an example demonstrating differential expression of a rat gene referred to as clone PD0210D09. The invention relates to a polypoptide comprising a sequence of at least 80% identity to residues 22 122 of the present sequence, or a sequence encoded by a nucleic acid hybridising under stringent conditions to the complement of the coding region comprising 1031 nucleotides, and having at least one biological sectivity of the polypoptide encoded by clone PD021009. The polypoptide and polynucleotides of the invention are useful for the treatment of cardiac, renal and inflammatory diseases. The polynucleotides are useful in antisense mediated gene inhibition and in gene therapy. The polypoptide are useful in assays for identifying lead compounds that may be used as therapeutic agents in the treatment of cardiac, kidney or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat, secreted factor polypeptide, cardiac disease, renal disease; kidney, inflammatory disease, congestive heart failure, myocarditis, aathma; 8s; dilated congestive cardiomyopathy, angina pectoris, cardiac arrhythmia; myocardial infarction; pulmonary hypertension; arteriosclerosis; stroke; atherosclerosis; cardiac tumour; glomerulonephritis; nephrotic syndrome;
                                                                                                                                                                                                                                                                                                                    Novel secreted factor encoded by clone P00210D09 useful for diagnosing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                            Phagemid vector; pCR2.1; rat; secreted factor; P00210D09; cardiant; nephrotropic; antiinflammatory; gene therapy; cardiac disease; renal disease; inflammatory disease; polylinker; ss.
                                                                                                                                                                                                                                                                                                                                and/or preventing various cardiac, renal and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.0%; Score 18; DB 1; Length 18;
100.0%; Pred. No. 2.6e+02;
ive 0; Mismatches 0; Indels
                                    Phagemid vector pCR2.1 polylinker oligonucleotide #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                factor DNA oligonucleotide probe #6.
                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 41; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1736 AAAAAAAAAAAAAAA 1753
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                                                                                                                                                                                        27-SEP-2000; 2000WO-US026582.
                                                                                                                                                                                                                   99US-0156277P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS94743 standard; DNA; 18
             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18; Conservative
                                                                                                                                                                                                                                                                  Stanton LW, Kapoun AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammatory diseases
                                                                                                                                                                                                                                                                                            WPI; 2001-328177/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                            (SCIO-) SCIOS INC.
                                                                                                                                       WO200123419-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat secreted
                                                                                                                                                                                                                   27-SEP-1999;
                                                                                                                                                                05-APR-2001.
             29-JUN-2001
                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS94743;
                                                                                                                                                                                                                                                                                                                                   treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                               diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anglogenesis inhibitor; ss; anglogenesis; solid tumour growth; tumour metastaais; precancerous lesion; rheumatorid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasis; rubeosis; osler-wbbber Syndrome; mycoardial anglogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; anglofibroma; wound granulation; intestinal adhesion; atherosclerosis;
                                 chronic renal failure; renal vein thrombosis; medullary sponge kidney; rheumatoid arthritis; osteoarthritis; psoriasis; restenosis; PCR primer; graft versus host reaction; Crohn's disease; ulcerative colitis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel secreted factor polypeptide useful for treating cardiac diseases such as arteriosclerosis, myocardial infarction, inflammatory diseases such as asthma, stroke, and rheumatoid arthritis and renal diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
renal infarction; hereditary nephritis; polycystic kidney disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.0%; Score 18; DB 1; I
100.0%; Pred. No. 2.6e+02;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 51; 189pp; English
                                                                                                                                                             Alzheimer's disease; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1736 AAAAAAAAAAAAAAA 1753
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ABS78455 standard; DNA; 18 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000; 2000US-0193548P.
14-MAR-2001; 2001US-00809545.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-2001; 2001WO-US009555.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stanton LW, White RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-010779/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SCIO-) SCIOS INC
                                                                                                                                                                                                                                                                                                                       WO200174901-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                      11-OCT-2001
                                                                                                                                                                                                                                            Synthetic.
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Best Local S
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tumour metastasis, precancerous lesion; rheumatoid arthritis, psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rubeosis; Osler-Webber Syndrome; myocārdial angiogenesis;
plaque neovascularisation; telangiectasia; haemophiliac joint;
angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
scleroderma; hypertrophic scar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Angiogenesis inhibitory oligonucleotide #913.
                                                                                                                                                                                                                    Claim 2; Page 36; 276pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1736 AAAAAAAAAAAAAAAA 1753
scleroderma; hypertrophic scar
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.0%; i
Best Local Similarity 100.0%;
Matches 18; Conservative 0
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                                                                                                                         (COLE-) COLEY PHARM GROUP INC
                                                                                                    14-DEC-2000; 2000US-0255534P.
                                                                                14-DEC-2001; 2001WO-US048458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           429/c
ABS78429 standard; DNA; 18
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                                                                                                                                                                                                                                                                                                                                                                           acid of the invention
                                                                                                                                                                 WPI; 2002-566690/60.
                                        40200253141-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200253141-A2
                                                                                                                                             Bratzler RL;
                                                            11-JUL-2002
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                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABS78429;
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The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antiangiogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, hemophiliac joints, angiofibroma, hypertrophic scars. The present sequence is an antiangiogenic nucleic
                                                                                                                                                                                                                             Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibody-induced cell lysis; cancer; immunostimulatory; CD20; angiogenesis; metastasis; cytostatic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.0%; Score 18; DB 1; Length 18;
100.0%; Pred. No. 2.6e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunostimulatory nucleic acid SEQ ID NO: 837.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                          Claim 2; Page 35; 276pp; English
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      \frac{\dot{z}_{i}^{\dagger}}{14}-DEC-2001; 2001WO-US048458.
                                                                                                    COLE-) COLEY PHARM GROUP INC
                                                             14-DEC-2000; 2000US-0255534P.
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ID ABL39401 standard; DNA; 18
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Best Local Similarity 100.0
Matches 18, Conservative
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/*tag=
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                                                                                                                                                                                     WPI; 2002-566690/60.
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modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-APR-2002
                                                                                                                                              Bratzler RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3ynthetic.
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XBXBXBXBXLLTTTTXSXXBXEXBXCXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   administering at least one antianglogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antianglogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metestasis, precancerous lesion, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of premutity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, tesanilation, intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. The present sequence is an antianglogenic nucleic
                                                                                                                                                                                                                                                                                                                                                                           Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to inhibiting angiogenesis in a subject, comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 18; DB 1; Length 18; Pred. No. 2.6e+02; 0; Mismatches 0; Indels
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Gaps

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/note= "phosphorothioate backbone"

WO200197843-A2

27-DEC-2001

22-JUN-2000; 2000US-0213346P 22-JUN-2001; 2001WO-US020154

(IOWA ) UNIV IOWA RES FOUND.

Hartmann G;

Weiner G,

Example 5; Page 37; 87pp; English.

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WPI; 2002-154611/20
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                                                                                                                                                                                                     developing
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Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies to a subject having or at risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Apoptosis; ion channel modulator; hyperproliferative disease; tumour; therapy; leukaemia; carcinoma; sarcoma; degenerative disease; melanoma; Alzheimer's disease; parkinson's disease; arteriosclerosis; heart disease; stroke; vascular disease; nootropic; neuroprotective; cerebroprotective; cardiant; cytotoxic protein; cyplasin L; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.0%; Score 18; DB 1; Length 18;
100.0%; Pred. No. 2.6e+02;
rative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                         Disclosure, Page 308; 312pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exemplification of the invention
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protein, factors for generating or detoxifying reactive oxygen species (ROS) and factors for plocking and/or by-passing of caspases. They are useful for tumour therapy. Cytocoxic proteins of the invention are useful for destroying tumours and/or selectively killing cells in tissues, for identifying novel targets for the development of pharmaceutical agents, preferably anti-tumour agents and as specific ion channel modulators, c.g., blockers or openers for therapy, diagnostic or research. They are useful for the diagnosis and therapy of hyperproliferative diseases, preferably tumours, e.g., leukaemia, carcinoma, sarcoma and melanoma. They are also useful for development of drugs for the treatment of degenerative diseases such as Alzaheimer's disease, Parkinson's disease, arteriosclerosis, heart diseases, stroke and vascular diseases. The present sequence is an oligonucleotide which is used for amplifying sea have cyplasin L DNA. This sequence is used in the exemplification of the invention
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                             The present invention relates to novel polypeptides having cytotoxic activity obtainable from sea hare Aplysia. Sequences of the invention are useful for the manufacture of cytotoxic agents against apoptosis, resistant cells, where the agents are useful for diagnosis, prevention, treatment of disorders associated with dysfunctions of GAP-SH3 binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Increasing efficiency of second strand cDNA synthesis using terminal continuation model before performing further RNA amplification by RNA transcription.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.0%; Score 18; DB 1; Length 18;
100.0%; Pred. No. 2.6e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
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14-FEB-2001; 2001US-0268664P.
18-JUL-2001; 2001US-0306216P.
07-NOV-2001; 2001US-034854P.
07-NOV-2001; 2001US-0348242P.
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1es 18; Conservative
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The present invention describes a method for the comparative detection of the amount of an RNA. The method comprises: (a) cDNAs obtained by transcribing respectively from at least two tissue RNAs are respectively from at least two tissue RNAs are respectively from at least two tissue RNAs are respectively.

I transcribing respectively from at least two tissue RNAs are respectively and a common adaptor are added to each of the cDNA fragments derived from the same or different tissues by the step (a); (c) the resultant adaptor-added cDNAs are mixed together; (d) an adaptor primer having the common sequence to said different adaptor and a gene-specific adaptor are used to amplify said adaptor-added cDNAs containing no region derived from c polyadenylic acid of the mRNA before the addition of the adaptor among the adaptor-added cDNAs prepared by the step (b); (e) the ratios of the cDNA amounts are measured between the tissues; (f) the RNA is detected from the measured result; (g) each different adaptor and a common adaptor are added to each of the genomic DNA fragments derived from a same or different individuals; (n) the resultant adaptor-added genomic DNAs are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Comparative detection of the amounts of RNA and DNA
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Example 7; Page 80; 128pp; English.
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18; Conservative
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Best Local (
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The invention relates to an acyclic linker-containing oligonucleotide comprising at least one modified deoxyribonucleotide. Oligonucleotides of the invention are useful for preventing or decreasing translation, reverse transcription and/or replication of a target RNA in a system. They are useful for selectively preventing gene expression in a sequence-specific manner, for hybridising to complementary RNA such as cellular mRNA or viral RNA, to hybridise to and induce cleavage of complementary RNA. They are also useful therapeutically in formulations or medicaments
mixed together; (i) the adaptor-added genomic DNAs are amplified by using an adaptor primer having the common sequence to the different adaptor and a sequence-specific adaptor; and (j) the ratios of the amplified amounts of the genomic DNAs are measured between the individuals. The method is used for the detection of the amounts of RNA and DNA. The present sequence represents an oligonucleotide which is used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Target RNA #1 used in the exemplification of the invention.
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                                                                                                                                                                                   Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                     Query Match
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                                               This invention relates to a novel method for increasing the efficiency of second strand cDNA synthesis through a mechanism of terminal continuation. In the method an RNA molecule is obtained and a first primer is added that comprises a region that hybridises to a complementary region of the molecule before a second primer is added comprising at least one riboguanine at the 3' end of the primer. A first complementary nucleic acid molecule is synthesised, the RNA molecule and second primer are removed and a second complementary nucleic acid molecule is synthesised to form a second hybrid with an extension product of the third primer bound to the first complementary molecule. The method of the invention is useful for increasing the efficiency of second strand cDNA synthesis and may be used for linear amplification of genetic signals from histologically stained issue. The present sequence represents a poly d(T) PCR primer used in the method of the invention
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Pred. No. 2.6e+02;
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100.0%; Pred. No. a...
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ö Ouery Match 1.0%; Score 18; DB 1; Length 18; Sest Local Similarity 100.0%; Pred. No. 2.6e+02; Matches 18; Conservative 0; Mismatches 0; Indels 1736 AAAAAAAAAAAAAAA 1753

Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

to prevent or treat a disease characterised by the expression of a particular target RNA. The invention is used in gene therapy. The present sequence is a target RNA, used in the exemplification of the invention

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Gaps

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Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an acyclic linker-containing oligonucleotide comprising at least one modified deoxyribonucleotide. Oligonucleotides of the invention are useful for preventing or decreasing translation, reverse transcription and/or replication of a target RNA in a system. They are useful for selectively preventing gene expression in a sequencement of the phybridising to complementary RNA such as cellular mRNA or viral RNA, to hybridise to and induce cleavage of complementary RNA. They are also useful therapeutically in formulations or medicaments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to prevent or treat a disease characterised by the expression of a particular targer RNA. The invention is used in gene therapy. The present sequence is an antisense oligo used to elicit human RNase (ribonuclease) H degradation of target RNA. This sequence is used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel acyclic linker-containing oligonucleotide useful for preventing or decreasing translation, reverse transcription and/or replication of a target RNA in a system, comprises a modified deoxyribonucleotide.
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                                                                                                                                                                                                                                                                                              Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                  Antisense oligo #1, to elicit RNase H degradation of target RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.0%; Score 18; DB 1; Length 18;
100.0%; Pred. No. 2.6e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Fig 9; 104pp; English
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    AAAAAAAAAAAAAA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-OCT-2002; 2002WO-CA001628.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-OCT-2001; 2001US-0330719P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD56446 standard; DNA; 18
                                                                                                               AADS6440 standard; DNA; 18
                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viazovkina E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
1es 18; Conservative
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                                                                                                                                                                                                                                                                                                                     antisense; ss
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                                                                                                                                                                                                                                                                                                                                                             Unidentified
                                                                                                                                                                                                   07-AUG-2003
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                                                                                                                                                         AAD56440;
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                                                                                   AMDS 440/0/10 AM
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AC AAD5

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The invention relates to an acyclic linker-containing oligonucleotide comprising at least one modified deoxyribonucleotide. Oligonucleotides of the invention are useful for preventing or decreasing translation, reverse transcription and/or replication of a target RNA in a system. They are useful for selectively preventing gene expression in a sequence-specific manner, for hybridising to complementary RNA such as cellular mRNA or viral RNA, to hybridise to and induce cleavage of complementary RNA. They are also useful therapeutically in formulations or medicaments to prevent or treat a disease characterised by the expression of a particular target RNA. The invention is used in gene therapy. The present sequence is an antisense oligo used to elicit human RNase (ribonuclasse) H degradation of target RNA. This sequence is used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel acyclic linker-containing oligonucleotide useful for preventing decreasing translation, reverse transcription and/or replication of a target RNA in a system, comprises a modified deoxyribonucleotide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                           /note= "2'-deoxy-2'-fluoroarabinothymidine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      콗
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.0%; Score 18; DB 1; Length 18;
100.0%; Pred. No. 2.6e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parniak MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mangos MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunostimulatory nucleic acid #882.
                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Fig 7; 104pp; English.
                                                                                                                                                                                                          base= OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-OCT-2002; 2002WO-CA001628.
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                                                                                                                                                                    ...18
*tag= a
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nes 18; Conservative
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                                                                                                                                                                                                                                                                                                                                 WO2003037909-A1
antisense; ss.
                                                                                                                             Key
modified base
                                                           Unidentified
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The present invention relates to a new oligonucleoside which comprises at alternating first and second segments. The first segment comprises at least one 8 ugar modified nucleoside. The second segment comprises at least one 2 -deoxynucleoside. The oligonucleoside comprises at least 2 cach of the first and second segments, so that it comprises at least 4 alternating segments. The oligonucleoside comprises at least 4 capternating segments. The oligonucleoside clavage of a target RNA in a system, preventing or decreasing translation, transcription or system, preventing or decreasing translation, transcription or target RNA in a system, as system, detecting the presence of a target RNA in a system, validating a gene target corresponding to a target RNA in a system, or preventing or treating a disease related to a target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS) or hepatitis B. The invention is useful in gene therapy. The present sequence is an antisense oligonucleotide used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antisense DNA-RNA hybrid #2 used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS; hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;
                                                                                                                                                                                                                                                                                                                                                                                                                  1.0%; Score 18; DB 1; Length 18;
100.0%; Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                             Seguence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
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/label= RNA
/note= "2'-O-methyl-D-uridine"
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/label= RNA
/note= "2'-O-methyl-D-uridine"
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|label= RNA
'note= "2'-O-methyl-D-uridine'
                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Preα. ...
tive 0; Mismatches
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  Example 2; Page 35; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1736 AAAAAAAAAAAAAAAA 1753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 AAAAAAAAAAAAAA 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                      the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD57878;
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc RNA
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AAD57878/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic contect dermatisi, latex dermatitis or inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease. This sequence represents an immunostimulatory nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS; hepatitis B; gene therapy; virucide; anti-HIV; antisense; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                          Treating non-allergic inflammatory diseases, such as psoriasis, ecze allergic contact dermatitis, latex dermatitis or inflammatory bowel disease by administering an immunostimulatory nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antisense oligo #1 used in the exemplification of the invention.
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Pred. No. 2.6e+02;
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100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                        29-MAR-2001; 2001US-0279642P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-NOV-2003 (first entry)
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Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                    WPI; 2003-521815/49
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                                                                                                                                                                                                                           Krieg AM, Berg DJ;
                                                                                                                                                             (KRIE/) KRIEG A M. (BERG/) BERG D J.
US2003050268-A1
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                                        13-MAR-2003
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RESULT 558 AAD57871/c

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                                                                                                                                                                                                                                                                                                                                                  RESULT 561
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                                                   The present invention relates to a new oligonucleoside which comprises at least one sugar modified nucleoside. The first segment comprises at least one agar modified nucleoside. The second segment comprises at least one 2 -deoxynucleoside. The oligonucleoside comprises at least 2 of each of the first and second segments, so that it comprises at least 4 alternating segments. The oligonucleotide is useful for preparing a composition for inducing RNAse H-mediated cleavage of a target RNA in a system, preventing or decreasing translation, transcription or resplication of a target RNA in a system, detecting the presence of a target RNA in a system, validating a gene target corresponding to a target RNA in a system or preventing or treating a disease related to a target RNA in a system or preventing or treating a disease related to a target RNA in a system or preventing or treating a disease related to a target RNA in a system is useful in gene therespy. The present or hepatitis B. The invention is useful in gene therapy. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS; hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense DNA-RNA hybrid #3 used in the exemplification of the invention.
New oligonucleotide, useful for preventing or treating a disease related to a target RNA in a system, e.g., AIDS or hepatitis B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New oligonucleotide, useful for preventing or treating a disease related
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                                                                                                                                                                                                                                                             Length 18;
                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                      Sequence 18 BP; 0 A; 0 C; 0 G; 9 T; 9 U; 0 Other;
                                                                                                                                                                                                                                                          Score 18; DB 1; Le
Pred. No. 2.6e+02;
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|label= RNA
|note= "2'-O-methyl-D-uridine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *tag= b
|abel= RNA
|note= "2'-O-methyl-D-uridine"
                                                                                                                                                                                                                                                / Match 1.0%; Score 18; ub. Local Similarity 100.0%; Pred. No. 2.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             location/Qualifiers
                                Example 2; Page 35; 73pp; English
                                                                                                                                                                                                                                                                                                       1736 AAAAAAAAAAAAAAA 1753
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                                                                                                                                                                                                                                                                                                                                                                            879/c
AAD57879 standard; DNA; 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Damha MJ, Parniak MA;
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                                                                                                                                                                                                                  the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                         AAD57879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
misc_RNA
                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                 The present invention relates to a new oligonucleoside which comprises allerating first and second segments. The first segment comprises at least one sugar modified nucleoside. The second segment comprises at least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 each of the first and second segments, so that it comprises at least 4 alternating segments. The oligonucleoside is useful for preparing a composition for inducing Names H-mediated cleavage of a target RNA in a system, preventing or decreasing translation, transcription or replication of a target RNA in a system, detecting the presence of a target RNA in a system, validating a gene target corresponding to a target RNA in a system or preventing or treating a disease related to a target RNA in a system or preventing or treating a disease related to a target RNA in a system or preventing in gene target corresponding to a target RNA in a system or preventing or treating a disease related to a target RNA in a system, each is a section of exequence is an antisense DNA-RNA hybrid used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS; hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antisense DNA-RNA hybrid #1 used in the exemplification of the invention.
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100.0%; Pred. No. 2.6e+02;
iive 0; Mismatches 0; Indels
to a target RNA in a system, e.g., AIDS or hepatitis B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18 BP; 0 A; 0 C; 0 G; 6 T; 12 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/label= RNA
/note= "2'-0-methyl-D-uridine"
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|label= RNA
'note= "2'-O-methyl-D-uridine"
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|label= RNA
'note= "2'-O-methyl-D-uridine"
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|abel= RNA
'note= "2'-O-methyl-D-uridine'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  location/Qualifiers
                                                                        Example 2; Page 35; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1736 AAAAAAAAAAAAAAA 1753
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ID AAD57877 standard; DNA; 18 BP.
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/label= RNA
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label= RNA
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ses 18; Conservative
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misc_RNA

misc_RNA

07-AUG-2003

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WO2003064441-A2
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                                        07-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a new oligonucleoside which comprises at least one sugar modified nucleoside. The first segment comprises at least one by an addition of the first segment comprises at least one 2 deoxymucleoside. The second segment comprises at least 2 deach of the first and second segments, so that it comprises at least 4 alternating segments. The oligonucleotide is useful for preparing a composition for inducing RNses H-mediated cleavage of a target RNA in a system, preventing or decreasing translation, transcription or replication of a target RNA in a system, validating a gene target corresponding to a target RNA in a system, validating a gene target corresponding to a target RNA in a system, e.g., acquired immune deficiency syndrome (ADS) or hepatitis B. The invention is useful in gene therapy. The present sequence is an antisense DNA-RNA hybrid used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New oligonucleotide, useful for preventing or treating a disease related to a target RNA in a system, e.g., AIDS or hepatitis B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS; hepatitis B; gene therapy; virucide; anti-HIV; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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100.0%; Pred. No. 2.6e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 BP; 0 A; 0 C; 0 G; 9 T; 9 U; 0 Other;
    /*tag= g
/label= RNA
/note= "2'-O-methyl-D-uridine"
                                                                                                              /note= "2'-0-methyl-D-uridine"
                                                                                                                                                                                             /note= "2'-0-methyl-D-uridine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Target RNA #1 used in RNase H assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 35; 73pp; English
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/label= RNA
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                                                                              /*tag= h
/label= RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Damha MJ, Parniak MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-689523/65.
                                                                                                                                                                                                                                                                                                                                                                                          (UYMC-) UNIV MCGILL.
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Matches 18; Conserv
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Unidentified

AAD57890;

**Ouery Match** 

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The present invention relates to a new oligonucleoside which comprises at alternating first and second segments. The first segment comprises at least one sugar modified nucleoside. The second segment comprises at least 2 of least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of each of the first and second segments, so that it comprises at least 4 composition for inducing RNase H-mediated cleavage of a target RNA in a system, preventing or decreasing translation, transcription or creptication of a target RNA in a system, detecting the presence of a target RNA in a system or preventing or treating a disease related to a carget RNA in a system or preventing or treating a disease related to a target RNA in a system, e.g., acquired immune deficiency syndrome (ADS) or hepatitis B. The invention is useful in gene therapy. The present
                                                                                                                                                                                                                         New oligonucleotide, useful for preventing or treating a disease related to a target RNA in a system, e.g., AIDS or hepatitis B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ds; allergy; asthma; poly-G nucleic acid; aerosol formulation; hypo-responsive subject; immunostimulatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.0%; Score 18; DB 1; Length 18; 100.0%; Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
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Local Similarity 100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the exemplification of the invention
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                                                                                                                                                                                                                                                                                                Example 4; Page 38; 73pp; English
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31-JAN-2003; 2003WO-CA000129
                                            01-FEB-2002; 2002US-0352873P
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                                                                                                                                      Jamha MJ, Parniak MA;
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PETERSEN D M
FOURON Y.
                                                                                                                                                                                 PI; 2003-689523/65
                                                                                         (UYMC-) UNIV MCGILL
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(PETE/)
(FOUR/)
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Pred. No. 2.6e+02;

Best Local Similarity

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The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G nucleic acid in an ascrosol formulation. The methods and compositions of the present invention are useful for diagnosing and/or treating asthma and allergy especially in a hypo-responsive subject. The present sequence represents an immunostimulatory nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G nucleic acid in an aerosol formulation. The methods and compositions of the present invention are useful for diagnosing and/or treating asthma and allergy especially in a hypo-responsive subject. The present sequence represents
                                                                    Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ds; allergy; asthma; poly-G nucleic acid; aerosol formulation; hypo-responsive subject; immunostimulatory.
                                                                                                                                                                                                                                                                                                           1.0%; Score 18; DB 1; Length 18;
100.0%; Pred. No. 2.6e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                             Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        an immunostimulatory nucleic acid of the invention
   Fouron Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bratzler RL, Petersen DM, Fouron Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Page 18; 221pp; English.
                                                                                                                        Disclosure; Page 17; 221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunostimulatory nucleic acid #850.
                                                                                                                                                                                                                                                                                                                                                                                   1736 AAAAAAAAAAAAAAA 1753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-FEB-2000; 2000US-0179991P.
 Petersen DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADB37236 standard; DNA; 18
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Matches 18; Conservative
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(PETE/) PETERSEN D M.
(FOUR/) FOURON Y.
                                   WPI; 2003-657977/62
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 Bratzler RL,
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                                                                                                                                                                                                                                                                                                               Query Match
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1.0%; Score 18; DB 1; Length 18;

Query Match

Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

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Gaps ;

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This invention relates to a novel method for the concurrent interrogation of a number of polymorphic sites in the presence of, and without interference from, non-designated polymorphic sites. Specifically, it comprises conducting a multiplexed elongation assay by applying one or comprises conducting a multiplexed elongation assay by applying one or more temperature cycles to achieve linear amplification of the target or a combination of annealing and elongation steps under temperature.

CC a combination of annealing and elongation steps under temperature-cc controlled conditions. Furthermore, this detection method uses probe extension or elongation and relies on enzymatic recognition, a superior cc technique that no longer depends on differential hybridisation. The present invention describes probes and methods useful for identifying or detecting polymorphisms at one or more designated sites, such that they can identify mutations within the cystic fibrosis conductance transmembrane regulator (GFTR) or the human leukocyte enrigen (HLA) genes. In addition, concurrent interrogation of a multiplicity of genetic profiling, and identity testing. This genotyping or genetic profiling, and identity testing. This concurrent interval probe used for the elongation in mediated multiplexed analysis of HLA-DR, in an exemplification of the
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                                                                                                                                                                                                                                                                                                                                                        probe; ss; negative control; CFTR; human leukocyte antigen; HLA; genetic testing; carrier screening; genotyping; profiling; polymorphic; multiplexed elongation assay; enzymatic recognition; cystic fibrosis conductance transmembrane regulator.
                                                                                                                                                                                                                                                                                                                   Human probe NEG for elongation mediated multiplexed analysis of HLA-DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Concurrent interrogation of a number of polymorphic sites, useful for genetic testing, carrier screening, genetic profiling, and identity testing, comprises conducting a multiplexed elongation assay using
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                      Indels
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                  0; Mismatches
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                                                         1736 AAAAAAAAAAAAAAAA 1753
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                                                                                                 18 AAAAAAAAAAAAAA 1
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100.08;
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15-OCT-2001; 2001US-0329428P.
15-OCT-2001; 2001US-0329619P.
15-OCT-2001; 2001US-0329620P.
14-MAR-2002; 2002US-0364416P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-OCT-2002; 2002WO-US033012.
                                                                                                                                                                                                  ADE77617 standard; DNA; 18
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                                                                                                                                                                                                                                                                                (first entry)
                    18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003034029-A2.
                                                                                                                                                                                                                                                                                29-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
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                  Matches
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us10008789-3.rng

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A method for the analysis of cDNA comprises (a) preparing an aggregate of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18; DB 1; Length 19;
Pred. No. 2.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 5; 11pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aggregate; restriction enzyme; ss
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                                                                                              JP06303997-A.
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                                         Synthetic.
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of
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                                                                        Gaps
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Pred. No. 2.8e+02;
                          Length 18;
                                                                      Indels
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Score 18; DB 1; Ler
Pred. No. 2.6e+02;
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       1.0%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Analysis; gene expression; reverse
aggregate; restriction enzyme; ss
                                                                                                                    1736 AAAAAAAAAAAAAA 1753
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                                                                      Conservative
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Best Local Similarity
                                                Similarity
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                                                                      18;
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includes an extendable terminus, under conditions where hybrids form; (c) treating any hybrids formed with a non-remplate dependent chain elongating enzyme and its substrates, where any hybridised probe is extended. The method is useful for identifying and detecting nucleic acids, particularly DNA hybridisation probes. The present sequence represents a tailing reaction exemplary primer, which is used in an example from the present invention
     hybridising the treated molecules with a nucleic acid probe that
                                                                                                                                                                                                                                                                         1.0%; Score 18; DB 1; Length 19;
100.0%; Pred. No. 2.8e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                             Seguence 19 BP; 18 A; 0 C; 0 G; 0 T; 1 U; 0 Other;
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Matches 18; Conservative
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Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ISIS-) ISIS PHARM INC.
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modified_base
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double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying and detecting nucleic acids, particularly DNA hybridization probes, involves employing chain extending enzymes (e.g. telomerase) to elongate probes to render them readily detectable.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a method for detecting a nucleic acid
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100.0%; Pred. No. 2.88+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                   Sequence 19 BP; 0 A; 0 C; 2 G; 17 T; 0 U; 0 Other;
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25-MAY-2000; 2000US-00580358.
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                                                                                                                                                                                                                                                                              Local Similarity
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100.0%; Pred. No. 2.8e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                       Synthetic nuclease-resistant oligomeric compound #54.
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/mod base= OTHER
1 AAAAAAAAAAAAAAA 18
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28-NOV-2001; 2001US-00996292.
10-DEC-2001; 2001US-00013295.
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ABZ75398 standard; DNA; 19
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RESULT 57 ABZ75399/

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Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
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                                Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
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 Reverse transcription primer used in cDNA analysis technique.
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100.0%; Pred. No. 2.9e+02;
iive 0; Mismatches 0; Indels
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100.0%; Pred. No. 2.8e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                          Synthetic nuclease-resistant oligomeric compound #55.
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              1736 AAAAAAAAAAAAAAA 1753
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1es 18; Conservative
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Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.

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RESULT 575
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                                   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAG75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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Pred. No. 2.9e+02;
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Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
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                                                                                                                               Reverse transcription primer used in cDNA analysis technique.
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Pred. No. 2.9e+02;
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AAQ75563 standard; DNA; 20 BP
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                                           AAQ75563;
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Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                           Analysis; gene
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                                                                                                Analysis of cDNA and gene expression – by amplification of mRNA followed by digestion with restriction enzymes.
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                                                                                                                                                                                                                                                                                                  1.0%; Score 18; DB 1; Length 20;
100.0%; Pred. No. 2.9e+02;
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                                                                                                                                                                                                                                                                                                           100.0%; Prec. ...
                                                (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
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                                                                                                                                      Disclosure; Page 5; 11pp; Japanese
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93JP-00112515
                       93JP-00112515
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Matches 18; Conservative
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16-APR-1993;
                       16-APR-1993;
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Query Match
1.0%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels
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.00.0%; Pred. No. 2.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aggregate; restriction enzyme; ss
                                                                                                                        1735 CAAAAAAAAAAAAAAA 1752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression;
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cycostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
                                                                                                                                                                                                                                                                               cDNA and gene expression - by amplification of mRNA followed
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               expression; reverse transcription; primer; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.0%; Score 18; DB 1; Length 20;
100.0%; Pred. No. 2.9e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                               by digestion with restriction enzymes.
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                               aggregate; restriction enzyme; ss
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                   gene
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                                                              Synthetic.
               Analysis;
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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a cuse in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antisinflammatory steroid in a subject, for reducing levels of adenosine receptor, producing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO
                                                                               Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
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100.0%; Pred. No. 2.9e+02;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                   Claim 15; SEQ ID NO 554; 872pp; English
Shahabuddin S;
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Matches 18; Conserva
                                        WPI; 2003-229219/22
Tang L,
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Miller S,
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Pabalan J, Aguilar D;

Katz E,

Li Y, Sandrasagra A,

Nyce JW,

Katz E, Pabalan J, Aguilar D;

Li Y, Sandrasagra A,

Nyce JW,

24-APR-2001; 2001US-0286137P. 23-APR-2002; 2002WO-US013135

(EPIG-) EPIGENESIS PHARM INC

23-APR-2002; 2002WO-US013135. 24-APR-2001; 2001US-0286137P. (EPIG-) EPIGENESIS PHARM INC.

24-APR-2001; 2001US-0286137P (EPIG-) EPIGENESIS PHARM INC Homo sapiens. 31-OCT-2002 ubiquinone. ABZ89301; Query Match Matches ABZ89301 ઠ g

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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an national antinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiathmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an preventing sensitivity to adenosine, reducing levels of denosine receptor, producing bronchodilation, increasing levels of ubiquinone or ung inflammation, lung allergies, or a respiratory disease or condition, lung inflammation, lung allergies, or a respiratory disease or condition.

Note: The sequence date for this patent is not represented in the printed or fer in the printed or fer in the condition.
                                                                                                                                                                                              Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 4180; 872pp; English.
     Shahabuddin S
                                                                                                          WPI; 2003-229219/22.
     Tang L,
Miller S,
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Gaps
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1.0%; Score 18; DB 1; Length 20; 100.0%; Pred. No. 2.9e+02;
                         0; Indels
       100.0%; Prec. ....
                                                     1735 CAAAAAAAAAAAAAA 1752
                                                                    3 CAAAAAAAAAAAAAAAA 20
           Local Similarity 100.
168 18; Conservative
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Human oligonucleotide sequence. ABZ89301 standard; DNA; 20 BP 17-OCT-2003 (first entry)

Human; antisense; lung dysfunction; nasal airway dysfunction; antilnflammatory steroid; ubiquinone; antilnflammatory; antiallergic; antiasthmatic; pypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

23-APR-2002; 2002WO-US013135 WO200285308-A2

Pabalan J, Aguilar D; Li Y, Sandrasagra A, Katz E, Nyce JW,

Analysis of cDNA and gene expression - by amplification of mRNA followed

by digestion with restriction enzymes.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation coodon, coding regalon, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an entiinflammatory steroid and ubjudinone. A composition of the invention has antiinflammatory, antiallergic, antisethmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therappy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an extension sensitivity to adenosine, reducing a subject, for reducing levels of adenosine receptor, producing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing levels of ung surfactant in a subject's tissue, or treating bronchoconstriction, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obsained in electronic format directly from WIPO ö Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or Gaps Analysis; gene expression; reverse transcription; primer; cDNA; ö Reverse transcription primer used in cDNA analysis technique. 1.0%; Score 18; DB 1; Length 20; 100.0%; Pred. No. 2.9e+02; 0; Indels Sequence 20 BP; 17 A; 2 C; 0 G; 1 T; 0 U; 0 Other; ftp.wipo.int/pub/published_pct_sequences 100.0%; Prec. ... Disclosure; SEQ ID NO 4543; 872pp; English. (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP Shahabuddin S; aggregate; restriction enzyme; 88. 1735 CAAAAAAAAAAAAAAA 1752 20 AAQ75622 standard; DNA; 21 BP 93JP-00112515 93JP-00112515 CAAAAAAAAAAAAAAAA 04-AUG-1995 (first entry) 18; Conservative WPI; 2003-229219/22 WPI; 1995-018287/03 Tang L, Local Similarity JP06303997-A. 16-APR-1993; 16-APR-1993; 01-NOV-1994. ubiquinone. Synthetic. Miller S, AAQ75622; Query Match Matches AAQ75622/ RESULT 8 셤 

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEC files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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1es 18; Conservative
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Disclosure; Page 7; 11pp; Japanese.

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                            double-stranded cDNA y using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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cive 0; Mismatches 0; Indels
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es 18; Conserv
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
                                                                                                                  Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
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Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
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Reverse transcription primer used in cDNA analysis technique.
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Analysis; gene expression; reverse transcription; primer; cDNA; aggregate, restriction enzyme; ss

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily

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100.0%; Pred. No. co.
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                                                        1735 CAAAAAAAAAAAAAAA 1752
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Matches 18; Conserv
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  Query Match
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Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
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double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESGO files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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aggregate; restriction enzyme; вв.
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                                                                                                                                                            1.0%; Score 18; DB 1; Length 21;
100.0%; Pred. No. 3e+02;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 3e+02;
ive 0; Mismatches 0; Indels
                                                                                                                               Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
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1es 18; Conservative
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                                                                                                                                                               Query Match
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AAQ75621/c
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100.0%; Pred. No. 3e+02;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                            by digestion with restriction enzymes.
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aggregate; restriction enzyme; ss
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Best Local Similarity 100.7
Matches 18; Conservative
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Pred. No. 3e+02;
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                                                                               aggregate; restriction enzyme; ss.
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Best Local Similarity 100.
Matches 18; Conservative
AAQ75621 standard; DNA;
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AAQ75656/
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                                                                                                                                           Analysis of cDNA and gene expression – by amplification of mRNA followed by digestion with restriction enzymes.
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100.0%; Pred. No. 3e+02;
iive 0; Mismatches 0; Indels
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(NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
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                                                                                                                                                                                                                                                 Disclosure, Page 6; 11pp; Japanese.
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Matches 18; Conservative
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1.0%; Score 18; DB 1; Length 21;

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WPI; 1995-018287/03.
                                                                                                             WPI; 1995-018287/03
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                   JP06303997-A
                                                       16-APR-1993;
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                                      01-NOV-1994,
 Synthetic.
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Matches
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                                                                                                                                                                                                                                                                                                                                 Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
                                                                                                                                                                                                                                                                                                                                                                              A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of abbelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Analysis, gene expression, reverse transcription; primer, cDNA, aggregate, restriction enzyme; 88.
                                                                                                                                                                    Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
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                                                                                                                                                   Reverse transcription primer used in cDNA analysis technique.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.0%; Score 18; DB 1; Length 21; Local Similarity 100.0%; Pred. No. 3e+02; les 18; Conservative 0; Mismatches 0; Indels
          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
Pred. No. 3e+02;
; Mismatches 0;
                                                                                                                                                                                                                                                                                             (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 6; 11pp; Japanese.
                                                                              1735 CAAAAAAAAAAAAAA 1752
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ilarity 100.0%; Pr
Conservative 0;
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Best Local Similarity
Matches 18; Conserv
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double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAG75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) alectrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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                                                                                                                                                                                                                                                                                                       Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.0%; Score 18; DB 1; Length 21; Best Local Similarity 100.0%; Pred. No. 3e+02; Matches 18; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                 (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP
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93JP-00112515.
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Analysis;
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              AAQ75658;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - by amplification of mRNA followed
            and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
 labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                               expression; reverse transcription; primer; cDNA;
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                                                                                                                1.0%; Score 18; DB 1; Length 21;
100.0%; Pred. No. 3e+02;
vative 0; Mismatches 0; Indels
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                                                                                        Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by digestion with restriction enzymes.
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                                                                                                                                                                                                                                                                                                                                                                              aggregate; restriction enzyme; ss
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                                                                                                                                           18; Conservative
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                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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18

AAQ75658 standard; DNA; 21 BP.

RESULT 613

AAQ75658/ ID AAQ7

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
                                                                                                                                                                                                                                                                                                                                                                                                                                     Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
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                                                                                  expression; reverse transcription; primer; cDNA;
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                                         Reverse transcription primer used in cDNA analysis technique.
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Pred. No. 3e+02;
0; Mismatches 0; Indels
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100.0%; Pred. No. ser.
... 0; Mismatches
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                                                                                                     aggregate; restriction enzyme; ss
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ID AAQ75638 standard; DNA; 21
(first entry)
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Best Local Similarity 100.
Matches 18; Conservative
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04-AUG-1995
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Best Local Similarity
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04-JAN-1995
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                                             Query Match
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                                                                            AAQ64706;
                                                  Matches
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This invention describes a novel genetically modified glucocorticoid receptor, which has transrepression protein-protein reciprocal effects and is transactivation deficient. The invention also describes (1) a gene construct comprising at least a nucleic acid encoding the glucocorticoid receptor, operably linked with regulatory sequences of a reporter gene, preferably a DNA-binding domain for a reporter gene; (2) identifying a gene encoding a cofactor involved in glucocorticoid receptor modulation of at least another transcription factor comprising; (a) using the above construct with an expression bank of a eukaryotic cell expressed in a yeast two hybrid system; (b) detecting a specific protein-protein complex or the receptor and a cofactor through growth in a selective medium for the reporter and (c) isolating and characterising the nucleic acid encoding the cofactor in the CDNA clone; (3) a cofactor with in a transrepression specific for the glucocorticoid receptor with in a
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                   Example 1; Page 68; 86pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                               22 AAAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABX94933 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                 Conservative
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les 18; Conserval
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Matches
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X & X & O O O O O O O O X & S
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                                                                                                                                                                g g
                                                         Analysis of cDNA and gene expression – by amplification of mRNA followed by digestion with restriction enzymes.
                                                                                                                                                        A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of ababelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= 2',5'-linked tetraadenylate
/note= "nucleotides Tinked through phosphodiester bonds
at hydroxyl groups of 2' and 5' carbons"
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antisense; 2',5'-tetraadenylate; 2-5A dependent RNase activator; RNA cleavage; antiviral therapy; chimeric molecule; ss.
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                                                                                                                                                                                                                                                                                                                                                                                         1.0%; Score 18; DB 1; Length 21;
100.0%; Pred. No. 3e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                  Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
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/note= "antisense region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ64706 standard; cDNA to mRNA; 22 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maitra R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                   Disclosure, Page 6; 11pp; Japanese.
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93US-00123449.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                  18; Conservative
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                 WPI; 1995-018287/03.
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This sequence is an example of a 2-5A-antisense oligonucleotide chimeric molecule. The antisense region targets the chimeric molecule to a particular region of RNA to be specifically cleaved and the 2',5'-linked tetraadenylate tail activates the 2-5A RNase. Typical applications are treatment of viral infections (esp. for cleavage of an RNA virus genome), cancer, leukaemia, cardiovascular disorders (e.g. restenosis after angioplasty), genetic disorders, osteoarchritis or rheumatoid arthritis. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A genetically modified glucocorticoid receptor which is transactivation deficient is used to identify cofactors which will be useful to provide inflammation-inhibiting and immunosuppressive treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Luciferase; ubiquitin promoter; glucocorticoid receptor; PCR; primer; transrepression protein-protein reciprocal effect; immunosuppressive; transactivation deficient inflammation; ss.
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100.0%; Pred. No. 3.1e+02;
iive 0; Mismatches 0;
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Sequence 23 BP; 18 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

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downstream segment the N-terminal AP-1 and the DNA-binding domain of the receptors are bound; (4) identifying an agent which affects the reciprocal effect of the glucocorticoid receptor with other transcription factors and/or offactors, whereby the receptor or construct is contacted with a potential agent and modulation of the interaction of the protein contacted by expression of the reporter game or detecting protein complex binding; (5) an agent for modulating interaction of the glucocorticoid receptor with a cofactor which binds either at the binding site of a physiological hormone or at a separate binding place of (6) a compound with an inflammation-inhibiting or immunosuppressive effect comprising the above agent. The genetically modified glucocorticoid receptor is useful to identify coreceptors which are used to produce an inflammation-inhibiting or immunosuppressive treatment. This sequence represents a PCR primer #1986orw used to amplify a Renilla reniformis luciferase gene which is then cloned into a reporter construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      molecular array. The method involves employing calibration probes that generate signals proportional to the total concentrations of labelled generate signals proportional to the total concentrations of labelled entire range of sample solutions and molecular array process are directed over an entire range of sample solutions and molecular arrays incorporating sets of calibration probes. Method is useful for calibrating different types of signals scanned from a molecular array, or calibrating signals scanned from different molecular arrays. The present sequence is poly (A) normalisation probe used in calibration of molecular array data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Calibration of molecular array data by employing calibration probes that generate signals proportional to total concentrations of labeled target molecules, and molecular arrays incorporating sets of calibration probes.
protein-protein interaction achieves a reciprocal effect, whereby within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a method for calibrating data scanned from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T7T18Apad_PS13-23-0001 probe for calibration of molecular array data.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.0%; Score 18; DB 1; Length 22;
100.0%; Pred. No. 3.1e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22 BP; 5 A; 5 C; 8 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 Trccaeeccarercees 22
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                                                                                                                                                                                                                                                                                                                                                               behind a ubiquitin promoter
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Best Local Similarity 100.0
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                          an; S4 ribosomal protein 13.97; malignant tumour; haemopathy; infection; immunological disease; inflammation; cytostatic; anti-HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human S4 ribosomal protein 13.97 polypeptide and encoding polynucleotide, useful for treating malignant tumor, inflammation, hemopathy, human immunodeficiency virus infection, immunological disease and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to human S4 ribosomal protein 13.97 (see 8883339). The ribosomal protein and its coding sequence are useful for treating malignant tumours, haemoopthy, HIV infection, immunological diseases and various inflammations. The present sequence is a PCR primer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T7T18Apad_PS12-24-0001 probe for calibration of molecular array data.
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 Length 23;
                               0; Indels
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 Score 18; DB 1; Le
Pred. No. 3.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        which was used in an example from the invention
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                                                                                                                                                                                                                                                               Human S4 ribosomal protein 13.97 PCR primer #2.
1.0%; Score 18; DB Local Similarity 100.0%; Pred. No. 3.2 les 18; Conservative 0; Mismatches
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                                                                                                                                                                       ABN85073 standard; DNA; 24
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                                                                                                                                                                                                                                    entry)
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Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                             Human; S4 ribosomal
                                                                                                                                                                                                                                                                                                                           PCR; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                    ABN85073;
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEC files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEC files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
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                                                                                                                                                                                                                                                                                                                        Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              1733 TACAAAAAAAAAAAAAAA 1753
                                                                     Disclosure, Page 8; 11pp; Japanese.
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Best Local Similarity 90.5
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Calibration of molecular array data by employing calibration probes that generate signals proportional to total concentrations of labeled target molecules, and molecular arrays incorporating sets of calibration probes.
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                       Molecular array; probe;
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RESULT 62 AAQ75736/

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Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEC files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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                                                                aggregate; restriction enzyme; ss.
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Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
                                                                                                                                                             Reverse transcription primer used in cDNA analysis technique.
                                                                                                                                                                                                                                                                                                                                                                                   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
                                                                      AAQ75694 standard; DNA; 21 BP
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                                                                                                      AAQ75694;
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                                                      A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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                                                                                                                                                                                                                    1.0%; Score 17.8; DB 1; Length 21; 90.5%; Pred. No. 3.2e+02; ve 0; Mismatches 2; Indels
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by digestion with restriction enzymes
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                             Disclosure; Page 7; 11pp; Japanese.
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nes 19; Conservative
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AAQ75753/
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Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
                                                                                                                                                 double-stranded cDNAs by using an aggregate of mENAs and a plural type labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mENAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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                                                                            Disclosure; Page 7; 11pp; Japanese.
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                                                          (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP
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Warches 19; Conservative
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Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
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                                                      1.0%; Score 17.8; DB 1; Length 90.5%; Pred. No. 3.2e+02; tive 0; Mismatches 2; Indels
Seguence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of abblied reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEC files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
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            Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
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AAQ75692 standard; DNA; 21
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             Seguence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
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Pred. No. 3.2e+02;
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Match 1.0%; Score 17.8; DB 1; Length Local Similarity 90.5%; Pred. No. 3.2e+02; Length 9; Conservative 0; Mismatches 2; Indels
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Analysis of cDNA and gene expression - by amplification of mRNA followed
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Disclosure; Page 7; 11pp; Japanese.
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Analysis of cDNA and gene expression - by amplification of mRNA followed
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93JP-00112515 93JP-00112515

Length 21; 2; Indels

1.0%; Score 17.8; DB 1; 90.5%; Pred. No. 3.2e+02; 0; Mismatches

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                                        1.0%; Score 17.8; DB 1; Length 90.5%; Pred. No. 3.2e+02; ive 0; Mismatches 2; Indels
Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;
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AAQ75704 standard; DNA; 21
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Matches 19; Conservative
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Best Local Similarity 90.5
Matches 19; Conservative
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Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
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Best Local Similarity 90.5
Matches 19; Conservative
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expression - by amplification of mRNA followed
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by digestion with restriction enzymes.
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Matches 19; Conservative
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  expression; reverse transcription; primer; cDNA;
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Pred. No. 3.2e+02;
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aggregate; restriction enzyme; ss
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                 AAQ75734 standard; DNA; 21
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TELEGRAPH & TELEPHONE CORP.
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es 19; Conserv
(NITE ) NIPPON
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ággregate; restriction enzyme; ss.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                            - by amplification of mRNA followed
                              Gaps
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        Length 21;
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      Query Match
1.0%; Score 17.8; DB 1;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                        digestion with restriction enzymes.
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                                                 1733 TACAAAAAAAAAAAAAAAA 1753
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AAQ75710 standard; DNA; 21 BP.
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Analysis of cDNA and gene expression - by amplification of mRNA followed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  double-stranded cDNAs by using an aggregate of mRNAs and a plural type labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 1.0%; Score 17.8; DB 1; Length 21; Local Similarity 90.5%; Pred. No. 3.2e+02; Nes 19; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                 by digestion with restriction enzymes.
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                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 8; 11pp; Japanese.
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93JP-00112515
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method for the analysis of cDNA comprises (a) preparing an aggregate of wble-stranded cDNAs by using an aggregate of mRNAs and a plural type of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polymorphism; human, inhibitor; cancer; treatment; cell growth; LOH; cell viability; loss of heterozygosity; precancerous condition; ASI; allele specific inhibitor; somatic cell; diagnosis; prevention; atherosclerotic plaque; premalignant metaplastic lesion; endometriosis; dysplastic lesion; benign tumour; polycystic kidney disease; transplant; graft versus host disease; malignant cell removal; bone marrow; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying target genes for allele-specific drugs - used for diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic plaque, dysplastic lesions, endometriosis or graft versus host disease.
                      double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GRNESGO files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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                                                                                                                                                                                                                                         1.0%; Score 17.8; DB 1; Length 21; 90.5%; Pred. No. 3.2e+02; ve 0; Mismatches 2; Indels
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Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
               graft versus host disease. The method can also be used to remove malignant cells from bone marrow transplants. AAZ25812-Z26825 represent human polymorphic sites described in the method of the invention
endometriosis, polycystic kidney disease, and
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                                                                                                          ch 1.0%; Score 17.8; DB 1; Length 21; al Similarity 90.5%; Pred. No. 3.2e+02; 19; Conservative 0; Mismatches 2; Indels
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es 18; Conservative
 lesions, benign tumours,
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                                                                                                                      A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEG files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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of
      Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
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                                                                                                                                                                                                                                                                                                                                                                      Score 17.4; DB 1; Length 19;
Pred. No. 3.3e+02;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                        Sequence 19 BP; 1 A; 0 C; 1 G; 17 T; 0 U; 0 Other;
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                                                                                  Disclosure; Page 5; 11pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aggregate; restriction enzyme; ss
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Best Local Similarity 94.7%;
Matches 18; Conservative 0
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                                                                                                      Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
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                                                             Reverse transcription primer used in cDNA analysis technique.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19 BP; 1 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
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                    (first entry)
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Best Local Similarity
Matches 18; Conserv
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psoriasis; inflammatory bowel disease; drug screening;
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                                   Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                        Analysis of cDNA and gene expression - by amplification of mRNA followed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   short interfering nucleic acid; siNA; downregulation; inhibition; mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference; cytostatic; anorectic; antidiabbtic; antiinflammatory; antiasthmatic; immunosuppressive; antibacterial; antirheumatic; antiarthritic; antipporiatic; gastrointestinal; obesity; diabetes; tumour; inflammatory disease; asthma; septic shock; rheumatoid arthritis;
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                                                                                                                                                                               Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
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                                                                                                                                                         Reverse transcription primer used in cDNA analysis technique.
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                                                                                                                                                                                                                                                                                                                                                                                                     by digestion with restriction enzymes.
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1735 CAAAAAAAAAAAAAAAA 1753
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             CGAAAAAAAAAAAAAAA
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                                                                                AAQ75557 standard; DNA; 19
                                                                                                                                04-AUG-1995 (first entry)
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Best Local Similarity
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                                                                                                        AAQ75557;
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ADE29541
ID ADE2
XX
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AC ADE
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The present invention describes a short interfering nucleic acid (siNA) that downregulates expression of a mitogen-activated protein kinase (MARK) genes by RNA interference. Also described: (1) a method for modulating expression of MARK genes in cells, tissue explants or organisms by introduction of siNA; (2) kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or complexes of siNA; and (4) conjugates and/or complexes of siNA; and (4) vectors that express siNA and cells containing these vectors. MAPK siNAs have cytostatic, anorectic, antidacterial, antirheumatic, antisportatic and gastrointestinal activities. The MAPK siNAs can be used to modulate the expression of MAPK genes, in cells, tissue explants or organisms, e.g. for treating obesity; diabetes types I will a wide range of tumours, and inflammatory diseases (asthma, septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel disease). They can also be used for drug screening; diagnosis; target dentification and validation; genetic engineering; pharmacogenomics; studying gene function and gene mapping (e.g. of single-nucleotide colymorphisms). The present sequence represente a MAPK sinA which is used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New short interfering nucleic acid, useful e.g. for treatment and diagnosis of cancer, downregulates expression of mitogen-activated protein kinase genes.
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genetic engineering; pharmacogenomic; gene mapping; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP.
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2002US-0408378P.
2002US-0409293P.
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Best Local Similarity 89.5'
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                                                                                                                                                 WO2003072590-A1.
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Transgenic plants; altered petal colour; polymerase chain reaction; ss.

Cytochrome P450 sequence amplification PCR primer polyT

(first entry)

(revised)

25-MAR-2003

27-APR-1994

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The present invention describes a short interfering nucleic acid (siNh) that downregulates expression of a mitogen-activated protein kinase (MAPK) genes by RNA interference. Also described: (1) a method for modulating expression of MAPK genes in cells, tissue explants or corganisms by introduction of siNa; (2) kits for in vitro or in vivo delivery of siNa; (3) conjugates and/or complexes of siNa; and (4) conjugates and/or complexes of siNa; and (4) vectors that express siNa and cells containing these vectors. MAPK siNas have cytostatic, anorectic, antidabetic, antiinflammatory, antiarthritic, antispsoriatic and gastrointestinal activities. The MAPK siNas can starthritic; antispsoriatic and gastrointestinal activities. The MAPK siNas can be used to modulate the expression of MAPK genes, in cells, tissue explants or organisms, e.g. for treating obesity; diabetes types I can il a wide range of tumours, and inflammatory diseases (asthma, septic shock, rheumatoid arthritis, psoriatis and inflammatory bowel disease). They can also be used for drug screening; diagnosis; target clentification and validation; genetic engineering; pharmacogenomics; studying gene function and gene mapping (e.g. of single-nucleotide polymorphisms). The present sequence represents a MAPK siNa which is used in the exemplification of the present invention.
mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference; cytodetatic; anorectic; antidabetic; antidiamatory; antiaethmatic; immunosuppressive; antibacterial; antirheumatic; antiarthritic; antipsoriatic; gastrointestinal; obesity; diabetes; tumour; inflammatory disease; asthma; septic shock; rheumatori darthritis; psoriasis; inflammatory bowel disease; drug screening; genetic engineering; pharmacogenomic; gene mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New short interfering nucleic acid, useful e.g. for treatment and diagnosis of cancer, downregulates expression of mitogen-activated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SIRN-) SIRNA THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                , 2002US-0358580P.
; 2002US-0363124P.
; 2002US-0364782P.
; 2002US-0406784P.
; 2002US-0408378P.
; 2002US-0409233P.
                                                                                                                                                                                                                                                                                                       28-JAN-2003; 2003WO-US002510.
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Best Local Similarity 94.7%;
Matches 18; Conservative
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09-SEP-2002;
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ch 1.0%; Score 17.4; DB 1; Length 20; 1 Similarity 94.7%; Pred. No. 3.4e+02; 18; Conservative 0; Mismatches 1; Indels

Local Similarity

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1735 CAAAAAAAAAAAAAAAA 1753

Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

The sequence is that of a PCR primer which was used in polymerase ch reactions for the amplification of cloned cytochrome P450 sequences. (Updated on 25-MAR-2003 to correct PN field.)

Nucleic acid isolate encoding flavonoid-3'-hydroxylase - is used to create transgenic plants with altered petal colour.

Tanaka Y;

Holton TA, Cornish EC,

WPI; 1993-336914/42.

(ITFL-) INT FLOWER DEV PTY LTD

07-JAN-1993;

93WO-AU000127 92AU-00001538.

25-MAR-1993; 27-MAR-1992;

14-OCT-1993

WO9320206-A1

Synthetic.

Disclosure; Page 25; 86pp; English

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Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
                                                                                                                                                expression; reverse transcription; primer; cDNA;
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                                                            AAQ75591 standard; DNA; 20
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AAQ49436 standard; cDNA; 20

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AAQ49436

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us10008789-3.rng

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Analysis of cDNA and gene expression - by amplification of mRNA followed
                                                                                                                                                                      expression; reverse transcription; primer; cDNA;
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AAQ75586 standard; DNA; 20
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                                      A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GRNESEO files AA075547-075798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The
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Pred. No. 3.4e+02;
0; Mismatches 1; Indels
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             Disclosure; Page 5; 11pp; Japanese.
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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Disclosure; Page 5; 11pp; Japanese.
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Reverse transcription primer used in cDNA analysis technique.
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aggregate; restriction enzyme; ss.
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Pred. No. 3.4e+02;
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restriction enzyme; ss
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                                                                              Best_Local Similarity 94.7%;
Matches 18; Conservative
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Seguence 20 BP; 0 A;
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method can be used to analyse gene expression rapidly and easily
        Analysis; gene expression; reverse transcription; primer; cDNA;
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                                                                                                                                                                                                                                                                          Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
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                aggregate; restriction enzyme; ss
                                                                                                                                                                                                                                                                                                                             CTAAAAAAAAAAAAA 1
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nes 18; Conservative
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                                 A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNNs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily
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                                                                                                                                                                                                                                                                         Score 17.4; DB 1; Length 20;
Pred. No. 3.4e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                Sequence 20 BP; 0 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
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Disclosure; Page 5; 11pp; Japanese.
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Best Local Similarity 94.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ75582 standard; DNA; 20
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Pred. No. 3.4e+02;
0; Mismatches 1; Indels
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double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-075798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) diggesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
                                                                                                                                 gene expression - by amplification of mRNA followed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; antisense; lung dysfunction; nasal airway dysfunction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.0%; Score 17.4; DB 1; Length 20; 94.7%; Pred. No. 3.4e+02;
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S;
                                                       (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
                                                                                                                                   Analysis of cDNA and gene expression - by digestion with restriction enzymes.
                                                                                                                                                                                             Disclosure; Page 5; 11pp; Japanese.
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Tang L, Shahabuddin
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                  16-APR-1993;
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Miller S,
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                                                     AAQ75592 standard; DNA; 20 BP
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AAQ75576 standard; DNA; 20
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first active agent comprising an oligonucleotide antisense to the interactive agent comprising an oligonucleotide antisense to the intitation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an entilnflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotenaive, immunosuppressive, and cytostatic activity. The composition may have a cuse in antisense gene therapy. The composition is sectively a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO Sequence 20 BP; 17 A; 1 C; 1 G; 1 T; 0 U; 0 Other; at ftp.wipo.int/pub/published_pct_sequences 

ö Gaps ö 1.0%; Score 17.4; DB 1; Length 20; 94.7%; Pred. No. 3.4e+02; ve 0; Mismatches 1; Indels 94.78; 18; Conservative Local Similarity Query Match Best Loca Matches

1735 CAAAAAAAAAAAAAAA 1753 

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ABZ85534 standard; DNA; 20 ABZ85534; RESULT 677 ABZ85534

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(first entry) 17-OCT-2003

Human oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antianfmatic; hypotensive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Homo sapiens.

WO200285308-A2.

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

(EPIG-) EPIGENESIS PHARM INC.

24-APR-2001; 2001US-0286137P.

Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D; , Tang L, Shahabuddin S; Miller S, Nyce JW,

WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

Claim 15; SEQ ID NO 776; 872pp; English

ubiquinone

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a cuse in antisense gene therapy. The composition is useful for treating or preventing the prophylactic or therapeutic respiratory effect of an oriniflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of denosine receptor, producing bronchodilation, increasing levels of denosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this parent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences 

Sequence 20 BP; 18 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

Gaps ö / Match 1.0%; Score 17.4; DB 1; Length 20; Local Similarity 94.7%; Pred. No. 3.4e+02; nes 18; Conservative 0; Mismatches 1; Indels Query Match Matches

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1736 AAAAAAAAAAAAAAAA 1754

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RESULT 678 ABZ89487 뮵 ABZ89487 standard; DNA; 20

ABZ89487;

(first entry) 17-0CT-2003 Human oligonucleotide sequence.

Human, antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory; antiallergic; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Homo sapiens.

WO200285308-A2. 

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC.

Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D; Tang L, Shahabuddin S; Miller S, Nyce JW,

WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

Disclosure; SEQ ID NO 4729; 872pp; English

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the intistion codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antisinflammatory, antiallergic, antiathmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition of the invention has antiinflammatory, antiallergic, antiathmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a cuse in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing levels of adenosine creceptor, producing bronchodilation, increasing levels of denosine creceptor, producing bronchodilation, increasing levels of ubiquinone or lung inflammation, lung allergies, or a respiratory disease or condition.

Creceptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung allergies, or a respiratory disease or condition.

Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO Sequence 20 BP; 18 A; 2 C; 0 G; 0 T; 0 U; 0 Other; 

ö Gaps ô 1.0%; Score 17.4; DB 1; Length 20; 94.7%; Pred. No. 3.4e+02; 1; Indels 0; Mismatches 18; Conservative Query Match Best Local Similarity Matches

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ABZ88564 standard; DNA; 20 BP ABZ88564; RESULT 679 ABZ88564

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AAC ABZ8

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ABZ8

AAC ABZ8

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ABZ8

17-OCT-2003 (first entry)

Human; antisense; lung dysfunction; nasal airway dysfunction; Human oligonucleotide sequence.

antinflammatory steroid; ubiquinone; antinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Homo sapiens

WO200285308-A2.

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC.

Pabalan J, Aguilar D; Li Y, Sandrasagra A, Katz E, Tang L, Shahabuddin S; Nyce JW, I Miller S,

WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

Disclosure; SEQ ID NO 3806; 872pp; English.

Intraction cactive agent comprising an oligomedicotide antibenes to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 6' or and 3' intron-exon junctions, or regions within 2-10 nuclectides of inctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antinflammatory seroid and ubiquinone. A composition of the invention of thes antinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antinflammatory steroid in a subject, for reducing levels of adenosine receptor, producing bronchodilation, increasing bronchoconstriction, lung allergies, or a respiratory disease or condition.

Condition in a subject's tissue, or treating bronchoconstriction, lung surfactant in a subject's tissue, or treating bronchoconstriction, bote: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO ö composition, which has Gaps ö 1.0%; Score 17.4; DB 1; Length 20; 14.7%; Pred. No. 3.4e+02; ve 0; Mismatches 1; Indele Sequence 20 BP; 17 A; 1 C; 2 G; 0 T; 0 U; 0 Other; pharmaceutical 1734 ACAAAAAAAAAAAAAA 1752 invention relates to a novel 2 ACAGAAAAAAAAAAAAA 20 Query Match
Best Local Similarity 94.7%; 18; Conservative Matches ð g

RESULT 680

ABZ89703 standard; DNA; 20 BP ABZ89703;

17-OCT-2003 (first entry)

Human oligonucleotide sequence.

antiniflammatory steroid; ubiquinone; antiniflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds. Human; antisense; lung dysfunction; nasal airway dysfunction; 

Homo sapiens

WO200285308-A2.

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC.

Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D; Tang L, Shahabuddin S; Nyce JW, L Miller S,

WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

Disclosure, SEQ ID NO 4945; 872pp; English.

Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 U; 0 Other;

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first active agent comprising an oligomuclectide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nuclectides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antihiflammatory servoid and ubiquinone. A composition of the invention cantihiflammatory and ubiquinone. A composition may have a manisonable and cytostatic activity. The composition may have a cuse in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of antihiflammatory steroid in a subject, for reducing or depleting levels of of or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactent in a subject's tissue, or treating bronchoconstriction, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed of specification, but was obtained in electronic format directly from WIPO relates to a novel pharmaceutical composition, which has a 1.0%; Score 17.4; DB 1; Length 20; nilarity 94.7%; Pred. No. 3.46+02; Conservative 0; Mismarch... Sequence 20 BP; 16 A; 0 C; 0 G; 4 T; 0 U; 0 Other; at ftp.wipo.int/pub/published_pct_sequences 1731 TTTACAAAAAAAAAAAAAA 1749 2 TTTAAAAAAAAAAAAAA 20 Local Similarity Analysis; gene 04-AUG-1995 18; AAQ75735; Query Match AAQ75735/c Matches RESULT 681 ઠ g

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- by amplification of mRNA followed expression; reverse transcription; primer; cDNA; Reverse transcription primer used in cDNA analysis technique. (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP. Analysis of cDNA and gene expression - by digestion with restriction enzymes. Disclosure; Page 8; 11pp; Japanese. aggregate; restriction enzyme; ss. ВР 93JP-00112515 93JP-00112515 AAQ75735 standard; DNA; 21 (first entry) WPI; 1995-018287/03. JP06303997-A. 16-APR-1993; 16-APR-1993; 01-NOV-1994. Synthetic 

A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily

ö ô g g Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes. A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type clabelled reverse transcription primers (GENESES files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The Gaps Gaps method can be used to analyse gene expression rapidly and easily ; 0 expression; reverse transcription; primer; cDNA; ö Reverse transcription primer used in cDNA analysis technique. Reverse transcription primer used in cDNA analysis technique. 1.0%; Score 17.4; DB 1; Length 21; 94.7%; Pred. No. 3.6e+02; ive 0; Mismatches 1; Indels Length 21; 1; Indels Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other; DB 1; 1.0%; Score 17.4; DB 1; 94.7%; Pred. No. 3.6e+02; tive 0; Mismatches 1 (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP. Disclosure; Page 8; 11pp; Japanese. aggregate; restriction enzyme; ss 1735 CAAAAAAAAAAAAAAA 1753 19 CGAAAAAAAAAAAAAA 1 19 CGAAAAAAAAAAAAAAA 1 AAQ75719 standard; DNA; 21 BP B 93JP-00112515. AAQ75738 standard; DNA; 21 04-AUG-1995 (first entry) (first entry) Local Similarity 94.7 es 18; Conservative 18; Conservative WPI; 1995-018287/03. Best Local Similarity Matches 18; Conserv Analysis; gene JP06303997-A. 16-APR-1993; 04-AUG-1995 01-NOV-1994. Synthetic. AAQ75719; AAQ75738; Query Match Query Match RESULT 683 RESULT 682 AAQ75719/c Matches AAQ75738/ d ð 셤 ð

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Analysis of cDNA and gene expression – by amplification of mRNA followed
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                  A method for the analysis of cDNA comprises (a) preparing an aggregate double-stranded cDNAs by using an aggregate of mRNAs and a plural type labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
                                                                     Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
                                                                                                                                                                                                                                              Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
                        (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
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 93JP-00112515.
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Pred. No. 3.6e+02;
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1.0%; Score 17.4; DB 1; Length 21; 94.7%; Pred. No. 3.6e+02; ive 0; Mismatches 1; Indels
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Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
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aggregate; restriction enzyme; ss.
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1.0%; Score 17.4; DB 1; Length 21;
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ filles AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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Analysis; gene expression; reverse transcription; primer; cDNA;
aggregate; restriction enzyme; ss.
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706/c
AAQ75706 standard; DNA; 21
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Analysis; gene
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Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
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              Length 21;
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           1.0%; Score 17.4; DB 1;
94.7%; Pred. No. 3.6e+02;
ive 0; Mismatches 1;
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18; Conserv
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Matches 18;
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                                                                                                                                                                                      expression - by amplification of mRNA followed
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                                         (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
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                                                                                                                                                                                                                    by digestion with restriction enzymes.
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aggregate; restriction enzyme; ss.
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AAQ75717 standard; DNA; 21
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AAQ75750/c
ID AAQ75750 standard; DNA; 21
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Pred. No. 3.6e+02;
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Pred. No. 3.6e+02;
0; Mismatches 1; Indels
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Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
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(NITE ) NIPPON TELEGRAPH & TELEPHONE CORP
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                                                                                                                                                    Disclosure; Page 7; 11pp; Japanese.
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AAQ75749 standard; DNA; 21
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Query Match

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Gaps

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1; Indels

us10008789-3.rng

AAT94431 standard; mRNA; 19

RESULT 704

AAT94431

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The present sequence is one such mucleic acid sequence. Expression of [1].

The present sequence is one such mucleic acid sequence. Expression of [1] cresistance. (1) are useful as probes or primers for detecting, and or included the control of properties of control of properties. (1) are useful as probes or primers for detecting, as it is easier and for recombinant production of polypeptides. (1), cells containing these vectors and antibodies (Ab) against (II) are all useful for treatment/prevention of viral, tumour and cell degeneration diseases and schizophrenia). Analysing the expression of (1) is also useful for diagnosis and/or prognosis of such diseases. Transgenic animals carrying (I) are used for studying the actiology of these diseases (also immune and inflammatory diseases). Note: In the present specification, SEQ ID 1 to 2270 are shown in the specification.
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                                                                                                                                                                                                                                                                                                                                            Tumour, cytostatic, antiviral, neuroprotective, nootropic, neuroleptic, tumour suppression, tumour reversion, apploasion, tumour reversion, seems, neurodegeneration, viral infection; cell degeneration disease, neurodegeneration, ds; Alzheimer's disease, schizophrenia, immune disease, inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention relates to novel human nucleic acid sequences (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid implicated e.g. in tumor suppression, useful for diagnosis of tumors, viral infection and cellular degeneration and for
                                     Gaps
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Pred. No. 3.68+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23 BP; 15 A; 0 C; 3 G; 3 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                            Tumour suppression-related oligonucleotide #1870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Susini L;
                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tuijnder M,
                                                                     1732 TTACAAAAAAAAAAAA 1750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MOLE-) MOLECULAR ENGINES LAB SA.
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                                                                                                        19 TTAAAAAAAAAAAAA 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JAN-2001; 2001FR-00000899.
             94.7%;
                                                                                                                                                                                                ABQ96219 standard; DNA; 23
                                                                                                                                                                                                                                                                      28-OCT-2002 (first entry)
                                   18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Telerman A, Amson R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-610803/66.
                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUL-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FR2819824-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                    ABQ96219;
                                   Matches
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A method has been includes synthesising a double stranded (ds) cDNA from molecules which includes synthesising a double stranded (ds) cDNA from isolated mRNA, digesting the ds cDNA with a restriction endonuclease to produce cDNA fragments in which at least one end of the cDNA fragments in which at least one end of the cDNA fragments. (a) hybridising adaptor DNA sequences The improvement comprises: (a) hybridising adaptor DNA sequences to at least one end of the cDNA fragments; (b) ligating the adaptor DNA sequences to the cDNA fragments, where the primers that hybridise to the ends adaptor DNA sequences to the cDNA fragments, where the primers have at least one nucleotide at the contains, where the primers have at least one nucleotide at the 3' end that specifically hybridises to a subset of cDNA fragments. The present sequence represent a template poly-A tail used in the present sequence represent a template poly-A tail used in the present sequence represent a template poly-A tail used in the present sequence represent a template poly-A tail used in the present sequence represent a template poly-A tail used in the present sequence represent a template poly-A tail used in the present gene expressing cells based on their mRNA content, for representing expressed gene expression. The method is also useful for characterising cells of a variety of types and under a variety of physiological conditions. The method is also useful for individuals or species based on the fingerprint obtained from the mRNA content to isolated cells or tissue and comparing it to cells or tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detection and characterisation of mRNA by restriction display PCR -comprising synthesis of cDNA, digestion with a restriction endonuclease, ligation to an adaptor DNA and PCR amplification.
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                                                                                                                                                   detection; characterisation; mRNA; restriction display PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A method has been improved for detecting and characterising mRNA
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14.4%; Pred. No. 3.5e+02;
ve 1; Mismatches 0; Indels
                                                                                                         Template mRNA poly-A tail SEQ ID NO:1 from WO9729211.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19 BP; 17 A; 0 C; 0 G; 0 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 24; 40pp; English
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ID AAX18390 standard; DNA; 19 BP.
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                                                                                                                                                                                                                                                                                                                                                                    97WO-US002009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94.48;
                                                          (first entry)
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Best Local Similarity 94.4'
Matches 17; Conservative
                                                                                                                                                                       synthesis; cDNA; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-415362/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from a known source
                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                               WO9729211-A1
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                                                              02-MAR-1998
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                                                                                                                                                                                                                  Synthetic.
                      AAT94431;
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1731 TTTACAAAAAAAAAAAAA 1751

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Conservative

Local Similarity es 18; Conserv

Query Match Best Loca Matches TTTNGNAAAAAAAAAAAA 21

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This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta -N3'; or (X)m5'-(damma) k-delta-N3'; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, guanine or cytosine; N = adenine, guanine or thymine; gamma = thymine; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of repetition of gamma, in which thymine expressed by gamma is composed of 13 or large of a gamma is not sequences of a sequences for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibition; replication; herpes simplex virus; HSV; HIV; retard; human cytomegalovirus; influenza virus; inflammation; telomere length; neurological disorders; phospholipase A2 activity; hyperproliferation; malignancy; cardiovascular disease; snake bite; malignancy; aging; ss.
                                                                                                         RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
                                                                                                                                                                                                                                                                                                                                                          Peptides having at least two new nucleotides - useful as primers in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.0%; Score 17.2; DB 1; Length 19; 94.4%; Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                         RT-PCR primer of the invention SEQ ID 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Guanine quartet containing oligomer, #9.
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                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 12; 19pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1735 CAAAAAAAAAAAAAAA 1752
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(first entry)
                                             11-MAY-1999 (first entry)
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les 17; Conserv
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                                                                                                                                                                                                                                                                18-JUL-1997;
                                                                                                                                                                     JP11032765-A
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04-NOV-1994
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                AAX18390
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Gaps

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The sequences given in AAQ61990-2001 are oligonucleotides which contain G4 or G3 stretches and which may be used for inhibiting replication of herpes simplex virus (HSV), activity of HIV, human cytomegalovirus or influences avirus, or for treating inflammatory and neurological disorders caused by phospholipase A2 activity in cases of hyper- proliferation, malignancy, cardiovascular disease and snake bite. Oligonucleotides such as these, may be used for inhibiting division of malignant cells by modualting telomere length, which may also retard aging. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                     New modified oligo-nucleotide contg guanine quartet - inhibits activity of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibition; replication; herpes simplex virus; HSV; HIV; retard; human cytomegalovirus; influenza virus; inflammation; telomere length; neurological disorders; phospholipase A2 activity; hyperproliferation; malignancy; cardiovascular disease; snake bite; malignancy; aging; ss.
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                                                                                                                                                                             Brown-Driver VL;
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/note= "Phosphorothionate intersugar linkages"
/note= "Phosphorothionate intersugar linkages"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 1.0%; Score 17.2; DB 1; Length 22; I Similarity 86.4%; Pred. No. 3.9e+02; 19; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                               Chiang M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 22 BP; 0 A; 0 C; 16 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                            P, Bennett CF, Chian
Wyatt JR, Imbach JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Guanine quartet containing oligomer, #2.
                                                                                                                                                                                                                                                                                                                 Disclosure; Page 107; 144pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1015 GTGGTTGGGGATGGGGCTGGGG 1036
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                                                                                          93WO-US009297
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(first entry)
                                                                                                                                                                               Anderson KP,
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                                                                                                                                                                                           Vickers TA,
                                                                                                                                                 (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                          WPI; 1994-135613/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                    chromosomes
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misc_feature
                                                                                          29-SEP-1993;
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                               WO9408053-A1
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04-NOV-1994
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                                                            14-APR-1994
                                                                                                                                                                                             Ecker DJ,
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Matches
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WPI; 1994-135613/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequences given in AAQ61990-2001 are oligonucleotides which contain G4 or G3 stretches and which may be used for inhibiting replication of herpes simplex virus (HSV), activity of HIV, human cytomegalovirus or influenza virus, or for treating inflammatory and neurological disorders caused by phospholipase A2 activity in cases of hyper- proliferation, malignancy, cardiovascular disease and snake bite. Oligonucleotides such as these, may be used for inhibiting division of malignant cells by modualting telomere length, which may also retard aging. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                          New modified oligo-nucleotide contg guanine quartet - inhibits activity of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibition; replication, herpes simplex virus; HSV; HIV; human cytomegalovirus; influenza virus; inflammation; neurological disorders; phospholipase A2 activity; hyperproliferation; malignancy; cardiovascular disease; snake bite; malignancy; telomere length; retard; ss.
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                                                                                                                                 Brown-Driver VL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brown-Driver VL;
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/note= "Phosphorothionate intersugar linkages"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                        RC, Anderson KP, Bennett CF, Chiang M,
J, Vickers TA, Wyatt JR, Imbach JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22 BP; 0 A; 0 C; 16 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSV replication inhibiting oligomer, ISIS no 5677.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.0%; Score 17.2; DB 1;
86.4%; Pred. No. 3.9e+02;
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att JR, Imbach JL;
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Ecker DJ, Vickers TA, Wyatt JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
   92US-00954185
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                                                               (ISIS-) ISIS PHARM INC
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                                                                                                                                                                                                                 WPI; 1994-135613/16
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                                                                                                                                                                                                                                                                                                            of viruses, e.g of chromosomes.
   29-SEP-1992;
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04-NOV-1994
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New modified oligo-nucleotide contg guanine quartet - inhibits activity of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length of chromosomes.
                                                                                                                                                                                           The sequences given in AAQ61825-50 and AAQ61886-906 are oligonucleotides which contain a G4 or two G3 stretches and which may be used for inhibiting replication of herpes simplex virus (HSV). Oligonucleotides such as these may also be used for inhibiting activity of HIV, human cytomegalovirus or influenza virus, or for treating inflammatory and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New modified oligo-nucleotide contg guanine quartet - inhibits activity of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length of chromosomes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modualting telomere length, which may also retard aging. (Updated on 25-
MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                           neurological disorders caused by phospholipase A2 activity in cases of hyperproliferation, malignancy, cardiovascular disease and snake bite. They may also be used for inhibiting division of malignant cells by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inhibition, replication, herpes simplex virus, HSV, HIV, human cytomegalovirus, influenza virus, inflammation, neurological disorders, phospholipase A2 activity; hyperproliferation, malignancy; cardiovascular disease, snake bite, malignancy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.0%; Score 17.2; DB 1; Length 22; 66.4%; Pred. No. 3.9e+02; ve 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22 BP; 0 A; 0 C; 16 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSV replication inhibiting oligomer, ISIS no 5670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chiang M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P. Bennett CF, Chian Wyatt JR, Imbach JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1015 GTGGTTGGGGATGGGGCTGGGG 1036
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                                                                                                                                 Claim 5; Page 19; 144pp; English.
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Ecker DJ, Vickers TA, W
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04-NOV-1994
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(COLE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "at least one (and preferably all) of the backbone subunits are composed of N-acetyl N-(2-aminoethyl)glycine peptide residues, the nucleobase being attached covalently to the acetyl group and the peptide linkage being formmed by condensation of the glycine carboxy group of one residue with the amino group of the 2-aminoethyl moiety in the next residue.
                    The sequences given in AAQ61825-50 and AAQ61866-906 are oligonucleotides which contain a G4 or two G3 stretches and which may be used for inhibiting replication of herpes simplex virus (HSV). Oligonucleotides such as these may also be used for inhibiting activity of HIV, human cytomegalovirus or infilmenza virus, or for treating infilmamatory and neurological disorders caused by phospholipase A2 activity in cases of hyperproliferation, malignancy, cardiovascular disease and snake bite. They may also be used for inhibiting division of malignant cells by modualting telemere length, which may also retard aging. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligomer hybridisable to HIV sequence and contg. peptide nucleic acid sub:unit - binds in complementary manner to DNA and RNA, and useful for modulating HIV viral activity, e.g. in treating AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptide nucleic acid (PNA) oligomers are provided which (a) consist of naturally occurring nucleobases covalently bound to a polyamide
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       Peptide nucleic acid; PNA; HIV; human immunodeficiency virus; AIDS;
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                                                                                                                                                  Sequence 22 BP; 0 A; 0 C; 16 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                Peptide nucleic acid oligomer targetting HIV gene
                                                                                                                                                                      1.0%; Score 17.2; DB 1;
86.4%; Pred. No. 3.9e+02;
ative 0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                    antiviral, antisense, triple helix, ss.
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 Disclosure; Page 19; 144pp; English
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                                                                                                                                                                      Query Match
Best Local Similarity 86.4
Matches 19; Conservative
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backbone and (b) hybridise to the translation initiation AUG region, 5' untranslated region (5' UTR), 3' untranslated region (3' UTR), splice junctions or coding sequence of a human immunodeficiency virus gene chosen from env. gag, pol, rev and tat. The PNAs can be used to target RNA and single stranded DNA (88DNA) to produce antisense-type gene regulation modeltes. They have utility as gene-targetted frugs for modulating HIV processes. Hence they can be used to treat AIDS and other viral infections. They are also useful in diagnostic applications and as tranded DNA. They are also able to for triple helicas in which a first PNA strand binds with RNA or s9DNA and a second PNA strand binds with the first PNA strand binds with the first PNA strand. The PNAs possess no significant charge and are water soluble, which facilitates cellular uptake. Further, since they contain amides of non-biological amino acids, they are biostable and resistant to enzymatic degradation by proteases. The present sequence of nucleobases) targetting HIV genes. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vaccinating against tumors, infectious diseases, allergies and asthmausing immunostimulatory Py-rich and TG nucleic acids.
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immunostimulatory; tumour; viral infection; bacterial infection;
fungal infection; parasitic infection; cancer; asthma;
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27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
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nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpeviridae, retroviridae, and/or orthomyxoviridae), bantigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Thi to a Thi immune response and to activate immune cells. Note: the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth; tumour metestasis; pecancerous lesion; rheumatorid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisettion; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar.
                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                        Length 22;
                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                    present sequence may have a phosphorothioate backbone
                                                                                                                                                                                                                                            Sequence 22 BP; 0 A; 0 C; 2 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                 Score 17.2; DB 1;
Pred. No. 3.9e+02;
                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Angiogenesis inhibitory oligonucleotide #61.
                                                                                                                                                                                                                                                                                                                                                                        1734 ACAAAAAAAAAAAAAAAAA 1755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-DEC-2001; 2001WO-US048458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-DEC-2000; 2000US-025534P.
                                                                                                                                                                                                                                                                                                          86.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABS77577 standard; DNA; 22
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                                                                                                                                                                                                                                                                                                        Best Local Similarity 86.4
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic contact dermatitis, latex dermatitis or inflammatory bowel disease by administering an immunostimulatory nucleic acid.
wound granulation, intestinal adhesions, atherosclerosis, scleroderma hypertrophic scars. The present sequence is an antiangiogenic nucleic acid of the invention
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                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunostimulatory, antiinflammatory, dermatological, antipsoriatic, antiulcer, gene therapy, vaccine, non-allergic inflammatory disease, psoriasis, eczema, allergic contact dermatitis, latex dermatitis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, ss.
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86.4%; Pred. No. 3.9e+02;
ive 0; Mismatches 3; Indels
                                                                                                  Length 22;
                                                                                                                                      3; Indels
                                                                  Sequence 22 BP; 0 A; 0 C; 2 G; 20 T; 0 U; 0 Other;
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                                                                                                  1.0%; Score 17.2; DB 1;
16.4%; Pred. No. 3.9e+02;
.ve 0; Mismatches 3;
                                                                                                                                                                       1734 ACAAAAAAAAAAAAAAAA 1755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 10; 229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    Immunostimulatory nucleic acid #55.
                                                                                                                                                                                                         22 AAAAACAAAAAAACAAAAAA 1
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                                                                                                                    86.48;
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                                                                                                                                                                                                                                                                                             ACD99369 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                 25-SEP-2003 (first entry)
                                                                                                                    Best Local Similarity 86.4
Matches 19; Conservative
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nes 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Krieg AM, Berg DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (KRIE/) KRIEG A M. (BERG/) BERG D J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2003050268-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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                                                                                                      Query Match
Best Local 9
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Bellon L;

Beigelman L, Mcswiggen JA, Karpeisky A, Zwick M, Jarvis T, Woolf T, Haeberli P;

98US-0082404P.

99WO-US008547

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New nucleic acids that interact, and optionally cleave, target sequences,
                                                                                                                                                                                                                          The present invention describes nucleic acids (A) that interact stably
                                                                                                                                                                                                    Claim 77; Page 79; 148pp; English
                                                                              (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                               used to treat cancer
                                                                                                                                               WPI; 2000-013248/01.
                                                                                                                          Matulic-Adamic J;
                                                                                                    Thompson JD,
                         19-APR-1999;
                                              20-APR-1998;
23-JUN-1998;
28-oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                          invention
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                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G nucleic acid in an aerosol formulation. The methods and compositions of the present invention are useful for diagnosing and/or treating asthma and allergy especially in a hypo-responative subject. The present sequence represents an immunostimulatory nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                                                   Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                             ds; allergy; asthma; poly-G nucleic acid; aerosol formulation; hypo-responsive subject; immunostimulatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.0%; Score 17.2; DB 1; Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
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0; Mismatches 3
                                                                                                                                                                                                                                                                                                       Bratzler RL, Petersen DM, Fouron Y;
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                                                                                         Immunostimulatory nucleic acid #52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; Page 6; 221pp; English.
                         ADB36438 standard; DNA; 22 BP.
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                                                                                                                                                                                                                                      03-FEB-2000; 2000US-0179991P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.48;
                                                                   (first entry)
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nes 19; Conservative
                                                                                                                                                                                                                                                           (BRAT/) BRATZLER R L.
(PETE/) PETERSEN D M.
(FOUR/) FOURON Y.
                                                                                                                                                                                                                                                                                                                           WPI; 2003-657977/62.
                                                                                                                                                                   US2003087848-A1.
                                                                   04-DEC-2003
                                                                                                                                                                                          08-MAY-2003
                                                                                                                                               Synthetic.
                                              ADB36438
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  RESULT 714
ADB36438/c
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with a target sequence and contain at least one phosphoro(di)thioate
link, having endonuclease activity. (A), and more generally any catalytic
link, having endonuclease activity. (A), and more generally any catalytic
cucleic acid (A) that modulates expression of the oestrogen receptor
cgene, are used to treat cancer (particularly of breast or endometrium).

CG in vivo or by transforming cells ex vivo and implanting treated cells, or
correlate inhibition of gene expression with alterations in phenotype,
ccorrelate inhibition of gene expression with alterations in phenotype,
correlate inhibition of gene expression with alterations in phenotype,
correlate inhibition of gene expression with alteration in phenotype,
ccorrelate inhibition of gene expression with alteration in phenotype,
correlate inhibition of gene expression with alteration in phenotype,
ccorrelate inhibition of gene expression with alteration in phenotype,
ccorrelate inhibition of gene expression with alteration in phenotype,
ccorrelate inhibition of gene expression with alteration as research
creagents (for RNA, in the same way that restriction endonucleases are
cused with DNA). The combination of modifications in (A) improves
correspondences, bandling affinity and/or activity. AAA23503 to
AAA24748 to AAA2592 represent thair corresponding target sequences.
AAA2593 to AAA26105 represent thair corresponding target
sequences. and AAA26107 to AAA26211 represent their ribozyme sequences and
antisense oligonucleotides used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Destrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1949.
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Pred. No. 3.4e+02;
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Destrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1948.

AAA25450 standard; DNA; 17 BP

AAA25450/

19-JUL-2000 (first entry)

Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage; hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide; gene expression modification; cancer; phosphorothioate; endonuclease; anticancer; brasst cancer; endometrium cancer; ss

WO9954459-A2 Ното варіеля

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AAA25452/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Link, having endonuclease activity. (A), and more generally any catalytic nucleic acid (A') that modulates expression of the oestrogen receptor gene, are used to treat cancer (particularly of breast or endometrium), in vivo or by transforming cells ex vivo and implanting treated cells, or for other conditions associated with levels of oestrogen receptor.

Correlate inhibition of gene expression with alterations in phenotype, particularly for identification of therapeutic targets, and as research reagents (for RNA, in the same way that restriction endonucleases are used with DNA). The combination of modifications in (A) improves resistance to nucleases, binding affinity and/or activity. AAA23503 to AAA24747 represent oestrogen receptor hammerhead ribozyme sequences.

AAA24747 represent oestrogen receptor hammerhead ribozyme sequences.

AAA25105 represent their corresponding target sequences.

AAA25105 represent oestrogen receptor hammerhead sequences.

Correlated the particular of the present their corresponding target sequences.

AAA25105 represent oestrogen receptor hammerhead sequences.
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                                                                                                                                                            New nucleic acids that interact, and optionally cleave, target sequences, used to treat cancer.
                                                                                                                                                                                                                         The present invention describes nucleic acids (A) that interact stably
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                      a target sequence and contain at least one phosphoro(di)thioate
                                                                                     Bellon L;
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100.0%; Pred. No. 3.4e+02;
ative 0; Mismatches 0; Indels
                                                                                   Karpeisky A,
Haeberli P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;
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                                                                                   Beigelman L, Mcswiggen JA,
Zwick M, Jarvis T, Woolf T,
                                                                                                                                                                                                 Claim 77; Page 79; 148pp; English.
                                                                                                Zwick M, Jarvis T,
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99WO-US008547.
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                                                            (RIBO-) RIBOZYME PHARM INC.
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Matches 17; Conservative
                                                                                                                                   WPI; 2000-013248/01.
                                                                                                             Matulic-Adamic J;
                                                                                     Thompson JD,
 19-APR-1999;
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                        20-APR-1998;
23-JUN-1998;
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                                                                                                  Reynolds M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention
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The present invention describes nucleic acids (A) that interact stably with a target sequence and contain at least one phosphoro(di)thioate with a target sequence and contain at least one phosphoro(di)thioate with a tarying endomuclease activity. (A), and more generally any catalytic nucleic acid (A') that modulates expression of the oestrogen receptor gene, are used to treat cancer (particularly of breast or endometrium), or the transforming cells ax vivo and implanting treated cells, or for other conditions associated with levels of oestrogen receptor. Secause of the high selectivity for targeted RNA, (A) can also be used to correlate inhibition of gene expression with alterations in phenotype, particularly for identification of therapeutic targets, and as research reagents (for RNA, in the same way that restriction endomucleases are used with DNA). The combination of modifications in (A) improves to resistance to nucleases, binding affinity and/or activity. AAA23503 to AAA24747 represent oestrogen receptor hammerhead ribozyme sequences.

AAA24748 to AAA25010 represent their corresponding target sequences.

AAA25010 represent cestrogen receptor hairpin ribozyme sequences. and AAA25010 to AAA26107 to AAA26107 represent cestrogen receptor hairpin ribozyme sequences. and AAA26107 to AAA26171 represent their corresponding target sequences and antisense oligonucleotides used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acids that interact, and optionally cleave, target sequences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                 Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky Ä, Reynolds M, Zwick M, Jarvis T, Woolf T, Haeberli P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 77; Page 79; 148pp; English.
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98US-0082404P.
98US-00103636.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US008547.
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                                                                                                                     (RIBO-) RIBOZYME PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              used to treat cancer.
                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-013248/01.
                                                                                                                                                                                                                                                                                Matulic-Adamic J;
20-APR-1998;
23-JUN-1998;
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23-JUN-1998;
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AAA98232 standard; DNA; 17 BP
                                                                                                                                                                                                                                                                                                                       Human endogenous retrovirus.
     (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                             30-JAN-2001 (first entry)
                                                    used to treat cancer
                                   MPI; 2000-013248/01.
                                                                                                                                                                                                                                                                                                            PCR primer; 88.
                                                                                                                                                                                                                                                                                                                                WO200053789-A2
                                                                                                                                                                                                                                                                                                                                            14-SEP-2000.
                                                                                                                                                                           invention
                                                                                                                                                                                                                                                                   AAA98232;
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Matches
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10-MAR-1999;

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This invention describes a novel retroviral expression vector (A)

containing DNA sequences (I) for packaging vector RNA and for cell-
specific expression of proteins or peptides encoding by heterologous DNA

(II). The sequences controlling cell-specific expression contain a cell-
specifically regulatable promoter region (P) from a human endogenous

cretrovirus (HRNY) DNA sequence. The invention also describes (a) mRNA and

RNA of (A); (b) prokaryotic and eukaryotic cells containing (A); (c)

eukaryotic cells containing (A) in integrated form; (d) virions

containing a retroviral expression vector RNA derived from (A); (e) a

method for producing the virions of (d); (f) amethod for incorporating

protein-encoding nucleic acid sequences into a eukaryotic cell by

containing (A) and a packaging cell line, that contains at least one

(recombinant) retrovirus construct that encodes for the packaging

proteins of (A). (A) are used for cell- or tissue-specific expression of

proteins of (A). (A) are used for cell- or tissue-specific expression of

cortaining qenes for gene therapy and to produce virions for introducing

(II) into the chromosomal DNA of eukaryotic cells, preferably mammalian

and specifically human. (A) retain the advantages of usual retroviral

promoters with all the signal structures required for transcription in a

small region within the U3-R segment, but without their disadvantages

(Excessive strength and limited cell specificity). Since (A) are derived

controlled or produces into the genome and recombination will not create new

viral sequences into the genome and recombination will not create new

cypression, according to which HERV they are derived from
                                                                                 Retroviral expression vector, useful in gene therapy, contains a promoter from a human endogenous retrovirus to provide cell-specific expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "phosphorothioate internucleoside linkages"
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Pred. No. 3.4e+02;
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100.0%; Pred. No. J.
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                                                                                                                                                                  Disclosure; Page 27; 67pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1736 AAAAAAAAAAAAAA 1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAS0197 standard; DNA; 17 BP
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/note= "2'
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                            WPI; 2000-587442/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40200047593-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes nucleic acids (A) that interact stably with a target sequence and contain at least one phosphoro(di)thioate with a target sequence and contain at least one phosphoro(di)thioate contains and andonuclases eatroity. (A), and more generally any catalytic nucleic acid (A') that modulates expression of the oestrogen receptor. Gene, are used to treat cancer (particularly of breast or endometrium), con by transforming cells ex vivo and implanting treated cells, or for other conditions associated with levels of oestrogen receptor. Gecause of the high selectivity for targeted RNA, (A) can also be used to correlate inhibition of gene expression with alterations in phenotype, particularly for identification of therapeutic targets, and as research reagents (for RNA, in the same way that restriction endomucleases are used with DNA). The combination of modifications in (A) improves cellstance to nucleases; binding affinity and/or activity. AAA2303 to AAA2474 represent oestrogen receptor hammerhead ribozyme sequences.

AAA24748 to AAA2592 represent their corresponding target sequences.

AAA2593 to AAA26105 represent testrogen receptor hairpin ribozyme sequences.

Sequences, and AAA26107 to AAA26218 represent their corresponding target sequences and antisense oligonucleotides used in the exemplification of the present
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                                                                                                                                                                                                                                             nucleic acids that interact, and optionally cleave, target sequences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell-specific expression; tissue-specific expression; gene therapy; LTR; U3-R segment; long terminal repeat; retroviral expression vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                              Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L; Reynolds M, Zwick M, Jarvis T, Woolf T, Haeberli P; Matulic-Adamic J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                              Claim 77; Page 79; 148pp; English
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Gaps

12-FEB-1999;

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ABT34613 standard; DNA; 17 BP
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                                                                                                                                                                 17 AAAAAAAAAAAAAAA
                                                                                                                                                                                                     12-JUN-2003 (first entry)
                                                                                                                            tests on e.g. biologica.
and as antiviral agents
                     WPI; 2000-558188/51
                                                                                                                                                                                                                                             WO2003025175-A2
              Manoharan M,
                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                    27-MAR-2003.
                                                                                                                                                                                             ABT34613;
                                                                                                                                              Query Match
                                                                                                                                                                              RESULT 721
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The invention relates to a novel isolated 17 mer nucleic acid sequence, given in the specification, a sequence containing at least 15 consecutive mucleotides from the 17 mer sequence, a sequence with, after optimal alignment, at least 80 % identity to the 17 mer sequence that conditions to them. The sequence is a sequence that hybridizes to them under highly stringent conditions, or the complement of any of them, or the corresponding RNA. The novel isolated nucleic caids of the invention are useful as probes and primers for detecting, identifying and/or amplifying a nucleic acid, e.g. as one caids of the invention are useful any properties. Any of the nucleic acids, production of recombinant polypeptides. Nay of the nucleic acids, polypeptides, vectors containing the nucleic acids, cells containing the vector or antibodies directed against the polypeptides are useful for vector or antibodies directed against the polypeptides are useful for component of them and/or treatment of viral diseases that are characterised by development of tumours or cell diseases that are characterised by development of tumours or cell containing the containing the expression of the 17 mer nucleic acids in patient samples is useful for diagnosis and/or prognosis of these containing the containing the polypeptides and antibodies are useful as components of protein chips. The nucleic acid sequences of the invention can be used in gene therapy. This polymucleotide sequence represents a tumour suppression characy. This polymucleotide sequence represents a tumour suppression characy.
                                                                                                                                                                          New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MDZ3; MDZ4; MDZ12; chromosome 7q22.1;
chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 100.0%; Pred. No. 3.4e+02; 17; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                     Disclosure; Page 63; 720pp; French.
                                                           Tuijnder M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1644 GATCACTCTCCCTGACA 1660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP
   (MOLE-) MOLECULAR ENGINES LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GATCACTCTCCCTGACA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-AUG-2001; 2001US-00922181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUL-2002; 2002EP-00016874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        272/c
ADB04272 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome 6p21.3-22.2; chr
developmental disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                           Amson R,
                                                                                                                    WPI; 2003-313353/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AEOM-) AEOMICA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SP1281758-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17;
                                                               Telerman A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADB04272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB04272,
   요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of a phosphorothicate oligonucleotide containing 20 T nucleobases, each having a 2'-methoxyethoxy group on its 5 riboay! sugar moiety. It is an example of an oligomeric compound produced according to the methods of the invention. The invention of provides compounds and methods for the preparation of mixed backbone oligomeric, or chimeric, compounds having phosphoriser internucleoside linkages in addition to phosphorothoate and/or phosphoranidate internucleoside linkages. The methods utilise H-coranidate internucleoside linkages. The methods utilise H-coranidate internucleoside linkages. The methods utilise H-coranidate internucleoside linkages. The methods utilise H-coranidates that are coupled together forming contiguous regions of 1 or more H-phosphonate internucleoside linkages. Each contiguous region is subsequently oxidized to phosphodiester.

Contiguous region is subsequently oxidized to phosphodiester.

Contiguous region is subsequently oxidized to phosphodiester.

Contiguous region is ubsequently oxidized to phosphodiester.

Contiguous region in this manner by oxidizing adjacent regions with different reagents. Oligomeric compounds of the invention are prepared using novel oxidation steps that oxidize a region of 1 or more H-phosphonate compounds of the invention are prepared using novel oxidation steps that oxidize a region of 1 or more H-phosphonate content of primers in PCR, probes, linkers, gene fragments and for other dagnostic feets on e.g. biological tiskers, gene fragments and for other dagnostic feets on e.g. biological tiskers, gene fragments are seserch reagents,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                   Preparation of mixed backbone oligomeric compounds useful as e.g. primers for diagnostic tests, involves oxidation of H-phosphonate internucleoside linkages to phosphodiester internucleoside linkages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip; antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease; schizophrenia; protein chip; gene therapy; tumour suppression; human fukutin; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 1.0%; Score 17; DB 1; Length 17; Local Similarity 100.0%; Pred. No. 3.4e+02; nes 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                              Example 12; Page 34; 49pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1736 AAAAAAAAAAAAAA 1752
99US-00250075
                                                                                                                    Maier MA;
                                                        (ISIS-) ISIS PHARM INC.
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Gaps ö

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proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is encoded at chromosome 7g22.1, MD24 is encoded at chromosome 6p11.3-22.2, MD27 is more more for in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MD24. MD27, or MD21, e.g. cancer or developmental disorders. The nucleic acids and proteins are also useful for diagnosing or monitoring a disease caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic acids can also be used as probes to detect and characterize gross alterations in MD23, MD27, or MD212 genetic locus. The probes are
                                                                 New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7 or MDZ12, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                             useful in constructing microarrays for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as vaccines. The present sequence was used to illustrate the invention.
                                                                                                                                                                                   present invention relates to novel human zinc finger-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;
                                                                                                                                                   Example 8; SEQ ID NO 5258; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAAAAAAAAAAAAA 1
Gu Y, Nguyen C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-AUG-2003 (first entry)
                                     WPI; 2003-423107/40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified
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 Shannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD56441;
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Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H; Antisense oligo #2, to elicit RNase H degradation of target RNA 1735 CAAAAAAAAAAAAAAA 1751 AAD56441 standard; DNA; 17 BP

9. .10 /*tog= a /note= "Bases 9 and 10 are linked by a butanediol linker which is represented as B in page 49 and X in page 59, Fig 9 and 10 of the specification" Location/Qualifiers

(UYMC-) UNIV MCGILL

Parniak MA, Damha MJ, Viazovkina E, Mangos MM,

Min K;

29-OCT-2001; 2001US-0330719P. 29-OCT-2002; 2002WO-CA001628 WPI; 2003-421516/39. 402003037909-A1 08-MAY-2003

ö The invention relates to an acyclic linker-containing oligonucleotide comprising at least one modified decxyribonucleotide. Oligonucleotides of the invention are useful for preventing or decreasing translation, reverse transcription and/or replication of a target RNA in a system. They are useful for selectively preventing gene expression in a sequencespecific manner, for hybridising to complementary RNA such as cellular mRNA or viral RNA, to hybridise to and induce cleavage of complementary RNA. They are also useful therapeutically in formulations or medicaments to prevent or treat a disease characterised by the expression of a particular target RNA. The invention is used in gene therapy. The present sequence is an antienne oligo used to elicit human RNase (ribonuclasse) H degradation of target RNA. This sequence is used in the exemplification /*teg= b //*teg= b //note= "Bases 9 and 10 are linked by a butanediol linker which is represented as B in page 49 and Fig 5 and as X in page 52, 55 and Fig 6 of the specification" ö 2'F-ANA antisense oligo #3, to elicit RNase H degradation of target RNA Novel acyclic linker-containing oligonucleotide useful for preventing decreasing translation, reverse transcription and/or replication of a target RNA in a system, comprises a modified deoxyribonucleotide. Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H; Gaps ö /mod_base= OTHER /note= "2'-deoxy-2'-fluoroarabinothymidine" 1.0%; Score 17; DB 1; Length 17; .00.0%; Pred. No. 3.4e+02; 0; Indels Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other; / Match Local Similarity 100.0%; Pred. NO. J... Location/Qualifiers Example 2; Page 90; 104pp; English 1736 AAAAAAAAAAAAAA 1752 AAD56448 standard; DNA; 17 BP 17 AAAAAAAAAAAAAAA 1 (first entry) ಹ .17 of the invention antisense; ss. Key modified_base 07-AUG-2003 Unidentified misc_feature AAD56448; Query Match Novel Matches ઠ 셤 

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Gaps

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Novel acyclic linker-containing oligonucleotide useful for preventing or χ. Mangos MM, Parniak MA, Min Damha MJ, Viazovkina E, VPI; 2003-421516/39

29-OCT-2001; 2001US-0330719P 29-OCT-2002; 2002WO-CA001628

WO2003037909-A1

08-MAY-2003

(UYMC-) UNIV MCGILL

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                                                                                                                                                The invention relates to an acyclic linker-containing oligonucleotide comprising at least one modified deoxyribonucleotide. Oligonucleotides of the invention are useful for preventing or decreasing translation, reverse transcription and/or replication of a target RNA in a system. They are useful for selectively preventing gene expression in a sequence-specific manner, for hybridising to complementary RNA such as cellular mRNA or viral RNA, to hybridise to and induce cleavage of complementary RNA. They are also useful therapeutically in formulations or medicaments to prevent or treat a disease characterised by the expression of a particular target RNA. The invention is used in gene therapy: The present sequence is an antisense oligo used to elicit human RNase (ribonuclease) H degradation of target RNA. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mod_base= OTHER
/note= "2'-deoxy-2'-fluoroarabinothymidine"
12. .13
/rtag= bases 12 and 13 are linked by a butanediol linker
which is represented as B in page 49 and Fig 5 and as X
in page 55 and Fig 6 of the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2'F-ANA antisense oligo #4, to elicit RNase H degradation of target RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel acyclic linker-containing oligonuclectide useful for preventing decreasing translation, reverse transcription and/or replication of a target RNA in a system, comprises a modified deoxyribonucleotide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
translation, reverse transcription and/or replication of in a system, comprises a modified deoxyribonucleotide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.0%; Score 17; DB 1; Length 17; 100.0%; Pred. No. 3.4e+02; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
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                                                                                            Example 2; Fig 5; 104pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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target RNA i
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                                      The invention relates to an acyclic linker-containing oligonucleotide comprising at least one modified deoxyribonucleotide. Oligonucleotides of rehe invention are useful for preventing or decreasing translation, reverse translation, and/or replication of a target RNA in a system. They are useful for selectively preventing gene expression in a sequencespecific manner, for hybridising to complementary RNA such as cellular mRNA or viral RNA, to hybridise to and induce cleavage of complementary RNA. They are also useful therapeutically in formulations or medicaments to prevent or treat a disease characterised by the expression of a particular target RNA. The invention is used in gene therapy. The present sequence is an antisense oligo used to elicit human RNase (ribonuclease) and degradation of target RNA. This sequence is used in the exemplification
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/*tag= b
/*tog= "Bases 4 and 5 are linked by a butanediol linker
which is represented as B in page 49 and Fig 5 and as X
in page 55 and Fig 6 of the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2'F-ANA antisense oligo #2, to elicit RNase H degradation of target RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel acyclic linker-containing oligonuclectide useful for preventing decreasing translation, reverse transcription and/or replication of a target RNA in a system, comprises a modified deoxyribonuclectide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
                                                                                                                                                                                                                                                                                                                                         Gape
                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mod_base= ОТНБR
/note= "2'-deoxy-2'-fluoroarabinothymidine"
                                                                                                                                                                                                                                                                                                        Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Min K;
                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                         Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parniak MA,
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100.0%; Pred. No. 3.4e+02;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
               Example 2; Fig 5; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                        1736 AAAAAAAAAAAAAAA 1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD56447 standard; DNA; 17 BP
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                                                                                                                                                                                                                                                                                                                                                                                                         AAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                       17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Damha MJ, Viazovkina E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..17
*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYMC-) UNIV MCGILL.
                                                                                                                                                                                                                                           of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003037909-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antisense; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jnidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
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                                                                                                                                                                                                                                                                                                         Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 726
                                                                                                                                                                                                                                                                                                                                        Matches
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Example 2; Fig 5; 104pp; English.

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The invention relates to an acyclic linker-containing oligonucleotide comprising at least one modified deoxyribonucleotide. Oligonucleotides of the invention are useful for preventing or decreasing translation, reverse transcription and/or replication of a target RNA in a system. They are useful for selectively preventing gene expression in a sequence-specific manner, for hybridising to complementary RNA such as cellular mRNA or viral RNA, to hybridising to complementary RNA such as cellular RNA. They are also useful therapeutically in formulations or medicaments to prevent or treat a disease characterised by the expression of a particular target RNA. The invention is used in gene therapy. The present sequence is an antisense oligo used to elicit human RNase (ribonuclease) H degradation of target RNA. This sequence is used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                  of the invention
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Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Gaps ö Length 17; 1.0%; Score 17; DB 1; Length 17; 100.0%; Pred. No. 3.4e+02; tive 0; Mismatches 0; Indels Query Match Best Local Similarity 100. Matches 17; Conservative

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1736 AAAAAAAAAAAAAA 1752

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AAAAAAAAAAAAA 1 17

AADS6450 standard; DNA; 17 BP 07-AUG-2003 (first entry) antisense; ss AAD56450; RESULT 727 

2'F-ANA antisense oligo #5, to elicit RNase H degradation of target RNA Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;

Unidentified

/note= "2'-deoxy-2'-fluoroarabinothymidine" Location/Qualifiers /\*tag= a /mod\_base= OTHER Key modified\_base

misc\_feature

9. 10 /\*tag= b /\*tote= "bases 9 and 10 are linked by a secouridine linker which is represented as S in page 49 and X in page 57 and Fig 1, 2, 7 and 8 of the specification"

WO2003037909-A1

38-MAY-2003

29-OCT-2002; 2002WO-CA001628.

29-OCT-2001; 2001US-0330719P

(UYMC-) UNIV MCGILL.

Novel acyclic linker-containing oligonucleotide useful for preventing decreasing translation, reverse transcription and/or replication of a target RNA in a system, comprises a modified deoxyribonucleotide. WPI; 2003-421516/39.

Parniak MA, Min K;

Mangos MM,

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Damha MJ, Viazovkina

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The invention relates to the isolation of 6327 nucleotide sequences, fragments of at least 15 consecutive nucleotides of these nucleotides, a sequence having at least 80% identity, after optimal alignment, with the nucleotides, a sequence that hybridizes under stringent conditions with the nucleotides or the complement, or corresponding RNA, of the nucleotides or the nucleotides are used as probes or primers for detecting, identifying, quantifying and/or amplifying nucleotides as in vitro sense and antisense sequences, of nucleotides involved in tumour suppression or reversion, apoptosis and or viral resistence, to produce recombinant polypeptides, and to prepare transgenic animals, as experimental models. The nucleotides (also vectors containing them and

Example 2; Fig 7; 104pp; English

The invention relates to an acyclic linker-containing oligonucleotide

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comprising at least one modified deoxyribonucleotide. Oligonucleotides of the invention are useful for preventing or decreasing translation, reverse transcription and/or replication of a target RNA in a system. They are useful for selectively preventing gene expression in a sequence-specific manner, for hybridising to complementary RNA such as cellular RNA, or hybridise to and induce cleavage of complementary RNA. They are also useful therapeutically in formulations or medicaments to prevent or treat a disease characterised by the expression of a particular target RNA. The invention is used in gene therapy. The present sequence is an antisense oligo used to elicit human RNase (tibonuclasse) H degradation of target RNA. This sequence is used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic, antiviral; neuroprotective, nootropic, neuroleptic; ss;
primer; probe; tumour suppression; tumour reversion; apoptosis;
virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related polypeptide and antibodies.
                                                                                                                                                                                                                                                                          Gape
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                                                                                                                                                                                                                                        Score 17; DB 1; Length 17;
Pred. No. 3.4e+02;
                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pumour suppression/reversion associated nucleotide #2295.
                                                                                                                                                                                                          Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                                         / Match
Local Similarity 100.0%; Pred. No. 5.-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 300; 771pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tuijnder M;
                                                                                                                                                                                                                                                                                                        1736 AAAAAAAAAAAAAA 1752
                                                                                                                                                                                                                                                                                                                                                                                                                  ADB41972 standard; DNA; 17 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-SEP-2001; 2001FR-00011981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-SEP-2002; 2002WO-IB004219.
                                                                                                                                                                                                                                                                                                                                     17 AAAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 relerman A, Amson R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-441574/41.
                                                                                                                                                                               of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAY-2003.
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04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis.
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                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                          Matches
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Gaps

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Indels

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100.0%; Pred. No. 3.6e+02;

Mismatches

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Best Local Similarity 100.
Matches 17; Conservative
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                                  (Ab) against the polypeptide are useful for prevention and/or treatment of viral infections or diseases characterized by development of tumours or call degeneration (e.g. Alzheimer's disease or schizophrenia).

Analysis of the expression of the nucleotides can be used for diagnosis and/or prognosis of these diseases. The nucleotides and polypeptides can also be used to screen for their specific interactive molecules, potentially useful for treating diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P30313), vaccines contg. the immunogens and antibodies raised from them. The vaccines are useful in human and veterinary medicine and the antibodies are useful as diagnostic reagents. The DNA fragments are most esp. derived from the L1 region of human PV type 1a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA fragment coding for Papillomavirus antigenic proteins - and derived immunogen, vaccine and antibody.
   containing the vectors), the encoded polypeptides and antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence derived from the L1 region of the bovine papillomavirus (bPV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.0%; Score 17; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 3.4e+02; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diagnostioc reagent; vaccine; medicine; wart; tumour; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 BP; 16 A; 1 C; 1 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                          Seguence 17 BP; 4 A; 7 C; 2 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1644 GATCACTCTCCCTGACA 1660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yaniv M;
                                                                                                                                                                                                                                                                                                 expression of the nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAN30173 standard; DNA; 18 BP
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/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PASTEUR
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(DANO/) DANOS O.
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1.0%; Score 17; DB 1; Length 18;

Query Match

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                                                                                                                                                                                                                                                                                                                                                             Flavonoid 3' hydroxylase; pigmentation; flower colour; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel flavonoid 3'-hydroxylase(s) from flowering plants - and corresponding DNA, used in the manipulation of pigmentation in plants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.0%; Score 17; DB 1; Length 18;
100.0%; Pred. No. 3.6e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 BP; 1 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                              Anchored poly(T) oligonucleotide polyT-AnchA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Michael MZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 15; Page 59; 234pp; English.
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                                                                                                                                                                       BP.
                                                 2 CAAAAAAAAAAAAAA 18
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ID AAT94668 standard; DNA; 18
1735 CAAAAAAAAAAAAA
                                                                                                                                                                       AAT94667 standard; DNA; 18
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                                                                                                                                                                                                                                                               (first entry)
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Les 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brugliera F, Holton TA,
                                                                                                                                                                                                                                                                                                                                                                                        snapdragon; primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (FLOR-) FLORIGENE LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-448691/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-1997;
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                                                                                                                                                                                                                                                                  27-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
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                                                                                                                                                                                                                      AAT94667;
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                                                                                                                        RESULT 730
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                                                                                                                                                   AAT94667/
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Gape

WO9732023-A1

Synthetic

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This is the nucleotide sequence of a PCR primer used in the method of the invention, involving the use of novel apoptosis-related DNAs and proteins. The inventions can be used as diagnostic reagents for apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent in immunohistological staining, as a spoptosis inhibitors. It can also be used for treatment of apoptosis-related diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New secreted proteins and associated polynucleotides - obtained from murine adult spleen, human foetal kidney, human ovary, murine bone marrow and murine adult thymus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention describes novel proteins isolated from cDNA clones:
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                      apoptosis-related DNAs and proteins - for diagnosis, preventing or ing diseases associated with apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted protein; murine adult spleen; human foetal kidney; ovar;
bone marrow; thymus; AE648_1i; AE693_1i; AK438_1i; AK609_1i; AM1060_1i;
AQ2_1i; K433_1i; L256_1i; prevent; treat; ameliorate; medical; ds.
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                                                                                                                                                                                                                                                                                                 Score 17; DB 1; Length 18;
Pred. No. 3.6e+02;
                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                               Seguence 18 BP; 0 A; 0 C; 2 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human protein AQ2_1i 3'-portion and polyA tail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Racie LA,
                                                                                                                                                                                                                                                                                                                   100.0%; Pred. No. 3. trive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coy JM, Lavallie ER,
Agostino MJ;
                                                                                 Example 1; Page 48; 70pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Page 58; 75pp, English.
                                                                                                                                                                                                                                                                                                                                                                                  1734 ACAAAAAAAAAAAAA 1750
                                                                                                                                                                                                                                                                                                                                                                                                                       18 ACAAAAAAAAAAA 2
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97US-00960024
                                                                                                                                                                                                                                                                                                       1.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV37712 standard; cDNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                            17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-286946/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spaulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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29-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV37712;
                                         treating
                  Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 733
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    셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream region of a polyadenylation sequence. They were used to prime cDNA synthesis from snapdragon (Antirkhinum majus) petal and leaf RNA, and were also utilised in the PCR amplification of plant cytochrome P450 sequences (see also AAT94670-73). A cDNA clone (see AAT94657) encoding flavonoid 3' hydroxylase (see AAM95704) was isolated using a differential display approach. This can be used to manipulate the pigmentation of
Flavonoid 3' hydroxylase; pigmentation; flower colour; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                Novel flavonoid 3'-hydroxylase(s) from flowering plants - and corresponding DNA, used in the manipulation of pigmentation in plants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR; primer; amplification; apoptosis; antibody; inhibition; ss; immunohistological staining.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 18 BP; 0 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
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Pred. No. 3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                     Michael MZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 15; Page 59; 234pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleotide sequence PCR primer 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                97WO-AU000124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV54168 standard; cDNA; 18
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                                                                                                                                                                                                                                                                                                     Holton TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                      snapdragon; primer; ss
                                                                                                                                                                                                                                                           (FLOR-) FLORIGENE LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                          WPI; 1997-448691/41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transgenic plants
                                                                                                                                                                                                                                                                                                     Brugliera F,
                                                                                                                                                                              28-FEB-1997;
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409839437-A1

11-SEP-1998

Sakaki Y;

21-DEC-1998

AAV54168;

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Gaps

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The invention relates to an analytical method for determining the nucleotide sequence of nucleic acid analytes, including chemically nucleotide sequence of nucleic acid analytes, including chemically indiantial dignoucleotides. This new method utilises electrospray innisation-Fourier transform mass spectrometry. The ions are excited by sustained off-resonance excitation with single shot excitation, and the target fragmented by collisionally activated dissociation by a neutral gas, e.g. carbon dioxide. Alternatively, the excitation and dissociation can be nozzle skimmer dissociation. The method is used in molecular in biology and biomedical applications. The method is used in molecular in sextremely rapid and acts directly on the oligonucleotide. The method is extremely rapid and acts directly on the oligonucleotide. The method is effective for a variety of nucleic acid analytes, particularly successfully sequenced. The present sequence represents a propositional proposition of successfully sequenced. The present sequence represents a
haemostatic and thrombotic activity, receptor/ligand activity, anti-
hillammatory activity, cadherin/tumour invasion suppressor activity,
tumour inhibition activity and other activities. (Updated on 25-MAR-2003
to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Determining the nucleotide sequence of a nucleic acid analyte - using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/note= "phosphorothioate internucleotide linkages"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphorothicate; electrospray ionisation-Fourier transform; mass spectrometry; off-resonance excitation; ss.
                                                                                                                          1.0%; Score 17; DB 1; Length 18; 100.0%; Pred. No. 3.6e+02; tive 0; Mismatches 0; Indels
                                                                                        Sequence 18 BP; 17 A; 0 C; 1 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Phosphorothioate oligodeoxynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Fig 3A; 25pp; English.
                                                                                                                                                                                                    1736 AAAAAAAAAAAAAAA 1752
                                                                                                                                                                                                                                                                                                                                BP.
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                                                                                                                                                                                                                                                                                                                             AAV07750 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                           Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Secreted human proteins AS296-1i and AS34-1i, useful for treating tumors, autoimmune diseases, inflammatory disorders, wounds, microbial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic, immunostimulatory, antimicrobial, antiviral, immunostimulatory, antimicrobial, antiviral, immunosuppressive, antiinflammatory and vulnerary activity and which act as cytokine, cell proliferation of differentiation regulators. (1) is useful for treating tumors, autcoimmune diseases, inflammatory disorders, wounds, microbial infections and viral diseases. (1) is also useful for tengenessing graft versus host reaction. AAA40490-A40580 represent cDNA fragments that encode the secreted proteins AAB10226-B10288 described in the method of the invention
                                                                                                                                                                                                                                                                                                          Secreted protein, cytostatic, immunostimulatory; antimicrobial; antiviral; immunosuppressive; antiniflammatory; vulnerary; cytokine; cell proliferation; differentiation; regulator; treatment; tumor; autoimmune disease; inflammatory disorder; wound; microbial infection; viral disease; graft versus host reaction suppression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes novel secreted human proteins (I) which have
                                 Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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100.0%; Pred. No. 3.6e+02;
ive 0; Mismatches 0; Indels
1.0%; Score 17; DB 1; Length 18; 100.0%; Pred. No. 3.6e+02; ve 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                             Human adult ovary cDNA fragment AQ2_1i #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lavallie ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bowman MR;
                                                                   1736 AAAAAAAAAAAAAA 1752
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AAZ90644/c
ID AAZ90644 standard; DNA; 18 BP.
                                                                                                 1 AAAAAAAAAAAAAA 17
                  100.08;
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                                                                                                                                                                                 AAA40563 standard; cDNA; 18
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                                                                                                                                                                                                                                               (first entry)
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Best Local Similarity 100.
                                   17; Conservative
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Treacy M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and viral diseases.
                  Best Local Similarity
Matches 17; Conserv
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Merberg D,
                                                                                                                                                                                                                 AAA40563;
   Query Match
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                                                                                                                                                  RESULT 73
AAA40563
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                                                                                                                                                                                                                                                                                                                                                                                          tissue relating to obesity, particularly complications of visceral obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes (AA290631-631) and the proteins (AAV67598-V67600) are used in the genetic diagnosis, prevention and treatment of adipose tissue related diseases. Sequences AA290640-51 represent PCR primers amplifying the human adipose tissue genes
                                                                                                                                                                                                                                                                                                                          A physiologically active protein specifically derived from mammal tissue.
                                                                                                                                                                                                                                                                                                                                                                             The invention relates to identification of genes and proteins of adipose
                                                                                          Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human; arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.0%; Score 17; DB 1; Length 18; 100.0%; Pred. No. 3.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BEST; nucleic acid analysis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Binary encoded sequence tag method anchored primer #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 18 BP; 0 A; 0 C; 2 G; 16 T; 0 U; 0 Other;
                                                                 Human adipose tissue gene amplifying primer #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. ...
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gene expression; adaptor; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                  Example 2; Page 18; 50pp; Japanese
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06-APR-2000; 2000US-00544713.
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AAF75596 standard; DNA; 18
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                                       13-JUN-2000 (first entry)
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                                                                                                                                                                                                                                                                   (NISB ) JAPAN TOBACCO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
Les 17; Conservative
                                                                                                                                                                                                                                                                                               WPI; 2000-306578/27.
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                                                                                                                                                            JP2000037190-A
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                                                                                                                                                                                                                                          23-JUL-1998;
                                                                                                                                                                                                                23-JUL-1998;
                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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The invention relates to methods and kits for amplification of mRNA using a primer in PCR that contains an RNA polymerase (RNAP) promoter. The invention provides methods for amplification and detection of RNA derived from a population of cells, preferably eukaryotic cells and most preferably mammalian cells, which methods preserve fidelity with respect to sequence and transcript representation and additionally enable amplification of extremely small amounts of mRNA. The method and kit are useful for amplifying and detecting RNA derived from a population of cells, especially eukaryotic cells like mammals. The RNAs generated are
                                                                                                                                                                                                     The present invention describes a method of producing binary sequence tags from nucleic acid fragments in a sample, involving incubating the sample with cleaving reagents, mixing offest adaptors with the sample, incubating with more cleaving reagents and mixing the sample with adaptor incubating which more cleaving reagents and mixing the sample with adaptor are coupled to binary sequence tags. The method is useful in sequence analysis, including analysis and comparison
                                                                        Producing binary sequence tags, useful for analyzing nucleic acid sequence tags, gene expression or gene-expression patterns, involves generating nucleic acid fragments, which are mixed with offset adaptors
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNA polymerase; RNAP; RNA detection; IVT; in vitro transcription; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amplifying and detecting RNA derived from a population of cells employing a primer that contains an RNA polymerase promoter in polymerase chain reaction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA fragment used in 3' end PCR/IVT method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                             1.0%; Score 17; DB 1; Length 18;
100.0%; Pred. No. 3.6e+02;
tive 0; Mismatches 0; Indels
 Latimer DR;
                                                                                                                                                                                                                                                                                                                         of gene expression, nucleic acid samples and genomes
                                                                                                                                                                                                                                                                                                                                                          Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;
   Feng L,
                                                                                                                                                                    Disclosure; Page 100; 101pp; English.
 Lizardi PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ROSE-) ROSETTA INPHARMATICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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 Roth ME,
                                                                                                                                   and adaptor-indexers
                                     WPI; 2001-202878/20.
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 Kaufman JC,
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the templace for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
                                                                                                                                                                                                                                                                                                                                                                                                                           Analysis of cDNA and gene expression - by amplification of mRNA followed
                                                                               Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
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                                           Reverse transcription primer used in cDNA analysis technique.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 1.0%; Score 17; DB 1; Length 19; Local Similarity 100.0%; Pred. No. 3.7e+02; es 17; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                by digestion with restriction enzymes.
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    04-AUG-1995 (first entry)
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                                                                                                                                             Synthetic.
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useful for profiling gene expression in different populations of cells. The present sequence is a mRNA fragment used in 3' end PCR/IVT (in vitro transcription) method of the invention
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                                                                                                                                                                Gaps
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                                                                                                                  1.0%; Score 17; DB 1; Length 18;
100.0%; Pred. No. 3.68+02;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 3.7e+02;
vative 0; Mismatches 0; Indels
                                                                               Sequence 18 BP; 17 A; 0 C; 0 G; 0 T; 0 U; 1 Other;
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                                                                                                                                         Best Local Similarity 100. Matches 17; Conservative
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RESULT 740

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AAQ75556/ ID AAQ7 XX AC AAQ7

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Gaps

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The present sequence is a telomerase Oliog-dT-Primer, which can be used adding to a test sample a 1st primer, that serves as telomerase substrates, and nucleoside triphosphate (dhyp) and incubating to allow primer extension by the telomerase, amplifying the extension product, primer extension by the telomerase, amplifying the extension product, dualitative and/or quantitative detection of AP) on a solid phase and qualitative and/or quantitative detection of AP, where the substrate primer is preferably from the 5'-region of the long terminal repeat 2 (LTR-2) sequence of a retrovirus. The method can be used to diagnose tumours and screen compounds for effector activity. Immobilisation of AP provides a signal that is reproducibly representative of telomerase activity, eliminates the need for gel electrophoretic separation and
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of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Measuring telomerase activity, useful for tumour diagnosis and compound screening - by extending substrate primer, followed by amplification and immobilising product for detection.
Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
                                                                                                              double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GBNESGO files AAQTS547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
                                                                                            analysis of cDNA comprises (a) preparing an aggregate
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Pred. No. 3.7e+02;
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                                                         Disclosure; Page 5; 11pp; Japanese.
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Best Local Similarity 100.
Matches 17; Conservative
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provides high sensitivity. Radioactive labels are not required and the method can be automated for routine use. Specific detection is achieved by proper choice of hybridisation conditions, without separation of the telomerase extension product. A specific signal is generated by 1-10 cell equivalents, but for tumour analysis 10-1000 ng of tissue is usually used
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100.0%; Pred. No. 3.9e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                  1.0%; Score 17; DB 1; Length 19;
.00.0%; Pred. No. 3.7e+02;
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                                                                                                                                              100.0%; Pred. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aggregate; restriction enzyme; ss.
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RAQ75605/c
ID AAQ75605 standard; DNA; 20 BP.
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Best Local Similarity 100.
Matches 17; Conservative
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
                                                                                                                                                                                                                                                                                                               - by amplification of mRNA followed
                                                                             expression; reverse transcription; primer; cDNA;
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                                                     Reverse transcription primer used in cDNA analysis technique.
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Pred. No. 3.9e+02;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                            by digestion with restriction enzymes.
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                                                                                              aggregate; restriction enzyme; ss
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                                    gene expression - by amplification of mRNA followed
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                                                                                                                                                                                                                                          seperate lanes. The
                                                                                                                                              double-stranded cDNAs by using an aggregate of mRNAs and a plural type labelled reverse transcription primers (GRNESGO files AAQV5547-075798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of CDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily
                                                                                                                         A method for the analysis of cDNA comprises (a) preparing an aggregate
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                                    Analysis of cDNA and gene expression - by digestion with restriction enzymes.
                                                                                          Disclosure; Page 5; 11pp; Japanese.
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Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
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A method for the analysis of cDNA comprises (a) preparing an aggregate double-stranded cDNAs by using an aggregate of mRNAs and a plural type labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse

Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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                                                Reverse transcription primer used in cDNA analysis technique
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               the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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Pred. No. 3.9e+02;
0; Mismatches 0; Indels
                                                                                                               1.0%; Score 17; DB 1; Length 20; 100.0%; Pred. No. 3.9e+02; tive 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pr
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transcription primer; (b)
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Analysis; gene expression; reverse transcription; primer; cDNA;
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                                                                                                                                    aggregate; restriction enzyme; ss.
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AAQ75595 standard; DNA; 20 BP

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1.0%; Score 17; DB 1; Length 20; 100.0%; Pred. No. 3.9e+02; tive 0; Mismatches 0; Indels

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                                                                                                         A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GBNESEQ files AAQ75547-057598) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
                 - by amplification of mRNA followed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Analysis of cDNA and gene expression – by amplification of mRNA followed by digestion with restriction enzymes.
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100.0%; Pred. No. 3.9e+02;
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                 Analysis of cDNA and gene expression - by digestion with restriction enzymes.
                                                                         Disclosure, Page 5; 11pp; Japanese.
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Matches 17; Conservative
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Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
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                                                                                                                                                                                   reverse transcription; primer; cDNA;
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                                                                                                                                                       Reverse transcription primer used in cDNA analysis technique.
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100.0%; Pred. No. 3.9e+02;
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aggregate; restriction enzyme; ss.
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                                                                     AAQ75587 standard; DNA; 20
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ABQ79871/c
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Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.
                                                                                                                                                                                                                                                                                                                                                                                            Carrying out a thermal cycle of polymerase chain reaction (PCR) by using a substrate on which a DNA is immobilized used in medical, biochemical, molecular biological and gene engineering fields.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to performing a thermal cycle of PCR by using a substrate on which a deoxyribonucleic acid (DNA) is immobilized. The method is useful in the medical, biochemical, molecular biological and genetic engineering fields. Sequences ABQ79871-881 represent PCR primers used in the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.0%; Score 17; DB 1; Length 20; 100.0%; Pred. No. 3.9e+02; tive 0; Mismatches 0; Indels
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Tang L, Shahabuddin S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example; Page 9; 13pp; Japanese.
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                                                                                                27-DEC-2000; 2000JP-00399573.
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Miller S,
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AC ABZ89898
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XW Human,
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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antifinitammatory, antiallergic, antiasthmatic, hypotensive, in antisense gene therapy. The composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, communosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing levels of adenosine receptor, producing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung inflammation, lung allergies, or a respiratory disease or condition, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO
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                 Disclosure; SEQ ID NO 5138; 872pp; English.
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Tang L, Shahabuddin S;
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Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

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Aguilar

Pabalan J,

Katz E,

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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the intitation codon, coding regalon, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallargic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a immunosuppressive and cytostatic activity. The composition may have a preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an preventing sensitivity to adenosine reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject, for reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung inflammation, lung allergies, or a respiratory disease or condition, Note: The sequence data for this patent is not represented in the printed specification, but was obsained in electronic format directly from WIPO
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                            Claim 15; SEQ ID NO 774; 872pp; English.
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Seguence 20 BP; 17 A; 2 C; 1 G; 0 T; 0 U; 0 Other;

Gaps ô 1.0%; Score 17; DB 1; Length 20; 100.0%; Pred. No. 3.9e+02; ative 0; Mismatches 0; Indels Query Match Best Local Similarity 100.0 Matches 17; Conservative

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1735 CAAAAAAAAAAAAA 1751 CAAAAAAAAAAAAA 20

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ABZ89872 standard; DNA; 20 RESULT 758 AB289872 THE STANDARD 
17-OCT-2003 (first entry) ABZ89872;

Human oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; inflammation; respiratory disease; ds lung

Homo sapiens

WO200285308-A2.

31-OCT-2002

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC

Pabalan J, Aguilar Katz E, Li Y, Sandrasagra A, Ka Tang L, Shahabuddin S; Miller S, Nyce JW,

WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation coodon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 mucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an entilnflammatory steroid and ubjquinone. A composition of the invention has antiinflammatory, antiallergic, antistathmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene, therapy. The composition may have a preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antistralemmatory steroid in a subject, for reducing levels of denosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung surfactant in a subject's tissue, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO
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              Jaclosure, SEQ ID NO 5114; 872pp; English.
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BP ABZ89719 standard; DNA; 20 ABZ89719; RESULT 759 ABZ89719,

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Human oligonucleotide sequence 17-OCT-2003 (first entry) 

Human; antisense; lung dysfunction; nasal airway dysfunction; antinflammatory steroid; ubiquinone; antinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

WO200285308-A2.

31-OCT-2002

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC.

Aguilar D; Li Y, Sandrasagra A, Katz E, Pabalan J, , Tang L, Shahabuddin S; Nyce JW, I Miller S,

WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone

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by digestion with restriction enzymes.
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes. electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss. Reverse transcription primer used in cDNA analysis technique. 1.0%; Score 17; DB 1; Length 21; 100.0%; Pred. No. 4e+02; ive 0; Mismatches 0; Indels 1.0%; Score 17; DB 1; Length 21; 0; Indels Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 U; 0 Other; Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other; 0; Mismatches (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP. Disclosure; Page 8; 11pp; Japanese 1736 AAAAAAAAAAAAAA 1752 1736 AAAAAAAAAAAAAA 1752 BP. AAQ75752 standard; DNA; 21 BP 100.08; 93JP-00112515. 93JP-00112515. 17 AAAAAAAAAAAAAAAA 17 AAAAAAAAAAAAAAA AAQ75762 standard; DNA; 21 04-AUG-1995 (first entry) Query Match
Best Local Similarity 100.0
Matches 17; Conservative (first entry) Matches 17; Conservative WPI; 1995-018287/03. Best Local Similarity 16-APR-1993; JP06303997-A. 16-APR-1993; 04-AUG-1995 Synthetic. AAQ75752; AAQ75762; Query Match RESULT 761 RESULT 762 AAQ75762/c AAQ75752/ ន្តដ្ឋប្រ ð 셤 g ઠ The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding regalon, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory stretcid and ubiquinone. A composition of the invention has antiinflammatory, antiallargic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antifalmmatory steroid in a subject, for reducing levels of adenosine receptor, producing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing bronchoconstriction, lung surfactant in a subject stissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at fig. ö A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GRNESEQ files AAQ75547-075798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) Analysis of cDNA and gene expression - by amplification of mRNA followed Gaps Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss. ö Reverse transcription primer used in cDNA analysis technique. Query Match 1.0%; Score 17; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 3.9e+02; Matches 17; Conservative 0; Mismatches 0; Indels Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other; Disclosure; SEQ ID NO 4961; 872pp; English. (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP

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by digestion with restriction enzymes.
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                                                           Analysis; gene expression; reverse transcription; primer; cDNA;
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                   Reverse transcription primer used in cDNA analysis technique.
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                                                                                aggregate; restriction enzyme; ss
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                                                       A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-075798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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ive 0; Mismatches 0; Indels
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Disclosure; Page 9; 11pp; Japanese.
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Matches 17; Conservative
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Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
                                                                                                                                                                                                 Analysis of cDNA and gene expression - by amplification of mRNA followed
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                                                                                                            (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
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nes 17; Conservative
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AAQ75787/c
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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Reverse transcription primer used in cDNA analysis technique.
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method can be used to analyse gene expression rapidly and easily
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100.0%; Pred. No. 4e+02;
ive. 0; Mismatches 0; Indels
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1.0%; Score 17; DB 1; Length 21,
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                           Seguence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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                                                                                                                                                                                                                                                  1.0%; Score 17; DB 1; Length 21;
100.0%; Pred. No. 4e+02;
tive 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Fred. No. 4e+
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               Disclosure; Page 7; 11pp; Japanese
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AAQ75763/
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Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
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                                                                                                                                          expression; reverse transcription; primer; cDNA;
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                                                                                                             Reverse transcription primer used in cDNA analysis technique.
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Pred. No. 4e+02;
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                                                                                                                                                         aggregate; restriction enzyme; ss.
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                            AAQ75688 standard; DNA; 21 BP
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                                                        AAQ75688;
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RESULT 772
AAQ75688/c
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mkNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mkNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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                                                                                                                                             Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
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100.0%; Pred. No. 4e+02;
ative 0; Mismatches 0; Indels
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                                                                        (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
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Matches 17; Conservative
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16-APR-1993;
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Analysis of cDNA and gene expression – by amplification of mRNA followed
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                             DB 1; Length 21;
.4e+02;
thes 0; Indels
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Pred. No. 4e+02;
0; Mismatches 0; Indels
Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 U; 0 Other;
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tive 0; Mismatches
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tive 0; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                                                                      aggregate; restriction enzyme; ss
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Best Local Similarity 100.0
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                                             Best Local Similarity 100.
Matches 17; Conservative
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Disclosure; Page 9; 11pp; Japanese
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Best Local Similarity 100.0
Matches 17, Conservative
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     Analysis; gene
                          JP06303997-A
                                                    16-APR-1993;
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                                      A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of ababled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
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1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels
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Pred. No. 4e+02;
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Disclosure; Page 9; 11pp; Japanese.
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Best Local Similarity 100.0
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                                                                                                                                                                                                                                                                                                                                                                                                 Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
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                      expression; reverse transcription; primer; cDNA;
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100.0%; Pred. No. 4e+02;
tive 0; Mismatches 0; Indels
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                                           restriction enzyme; ss
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AAQ75790 standard; DNA; 21 BP.

RESULT 779 AAQ75790/c

(first entry)

04-AUG-1995

AAQ75790

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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEC files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) the digested aggregate of cDNAs in seperate lanes. The method can be used to analyse gene expression rapidly and easily
                                                                                                                                               Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
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                                                           (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
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Pred. No. 4e+02;
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Disclosure; Page 9; 11pp; Japanese.

WPI; 1995-018287/03

93JP-00112515 93JP-00112515

16-APR-1993; 16-APR-1993;

JP06303997-A

Synthetic

11-NOV-1994

1.0%; Scc. v 100.0%; Pre/ 0; N

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Conservative

Query Match Best Local Similarity Matches 17; Conserv

AAAAAAAAAAAAA 1

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AAQ75697 standard; DNA; 21

RESULT 780 AAQ75697/c (first entry)

04-AUG-1995

AAQ75697;

93JP-00112515.

16-APR-1993;

01-NOV-1994

JP06303997-A

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Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
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Analysis; gene expression; reverse transcription; primer; cDNA;
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100.0%; Pred. No. 4e+02;
ive 0; Mismatches 0; Indels
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                        aggregate; restriction enzyme; ss
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Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels
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Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
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Reverse transcription primer used in cDNA analysis technique.
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Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.
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aggregate; restriction enzyme; as
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A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of aballed reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in seperate lanes. The
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aggregate; restriction enzyme; ss.
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100.0%; Pred. No. 4e+02;
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tive 0; Mismatches 0; Indels
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This invention describes a novel method of determining a predisposition to disease by genotyping a subject's DNA sequence (A) of the human mismatch repair gene, MSH6 at specified positions and comparing with ceference DNA sequences, optionally taking into account all possible combinations of variations of the individual mutations, including any chosen absolute number of variations (A), and analysis of their chosen absolute number of variations (A), and analysis of their chosen absolute number of variations (A), and analysis of their chosen absolute number of variations (A), and analysis of their chosen absolute number of variations (A), and analysis of their constitutions, insertions and/or deletions) in eukaryotic cells; (iii) predicting the progression, severly and survival time of patients with neoplastic disease; (iv) the development of therapeutic and 'life-style' chosen chemotherapeutic agents (e.g. cis-lpiatin) or drugs developed from (iv); (vii) constructing genes and vectors, particularly for development of pharmaceuticals; (ix) developing diagnostic kits and other systems for september and (x) developing in vivo and in viro test systems for expressing individual forms of the MSH6 gene, e.g. for studying end (x) developing in vivo and in viro test systems for expressing individual forms of the MSH6 gene, e.g. for studying end
                                                                                                                                                                       Novel variants of the human mismatch repair gene, MSH6, useful e.g. for determining predisposition to cancer and for development of drugs.
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                                                                                      Schackert H;
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06-MAR-1999;
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                                                                                      Plaschke J,
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100.0%; Pred. No. 4e+02;
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               AAQ75783 standard; DNA; 21 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA98276 standard; DNA; 22
                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-018287/03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DE19909878-A1
                                                                                                     04-AUG-1995
                                                                                                                                                                                                                                                                                                 JP06303997-A.
                                                                                                                                                                                                                                                                                                                                                                                       16-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                16-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                            01-NOV-1994.
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                                                                                                                                                                                                                                                      Synthetic.
                                                          AAQ75783;
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Matches

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Gaps

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Disclosure; Page 107; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
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                                                                                                                                                                                                                                                                       RESULT 797
                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                  AAQ61896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New modified oligo-nucleotide contg guanine quartet - inhibits activity of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length of chromosomes.
                                                                                                                                                         These
                                                                                                                     The sequences given in AAQ7325-81 represent oligonucleotides which hybridise specifically with DNA or RNA from a herpes virus gene corresponding to one of the open reading frames ULS. *8, -9, -20, -20, -30, -30, -42, -52 or IE175 of herpes simplex virus type I (HSV-1). These oligos pref. hybridise with a translation initiation site, a coding region or a 5' untranslated region. These oligos may be used in compositions for the treatment and diagnosis of herpes viral infection, by contacting the virus or the animal, or its cells, tissues or body fluids with the oligo. (Updated on 25-MAR-2003 to correct PN field.)
                                                     New oligonucleotide(s) hybridising with DNA or RNA of herpesvirus gene are used in the treatment and diagnosis of herpes simplex virus, cytomegalovirus, Epstein Barr virus and varicella zoster infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibition; replication; herpes simplex virus; HSV; HIV; retard; human cytomegalovirus; influenza virus; inflammation; telomere length; neurological disorders; phospholipase A2 activity; hyperproliferation; malignancy; cardiovascular disease; snake bite; malignancy; aging; ss.
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chiang M, Brown-Driver VL;
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/note= "Phosphorothionate intersugar linkages"
 Hanecak R;
                                                                                                                                                                                                                                            1.0%; Score 16.8; DB 1; Length 20; Best Local Similarity 90.0%; Pred. No. 4.1e+02; Matches 18; Conservative 0; Mismarthron
                                                                                                                                                                                                                                    Sequence 20 BP; 0 A; 0 C; 12 G; 8 T; 0 U; 0 Other;
Crooke ST, Mirabelli CK, Ecker DJ,
Brown-Driver VL, Wyatt JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bennett CF, Chian
att JR, Imbach JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Guanine quartet containing oligomer, #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                      1019 TTGGGGATGGGGCTGGGGTT 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Anderson KP, Bennett
Vickers TA, Wyatt JR,
                                                                                                Claim 12; Page 36; 72pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1994-135613/16.
                                WPI; 1994-302552/37
          Anderson KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
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04-NOV-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hanecak RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ecker DJ,
 Draper KG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                         AAQ61999;
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The sequences given in AAQ61990-2001 are oligonucleotides which contain G4 or G3 stretches and which may be used for inhibiting replication of herpes simplex virus (HSV), activity of HIV, human cytomegalovirus or influenza virus, or for treating inflammatory and neurological disorders caused by phospholipase A2 activity in cases of hyper-proliferation, malignancy, cardiovascular disease and snake bite. Oligonucleotides such as these, may be used for inhibiting division of malignant cells by modualting telomere length, which may also retard aging. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New modified oligo-nucleotide contg guanine quartet - inhibits activity of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length of chromosomes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibition; replication; herpes simplex virus; HSV; HIV; human cytcomegalovirus; influenza virus; inflammation; neurological disorders; phospholipase A2 activity; hyperproliferation; nalignancy; cardiovascular disease; snake bite; malignancy; telomere length; retard; aging; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapa
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/note= "Phosphorothionate intersugar linkages"
                                                                                                                                                                                                                                                                                                                                                                                                        Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                              Seguence 20 BP; 0 A; 0 C; 12 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4SV replication inhibiting oligomer, ISIS no 5652.
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Ecker DJ, Vickers TA, Wyatt JR, Imbach JL;
                                                                                                                                                                                                                                                                                                                                                                                                     1.0%; Score 16.8; DB 1;
90.0%; Pred. No. 4.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1019 TTGGGGATGGGGCTGGGGTT 1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGGGGTIGGGGTIGGGGTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
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Best Local Similarity
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Gaps

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Length 20; Indels

Score 16.8; DB 1; Pred. No. 4.1e+02;

0; Mismatches

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New modified oligo-nucleotide contg guanine quartet - inhibits activity of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length of chromosomes.
                                                                                           human cytomegalovirus; influenza virus; inflammation; telomere length; neurological disorders; phospholipase A2 activity; hyperproliferation; malignancy; cardiovascular disease; snake bite; malignancy; aging; ss.
                                                                                                                                                                                                                                                                                             Chiang M, Brown-Driver VL;
                                                                                 Inhibition; replication; herpes simplex virus; HSV; HIV; retard;
                                                                                                                                                                      a
"Phosphorothionate intersugar linkages"
                                                                                                                                                                                                                                                                                             Bennett CF, Chian
itt JR, Imbach JL;
                                                               Guanine quartet containing oligomer, #6
                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 106; 144pp; English.
                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                     Wyatt JR,
BP
                                                                                                                                                                                                                                      93WO-US009297.
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20
                                             (first entry)
                                                                                                                                                                                                                                                                                             Anderson KP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New modified oligo-nucleotide contg guanine quartet - inhibits activity of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length of chromosomes.
                                                                                                                                                                                                                                                                                                                               human cytomegalovirus; influenza virus; inflammation;
neurological disorders; phospholipase A2 activity; hyperproliferation;
malignancy; cardiovascular disease; snake bite; malignancy;
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                                Gaps
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/note= "Phosphorothionate intersugar linkages"
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1.0%; Score 16.8; DB 1; Length 20; 90.0%; Pred. No. 4.18+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                  Inhibition; replication; herpes simplex virus; HSV; HIV;
                                                                                                                                                                                                                                                                                    HSV replication inhibiting oligomer, ISIS no 5650.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RC, Anderson KP, Bennett CF, Chiang
J, Vickers TA, Wyatt JR, Imbach JL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                              telomere length; retard; aging; ss.
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                                                               1019 TTGGGGATGGGGCTGGGGTT
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                                                                                                                                                                        AAQ61904 standard; DNA; 20
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                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Conservative
                                                                                                                                                                                                                                      (revised)
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 Query Match
Best Local Similarity
Matches 18; Conserv
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04-NOV-1994
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                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
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                                                                                                                                           RESULT 799
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1019 TTGGGGATGGGGCTGGGGTT 1038

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Sequence 20 BP; 0 A; 0 C; 12 G; 8 T; 0 U; 0 Other;

MAR-2003 to correct PN field.)

The sequences given in AAQ61990-2001 are oligonucleotides which contain G4 or G3 stretches and which may be used for inhibiting replication of herpes simplex virus (HSV), activity of HIV, human cytomegalovirus or influenza virus, or for treating inflammatory and neurological disorders caused by phospholipase A2 activity in cases of hyper-proliferation, andigmancy, cardiovascular disease and snake bite. Oligonucleotides such as these, may be used for inhibiting division of malignant cells by modualting telomere length, which may also retard aging. (Updated on 25-

Gaps

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2; Indels

Score 16.8; DB 1; Pred. No. 4.1e+02;

1.0%; Scc. 90.0%; Pred. No. ...

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(first entry)

Synthetic AAQ97982; Ecker DJ; 

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Primer; DNA analysis; amplification; hybridisation; ss.
                                                                                                                                                                                                   Oligonucleotide 7 for DNA analysis.
                                                       1019 TIGGGAIGGGCIGGGTI 1038
                                                                                                                                   AAZ09195 standard; DNA; 20 BP
Query Match
Best Local Similarity 90.07
Each Local Similarity 90.07
Each Local Similarity
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                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                        AAZ09195;
                                                                                                                                                         peptide residues, the nucleobase being attached covalently to the acetyl group and the peptide linkage being formed by condensation of the glycine carboxy group of one residue with the amino group of the 2-aminoethyl moiety in the next residue"
                                                                                                                                                                                                                                                  a
"at least one (and preferably all) of the backbone
                                                                                                                                                                                                                                                                       subunits are composed of N-acetyl N-(2-aminoethyl)glycine
                                                                                                                                                                    nucleic acid; PNA; HIV; human immunodeficiency virus; AIDS;
                                                                                                                                              Peptide nucleic acid oligomer targetting HIV gene.
                                                                                                                                                                               antiviral; antisense; triple helix; ss.
                                                                                                                                                                                                                          Location/Qualifiers
                                                                  AAQ97982 standard; DNA; 20 BP
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                                                                                                                           (first entry)
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                                                                                                              (revised)
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                                                                                                                                                                                                                                    misc_feature
                                                                                                              25-MAR-2003
19-OCT-1995
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98JP-00005399. 98JP-00005399.

18; Query Match Best Local & Matches of naturally occurring nucleobases covalently bound to a polyamide charbone and (b) hybridise to the translation initiation AUG region, 5' backbone and (b) hybridise to the translation initiation AUG region, 5' untranslated region (3' UTR), gplice (1) untranslated region (3' UTR), gplice (2) untranslated region (3' UTR), gplice (3' UTR), gplice (4) untranslated for graph (4) untranslation moleties. They have utility as gene-tragetted drugs for modulating MIV processes. Hence they can be used to treat AIDS and other (4) untranslating MIV processes. Hence they can be used to treat AIDS and other (5' viral infections. They are also useful in diagnostic applications and as cresearch tools. PNA oligomers have high affinity for complementary single stranded DNA. They are also able to form triple helices in which a first PNA strand binds with the first PNA strand binds with the constitution double helix or with the first PNA strand. The PNAs possess no significant charge and are water soluble, which facilitates collular uptake. Further, since they contain amides of non-biological amino acids, they are biostable and registant to enzymatic degradation by proteases. The present sequence is a specifically claimed PNA sequence (represented by the sequence of nucleobases) targetting HIV genes. (Updated on 25-MAR-2003) Oligomer hybridisable to HIV sequence and contg. peptide nucleic acid sub:unit - binds in complementary manner to DNA and RNA, and useful for peptide nucleic acid (PNA) oligomers are provided which (a) consist modulating HIV viral activity, e.g. in treating AIDS Claim 2; Page 176; 186pp; English. WPI; 1995-082179/11.

Seguence 20 BP; 0 A; 0 C; 12 G; 8 T; 0 U; 0 Other;

This invention descibes a novel method for the analysis of a DNA fragment which comprises: (i) addition of a known common oligonucleotide sequence to at least one terminal of each DNA fragment, (ii) amplification of the resultant DNA fragment as a primer using a first common primer containing a complementary nucleotide sequence to the above mentioned known common oligonucleotide sequence to the prepared known common oligonucleotide sequence to the prepared known common oligonucleotide sequence optionally having been introduced with complementary nucleotide sequence to the prepared known common oligonucleotide sequence optionally having been introduced with complementary nucleotide sequence at a terminal, and a specific primer complementary nucleotide sequence, to give amplified DNA, (iii) analysis of the amplified DNA to find the information of the DNA fragment of in which the specific primer is designed to prepare fragments of the common first and second primers and to give short fragment of amplified DNA and (iv) labelling them to make their differentiation. Differentiation of unknown gene and simultaneous monitoring of signals derived from minor genes. Purthermore, labelling of DNAs according to functions of known genes can be performed. AAZ09189-Z09201 represent oligonucleotide primers ö Analysis of DNA fragment - comprises addition of known common oligonucleotide, amplification of resultant DNA fragment and analysis and labelling of amplified DNA. Gaps ö Score 16.8; DB 1; Length 20; Pred. No. 4.1e+02; 0; Mismatches 2; Indels Sequence 20 BP; 15 A; 3 C; 0 G; 2 T; 0 U; 0 Other; used to illustrate the method of the invention Example 1; Page 12; 17pp; Japanese Similarity 90.0%; Conservative WPI; 1999-496652/42.

us10008789-3.rng

AAF72967;

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Composition for treating hormone-regulated cancer, e.g. breast and profestic tumors, comprising an antisense oligonucleotide that inhibits expression of insulin like growth factor binding protein-5 by hormone-regulated tumor cells.
                                                                                         Insulin-like growth factor binding protein-5; IGFBP-5; human;
antisense oligonucleotide; hormone-regulated cancer; prostatic cancer;
breast cancer; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 3 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 34; 45pp; English.
                                                                        Antisense IGFBP-5 inhibitor #13.
                  AAA91207 standard; DNA; 20 BP.
                                                                                                                                                                                                                        (UYBR-) UNIV BRITISH COLUMBIA.
(MIYA/) MIYAKE H.
                                                                                                                                                                                   19-JUL-2000; 2000WO-CA000853
                                                                                                                                                                                                        99US-0144495P
                                                       (first entry)
                                                                                                                                                                                                                                                                       WPI; 2001-168448/17.
                                                                                                                                                  WO200105435-A2.
                                                       08-MAY-2001
                                                                                                                                                                                                       19-JUL-1999;
                                                                                                                               Homo sapiens
                                                                                                                                                                   25-JAN-2001
                                                                                                                                                                                                                                                     Gleave M;
                                    AAA91207;
RESULT 80
AAA91207/
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This sequence represents an antisense oligonucleotide targeted against human insulin-like growth factor binding protein-5 (IGFBP-5). The invention relates to a composition for treatment of hormona-regulated cancer, comprising an antisense oligonucleotide (such as this sequence) which inhibits expression of IGFBP-5 by hormone-regulated tumour cells.

The compositions is useful for delaying progression of hormone-regulated tumour cells such as prostatic cancer cells or breast cancer cells, to an antisense sequence which inhibits expression of IGFBP-5 by the tumour cells and composition can also be used for treating a hormone-creponsive cancer in an individual, and administering the composition to the individual after initiation of hormone-withdrawal to induce apoptotic cell death of hormone-responsive cancer cells, and therefore delaying the progression of hormone-responsive cancer cells, and therefore delaying the corposatic boney progression of an IGF-1 sensitive tumour in a mammal, by administering the composition to inhibit the expression of IGFBP-5 by the hormone-responsive cancer cells, and therefore independent state in the composition to inhibit the expression of IGFBP-5 by the hormone-responsive cancer cells, and therefore inhibiting or delaying metastatic boney progression of inhibit the expression of IGFBP-5 by the hormone-responsive cancer cells, and therefore inhibiting or delaying metastatic boney progression of the tumour
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AAS05713;
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                                      Gaps
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1.0%; Score 16.8; DB 1; Length 20; 90.0%; Pred. No. 4.1e+02; ive 0; Mismatches 2; Indels
                                                                      1731 TITACAAAAAAAAAAAA 1750
                                                                                                         TTTGAAAAAAAAAAAA 1
 Query Match
Best Local Similarity 90.0%;
Matches 18; Conservative
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Synthetic

AAF72967 standard; DNA; 20 BP.

RESULT 803 AAF72967/c ID AAF7296

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The present invention describes an antisense compound (I) up to 30 nucleobases in length, where (I) inhibits expression of daxx (also known as Fas binding protein. CENP-C binding protein. GENP-C binding protein. GENP-C binding protein. (I) has cytostatic and protein 6 and EAP for Ets-1 associated protein). (I) has cytostatic and antiinflammatory activity, and can be used in antisense therapy and as a modulator of daxx. (I) is useful for inhibiting the expression of daxx in therapeutics for the treatment of diseases associated with the expression of daxx, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation and as research reagent. The present sequence represents an inhibitory human daxx antisense phosphorothicate oilgonucleotide which is used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel antisense compounds capable of modulating expression of daxx useful for diagnosis, prophylaxis and treatment of diseases associated with expression of daxx.
                                                                                    Human daxx inhibitory antisense phosphorothioate oligonucleotide SEQ:68
                                                                                                                   Antisense oligonucleotide; daxx; inhibition; phosphorothioate;
Fas binding protein; CENP-C binding protein; dap6; BAP; cytostatic;
antiinflammatory; death segociated protein 6; Ets-1 associated protein;
infection; inflammation; tumour formation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reverse phase triplex forming oligonucleotide; RP-TFO; protected nucleic acid sequence; PNAS; single nucleotide polymorphism; SNP; short tandem repeat; cancer; Factor V Leiden SNP; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.0%; Score 16.8; DB 1; Length 20; 90.0%; Pred. No. 4.18+02; ive 0; Mismatches 2; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 0 A; 11 C; 0 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polypyrimidine Crick strand oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               859 GCAGGAAGAGGAAGAGGAGG 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAGGAAGAAGAAGAGGAGG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Col 43; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS05713 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                   24-JAN-2000; 2000US-00490692.
                                                                                                                                                                                                                                                                                                                                                        24-JAN-2000; 2000US-00490692.
                                                 24-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 90.0
nes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                            Cowsert LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-217744/22.
                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                 US6180353-B1
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                                                                                                                                                                                                                                                                                    30-JAN-2001.
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Matches
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The sequence is a polypyrimidine oligonucleotide for binding a second reverse phase triplex forming oligonucleotide, RP-TFO, (3' to the SNP) to the target SNP used to analyse Factor V Leiden SNP using the method of sequences comprising restricting isolated DNA, hybridising at least one triplex forming oligonucleotide (TFO), adding a 3' to 5' exonuclease to form a protected nucleic acid sequence (PNMS) tail structure, hybridising the captured structure with a single nucleotide polymorphisms (SNP) identification probe and determining the SNP score. The methods can be used for analysing target nucleic acid sequences, especially genomic DNA sequences, to determine if they contain SNPs or short tandem repeats (STRS). The methods can be used to detect SNPs for use in population genetics, drug development, forensics, cancer, genetic disease research,
                                                                                                                                                                                                                                                                                                                                                        Analyzing target nucleic acid sequences, useful for population genetics, drug development and diagnosing cancer, comprises hybridizing triple forming oligonuclectide and probe to target sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genouic, usug development, forensics, cancer, genetic disease research, genomic analysis, diagnostics and therapeutics in humans, plants and animals
                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 66; 141pp; English.
                                                                                                                             99US-0163356P.
99US-0163416P.
99US-0171348P.
                                                                                           03-NOV-2000; 2000WO-US030534.
                                                                                                                                                                                    07-JUL-2000; 2000US-0216579P
                                                                                                                                                                                                                                                                                   Ramberg ER;
                                                                                                                                                                                                                                                                                                                       WPI; 2001-343488/36.
                                                                                                                                                                                                                           (CYGE-) CYGENE INC.
                                                                                                                                                                                                                                            OSTE C C.
                   WO200132929-A1
                                                                                                                               03-NOV-1999;
                                                                                                                                                03-NOV-1999;
21-DEC-1999;
                                                      10-MAY-2001
                                                                                                                                                                                                                                                                                 Oste CC,
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Gaps ö 1.0%; Score 16.8; DB 1; Length 20; 90.0%; Pred. No. 4.1e+02; ive 0; Mismatches 2; Indels Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other; Local Similarity 90.0 nes 18; Conservative Query Match Matches ઠે

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ABZ89676 standard; DNA; 20 BP 17-OCT-2003 (first entry) ABZ89676; ABZ89676 

Human oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction; antilnflammatory steroid; ubiquinone; antilnflammatory; antiallergic; antilasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antilsense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Homo sapiens

WO200285308-A2

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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the intiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention of as antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a immunosuppressive, and cytostatic activity. The composition may have a cuse in attisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing levels of adenosine receptor, producing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject, stissue, or treating bronchoconstriction, lung allergies, or a respiratory disease or condition. Once: The sequence data for this parent is not represented in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                             Pharmaceutical composition for treating ailments associated with impaired
                                                                                                                                                                                                                                                                                                                   respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                              Pabalan J, Aguilar D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.0%; Score 16.8; DB 1; Length 20; 90.0%; Pred. No. 4.1e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 17 A; 2 C; 0 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, SEQ ID NO 4918; 872pp; English.
                                                                                                                                                                            Katz E,
S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ACATCAAAAAAAAAAAA 20
                                                                                                                                                                            Li Y, Sandrasagra A,
Tang L, Shahabuddin
                                                                                       24-APR-2001; 2001US-0286137P.
                                          23-APR-2002; 2002WO-US013135.
                                                                                                                                 (EPIG-) EPIGENESIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.06;
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nes 18; Conservative
                                                                                                                                                                                                                                                 WPI; 2003-229219/22.
31-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                  ubiquinone.
                                                                                                                                                                              Nyce JW, 1
Miller S,
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ABZ85436 standard; DNA; 20 BP (first entry) 17-OCT-2003 ABZ85436; ABZ85436/ 

RESULT 806

Human oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction; antilnflammatory steroid; ubiquinone; antilnflammatory; antiallergic; antisathmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Homo sapiens

40200285308-A2

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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation coodon, coding regalon, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 muclootides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an entinflammatory steroid and ubjquinone. A composition of the invention has antiinflammatory, antiallergic, antiathmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an exceptor, producing sensitivity to adenosine, reducing levels of adenosine receptor, producing sensitivity to adenosine, reducing levels of adenosine receptor, producing subject's tissue, or treating bronchoconstriction, lung surfactent in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed appears to the printed and printed and prophylacial papers in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                             Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                          Aguilar D;
                                                                                                                                                                                             Katz E, Pabalan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 15; SEQ ID NO 678; 872pp; English
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                                                                                                                                                                                        Li Y, Sandrasagra A,
Tang L, Shahabuddin
                                               23-APR-2002; 2002WO-US013135.
                                                                                              24-APR-2001; 2001US-0286137P
                                                                                                                                           (EPIG-) EPIGENESIS PHARM INC
                                                                                                                                                                                                                                                                WPI; 2003-229219/22.
31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                  ubiquinone.
                                                                                                                                                                                        Nyce JW, I
Miller S,
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Gaps ö 1.0%; Score 16.8; DB 1; Length 20; 90.0%; Pred. No. 4.18+02; ive 0; Mismatches 2; Indels Sequence 20 BP; 3 A; 2 C; 1 G; 14 T; 0 U; 0 Other; Local Similarity 90.0 hes 18; Conservative Query Match Matches

1730 GITTACAAAAAAAAAAA 1749 20 GGTTTCAAAAAAAAAAA 1 ઠે a

ABZ92865 standard; DNA; 20 ABZ92865; 

В.

(first entry) 17-0CT-2003

Human oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction; antilnflammatory steroid; ubiquinone; antilnflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodiation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Homo sapiens.

WO200285308-A2

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC.

Pabalan J, Aguilar D; Katz E, Li Y, Sandrasagra A, Ka Tang L, Shahabuddin S; Nyce JW,

Miller S,

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or WPI; 2003-229219/22.

Disclosure; SEQ ID NO 8107; 872pp; English.

ubiquinone.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the intitiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an entile lammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antisthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antialmamatory steroid in a subject, for reducing or depleting levels of adenosine receptor, producing sensitivity to adenosine, reducing sensitivity to adenosine, reducing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung surfactant in a subject's tissue, or treating bronchoconstriction, lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition.

Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO te fifty. WiPo.int/pub/published\_pot\_agences

Seguence 20 BP; 18 A; 0 C; 1 G; 1 T; 0 U; 0 Other;

Gaps ö 1.0%; Score 16.8; DB 1; Length 20; 90.0%; Pred. No. 4.1e+02; ive 0; Mismatches 2; Indel8 90.06 Local Similarity 90.0 es 18; Conservative Query Match Best Loca Matches

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ABZ85669 standard; DNA; 20 BP ABZ85669; ABZ85669/ 

(first entry)

17-0CT-2003

Human oligonucleotide sequence.

Human, antisense; lung dysfunction, nasal airway dysfunction, antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Homo sapiens.

WO200285308-A2

23-APR-2002; 2002WO-US013135.

Pabalan J, Aguilar D;

Katz E,

31-OCT-2002.

```
The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding regain, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallargic, antiatchmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an entiantlammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing levels of ung animation, lung allergies, or a respiratory disease or condition, ung inflammation, lung allergies, or a respiratory disease or condition.

Note: The sequence data for this patent is not represented in the printed or specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                               Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                              Claim 15; SEQ ID NO 911; 872pp; English.
                                                                                                                                                     ii Y, Sandrasagra A, Ke
Tang L, Shahabuddin S;
                                       23-APR-2002; 2002WO-US013135.
                                                                         24-APR-2001; 2001US-0286137P
                                                                                                             (EPIG-) EPIGENESIS PHARM INC
                                                                                                                                                                                                             WPI; 2003-229219/22.
                                                                                                                                                     Li Y,
                                                                                                                                                                                                                                                                                                            ubiquinone
                                                                                                                                                                       Miller S,
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                                                                                                                                                   Nyce JW,
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ö Gaps ö 1.0%; Score 16.8; DB 1; Length 20; 90.0%; Pred. No. 4.1e+02; 2; Indels Sequence 20 BP; 0 A; 2 C; 0 G; 18 T; 0 U; 0 Other; 0; Mismatches 1734 ACAAAAAAAAAAAAAAA 1753 Conservative Query Match Best Local Similarity Matches 18; Conserv

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20 AGAAAAAAAAAAAAAAA 1

ABZ86569 standard; DNA; 20 BP

(first entry) 17-OCT-2003

Human oligonucleotide seguence.

Human; antisense; lung dysfunction; nasal airway dysfunction; antinflammatory steroid; ubiquinone; antinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Homo sapiens

WO200285308-A2

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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding regalon, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an entilellammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallargic, antiathmetic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an entistialmmatory steroid in a subject, for reducing levels of adenosine or ceceptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject or increasing levels of ubiquinone or lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence date for this patent is not represented in the printed specification, but was observed in electronic format directly from WIPO
                                                                                                                                                                                                                                                                              Pharmaceutical composition for treating ailments associated with impaired
                                                                                                                                                                                                                                                                                                  respiration, has oligo(8) antisense to specific gene(8) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapa
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                                                                                                                                                                    Aguilar
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                                                                                                                                                                    Pabalan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 1 A; 6 C; 8 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                    Sandrasagra A, Katz E,
L, Shahabuddin S;
                                                                                                                                                                                                                                                                                                                                                                                     Claim 15; SEQ ID NO 1811; 872pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177 GCTGCCCCCGAAGCAGCCGG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 GCTGCCACCAAAGCAGCCGG 1
                                                                                  24-APR-2001; 2001US-0286137P.
                                                                                                                          (EPIG-) EPIGENESIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 90.0
les 18; Conservative
                                                                                                                                                                                                                                    WPI; 2003-229219/22.
                                                                                                                                                                  Li Y, Sar
Tang L,
                                                                                                                                                                                                                                                                                                                                             ubiquinone.
                                                                                                                                                                                        Miller S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Human, antisense, lung dysfunction, nasal airway dysfunction, antiinflammatory; sntiallergic; antiinflammatory; antiallergic; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds. Human oligonucleotide sequence. 

ABZ88813 standard; DNA; 20 BP

(first entry)

17-OCT-2003

ABZ88813;

Homo sapiens

40200285308-A2

us10008789-3.rng

31-OCT-2002

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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation coodon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an entiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antisers expected in a subject, for reducing or depleting levels of, or reducing benetitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                          Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                        Katz E, Pabalan J, Aguilar D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 16 A; 0 C; 1 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 4055; 872pp; English.
                                                                                                                                                                                                              s,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAATTTAAAAAAAAAAAA 20
                                                                                                                                                                                        Li Y, Sandrasagra A,
Tang L, Shahabuddin
                                              23-APR-2002; 2002WO-US013135.
                                                                                             24-APR-2001; 2001US-0286137P.
                                                                                                                                         (EPIG-) EPIGENESIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Conservative
                                                                                                                                                                                                                                                             WPI; 2003-229219/22.
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  31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                               ubiquinone
                                                                                                                                                                                                                 Miller S,
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1.0%; Score 16.8; DB 1; Length 20; 90.0%; Pred. No. 4.1e+02;
                                  2; Indels
                                   0; Mismatches
                                                                    1728 GAGTTTACAAAAAAAAA 1747
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Gaps.

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Human; antisense; lung dysfunction; nasal airway dysfunction; antinflammatory steroid; ubiquinone; antinflammatory; antiallergic; antiatethmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
                                                                                                                              Human oligonucleotide sequence
                                 ABZ85535 standard; DNA; 20 BP
                                                                                              17-OCT-2003 (first entry)
                                                                ABZ85535;
RESULT 811
ABZ85535
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WO200285308-A2

WO200285308-A2 Homo sapiens.

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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the intitation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 mucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an entiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiathmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antifilammatory steroid in a subject, for reducing levels of denosine receptor, producing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                 Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiinsthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                 Katz E, Pabalan J, Aguilar D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.0%; Score 16.8; DB 1; Length 20;
90.0%; Pred. No. 4.1e+02;
ive 0; Mismatches 2; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 18 A; 0 C; 2 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                             Claim 15; SEQ ID NO 777; 872pp; English.
                                                                                                                                                                 Li Y, Sandrasagra A, K.
Tang L, Shahabuddin S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1736 AAAAAAAAAAAAAAAAA 1755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AAAAAAAGAAAAAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human oligonucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABZ89014 standard; DNA; 20 BP
                                         23-APR-2002; 2002WO-US013135.
                                                                                24-APR-2001; 2001US-0286137P.
                                                                                                                          (EPIG-) EPIGENESIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.08;
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nes 18; Conservative
                                                                                                                                                                                                                              WPI; 2003-229219/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                       ubiquinone.
                                                                                                                                                                                       Miller S,
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                                                                                                                                                                   Nyce JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
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us10008789-3.rng

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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation coodon, coding regains, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallargic, antiaschmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an exceptor, producing bronchodilation, increasing levels of adenosine receptor, producing sensitivity to adenosine, reducing levels of biquinone or lung surfactuant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                       Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                            Pabalan J, Aguilar D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 16 A; 2 C; 0 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 4256; 872pp; English
                                                                                                                            Katz E,
                                                                                                                         Li Y, Sandrasagra A, Ka
Tang L, Shahabuddin S;
                               23-APR-2002; 2002WO-US013135.
                                                             24-APR-2001; 2001US-0286137P
                                                                                             (EPIG-) EPIGENESIS PHARM INC
                                                                                                                                                                         WPI; 2003-229219/22
                                                                                                                                                                                                                                                         ubiquinone.
                                                                                                                                          Miller S,
                                                                                                                            Nyce JW,
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                            Gapa
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Score 16.8; DB 1; Length 20;
Pred. No. 4.18+02;
0; Mismatches 2; Indels
                                                 1733 TACAAAAAAAAAAAAAAA 1752
   1.0%;
                           Conservative
              Local Similarity
les 18; Conserv
    Query Match
                           Matches
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1 TACCTAAAAAAAAAAAA 20

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AAF95712 standard; DNA; 21 (first entry) 06-JUN-2001 AAF95712; RESULT 813 AAF95712 

Human gene single nucleotide polymorphism #473.

Human; variant thrombospondin 1; variant thrombospondin 4; SNP; polymorphism; vascular disease; coronary artery disease; forensics; myocardial infarction; atherosclerosis; stroke; venous thromboembolism; pulmonary embolism; paternity test; ds.

Homo sapiens

Variation

/standard\_name= "single nucleotide polymorphism" Location/Qualifiers replace (11, T)

genes. The sequences at a number of polymorphic sites are also provided in the specification. In particular, the method can be used in the diagnosis of atherosclerosis, myocardial infarction, coronary heart disease, stroke, peripheral vascular diseases, venous thromboembolism and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also useful in forensics, paternity testing, genetic analysis and phenotype correlations to diseases. The present sequence is an example of one of The present invention provides a method of diagnosing a vascular disease in an individual, involving determining the sequence at various polymorphic sites within the human thrombospondin 1 and thrombospondin 4 Mccarthy JJ; Nucleic acids comprising single nucleotide polymorphisms, useful in applications such as forensics, paternity testing, medicine, genetic analysis and phenotype correlations to diseases such as diabetes and ö Score 16.8; DB 1; Length 21; Pred. No. 4.3e+02; 0; Mismatches 2; Indels Daley GO, Seguence 21 BP; 5 A; 3 C; 10 G; 3 T; 0 U; 0 Other; the human gene SNPS shown in the specification Bolk S, (WHED ) WHITEHEAD INST BIOMEDICAL RES Ireland JS, Example; Page 81; 242pp; English. 37-SEP-2000; 2000WO-US024503. 10-SEP-1999; 99US-0153357P. 26-JUL-2000; 2000US-0220947P. 16-AUG-2000; 2000US-025724P. 1.0%; (MILL-) MILLENNIUM PHARM INC Query Match
Best Local Similarity 90.0
Matches 18; Conservative Gargill M, WPI; 2001-226749/23 atherosclerosis. #O200118250-A2. 15-MAR-2001. Lander ES,

Gaps 831 AGAGGAAGCTGCTGGGGTCT 850 2 AGAGGAAGCCGATGGGGTCT 21 ઠ

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ABS97317 standard; DNA; 21 BP (first entry) 23-DEC-2002 ABS97317; ABS97317, 

RESULT 814

Human; 88; primer; cytochrome P450 A1; CYP4501A1; UG72B4; MDR1; PCR; cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF; adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRB1; MRB12; aryl hydrocarbon neceptor nuclear translocator; ARM1; cathepsin S1; cyclooxagenase 2; COX2; diazapam binding inhibitor; BB1; haematological; epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP; glutathione-S-transferase 12; GST12; histamine-N-methyl transferase; HMWT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNWT; NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STW; UG72B7; UDP-glucuronosyl transferase 287; UG72B7; UG72B7; urokinase receptor; uPA; multidrug resistance 1; lactoransferrin; orphan nuclear receptor; multidrug resistance associated protein 3; cancer; prostate; multidrug resistance associated protein 3; cancer; prostate; acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5; altered drug metabolism; cardiovascular function; colorectal tumour; Aryl hydrocarbon nuclear translocation receptor sequencing primer #6

RESULT 815 ADD05293 ઠે 쉽 This invention relates to the sequence of an isolated nucleic acid
molecule comprising at least one base variation from that of a known
chann cytochrome P450 Al (CY4501Al), adrenergic receptor betal (ADBR1),
cytochrome P450 Al (CY4501Al), adrenergic receptor betal (ADBR1),
cytochrome P450 O2E1 (CY4501Al), adrenergic receptor betal (ADBR1),
aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
(ANR), cathepsin S (CYSS), cycloxogenaes 2 (CXC2), diazepam binding
cinhibitor (DBI), epoxide hydroxylase 2 [EPHX2), 5-lipoxygenaes activating
protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
transferase (HNMY), NADPH quinone oxidoreductase 2 (NQC2),
culfotransferase thermolabile (STM), UDF-glucuronosyl transferase 2Bf (UGT2B1), UDP-glucuronosyl
transferase (UGT2B1), urokinase receptor (UR), multidrug resistance
(MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
(MRD3), orphan nuclear receptor (UR), multidrug resistance
(MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
(MRD3), orphan nuclear receptor (NR12), or acceptor 1, 2, 3, 4, or 5 (CHMR), CHMR2, CHMR3, CHMR4 or CHMR5) sequence
(MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
(MRD3), orphan nuclear receptor (NR12), or acceptor 1, 2, 3, 4, or 5 (CHMR), CHMR2, CHMR3, CHMR4 or CHMR5) sequence
(MDR1), lactotransferrin (LTF), multidrug and characterising the genes that are responsible for a variety of disorder-related
traits as a result of their e.g., overexpression, constitutive
expression, mutation or underexpression, which may be used in diagnosing
and/or treating the disorders. The nucleic acid molecules comprising the
cypolymorphic sequences contained in CYP4501Al, Isolated nucleic acid molecules having polymorphisms in known human genes eg. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for disorder-related traits. susceptibility to colorectal tumours, in DBI or CHMR1 for altered central nervous system function, in FLAP and HNWT for altered pulmonary, immunological or haematological function, in KLMZ for altered serine protease activity in the prostate, in LFF for altered immunological or haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and peripheral nervous system function. The present sequence represents a PCR primer used to amplify the sequences of the invention 1.0%; Score 16.8; DB 1; Length 21; 30.0%; Pred. No. 4.3e+02; ved. No. 4.3e+02; Indels Sequence 21 BP; 3 A; 4 C; 0 G; 14 T; 0 U; 0 Other; central nervous system; pulmonary; immunological. Example 6; Page 109; 714pp; English. 28-NOV-2001; 2001WO-US044838. 28-NOV-2000; 2000US-00724389. 90.06; DNAS-) DNA SCI LAB INC WPI; 2002-698522/75. Local Similarity Guida M, Hall J; WO200257410-A2 Homo sapiens. 25-JUL-2002. Query Match Best Loca Matches

Novel proteins for binding, identifying and concentrating female sex

Goda Y;

Fujimoto S,

Katagiri M,

WPI; 2003-731681/69.

hormones.

28-FEB-2003; 2003WO-JP002311.

01-MAR-2002; 2002JP-00055669

(TAKE ) TAKEDA CHEM IND LTD.

female sex hormone; primer; ss.

WO2003074704-A1.

Synthetic.

12-SEP-2003.

Primer of the invention #6.

(first entry)

01-JAN-2004

ADD05293;

ADD05293 standard; DNA; 21 BP.

Example 8; SEQ ID NO 31; 101pp; Japanese.

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The present invention relates to proteins that bind to female sex hormones. The method is useful for binding, identifying and concentrating female sex hormones. The present invention represents a primer of the
                                                                                                                           Gaps
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                                                                                            1.0%; Score 16.8; DB 1; Length 21; 90.0%; Pred. No. 4.3e+02; ive 0; Mismatches 2; Indels
                                                                     Sequence 21 BP; 5 A; 2 C; 10 G; 4 T; 0 U; 0 Other;
                                                                                                                                                   1396 GAGGAGACTGTGAGAATTGT 1415
                                                                                                                                                                   2 GAGGAGACTGTGAGAGTGGT 21
                                                                                                                                                                                                                                                                                                                                                            female sex hormone; primer; ss.
                                                                                                                                                                                                                                                 ADD05286 standard; DNA; 22 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003; 2003WO-JP002311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002; 2002JP-00055669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TAKE ) TAKEDA CHEM IND LTD.
                                                                              Query Match
Best Local Similarity your
                                                                                                                                                                                                                                                                                                                                  Primer of the invention #2.
                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                      01-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                             invention
                                                                                                                                                                                                                                                                            ADD05286;
                                                                                                                                                                                                                         RESULT 816
                                                                                                                                                                                                                                       ADD05286/
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Gaps ;; 0

1728 GAGTTTACAAAAAAAAA 1747

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18; Conservative

20 GAGTTTGAAAAAAAAAA 1

us10008789-3.rng

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Gaps

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1; Indels

Pred. No. 4.3e+02; Mismatches

; 0

Best Local Similarity 94.4%; Matches 17; Conservative

1734 ACAAAAAAAAAAAAAA 1751

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18 АТАААААААААААААА

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)* Adelta-N3'; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, guanine or cytosine; N = adenine, guanine or thymine; A matural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of the sess of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene
                                                                                                                                             The present invention relates to proteins that bind to female sex hormones. The method is useful for binding, identifying and concentrating female sex hormones. The present invention represents a primer of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptides having at least two new nucleotides - useful as primers in RT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
                                                                                                                                                                                                                                                                                        Gaps
                                                                          Novel proteins for binding, identifying and concentrating female sex
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                                                                                                                                                                                                                                                        1; DB 1; Length 22;
4.4e+02;
                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                          Sequence 22 BP; 4 A; 10 C; 3 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                        Score 16.8; DE Pred. No. 4.4e+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RT-PCR primer of the invention SEQ ID 14.
                                                                                                                    Example 3; SEQ ID NO 24; 101pp; Japanese
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                                                                                                                                                                                                                                                                                                                    1396 GAGGACTGTGAGAATTGT 1415
               ×
               Goda
                                                                                                                                                                                                                                                                                                                                                  GAGGACTGTGAGAGTGGT
                                                                                                                                                                                                                                                        1.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                            AAX18373 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 90.0
Matches 18; Conservative
              Fujimoto S,
                                            WPI; 2003-731681/69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-183822/16
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              Katagiri M,
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                                                                                                                                                                                                invention
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                                                                                         hormones
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0.9%; Score 16.4; DB 1; Length 18;

Sequence 18 BP; 1 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

sednences

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene
                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptides having at least two new nucleotides - useful as primers in RT-
                                                                                                                                                                 XT-PCR primer; DNA sequence determination; gene sequence analysis; ss
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Pred. No. 4.3e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18 BP; 2 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
                                                                                                                                RT-PCR primer of the invention SEQ ID 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 11; 19pp; Japanese.
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                                  ВЪ
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Matches 17; Conservative
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ABK13935 standard; DNA; 18
                                AAX18372 standard; DNA; 18
                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                   (TAKI ) TAKARA SHUZO
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-183822/16
                                                                                                                                                                                                                                  JP11032765-A.
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                                                                                                11-MAY-1999
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                                                                                                                                                                                                  Synthetic.
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                                                                 AAX18372
RESULT 818
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                  AAX18372
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Ernfors P;

us10008789-3.rng

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Nucleotide sequence of a double stranded product DNA fragment.
                                                                                                                                                                                                                                                                                                   Gene variant identification; restriction enzyme; HaeII; ds.
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                                                                                                                                                                                                                                                               ACF36339 standard; DNA; 18
                                                                                                                                                                                                                                                                                 (first entry)
                                                                             Ernfors
                                                                                      WPI; 2002-217065/27.
                                                                                                                                                                                           present invention
                                                                                                                                                                                                                                                                                                                     WO2003064689-A2,
                           WO200208461-A2.
                                                                             Linnarsson S,
                                                                                                                                                                                                                                                                                                                              07-AUG-2003.
                                    31-JAN-2002
                  Synthetic
                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                            Query Match
Best Local S
                                                                                                                                                                                                                                                                        ACF36339
                                                                                                                                                                                                                                                      RESULT 820
                                                                                                                                                                                                                     Matches
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Determining polyadenylation sites within transcribed gene sequences present in a sample comprises assigning to gene fragments gene candidates within a database by comparing signals in the dataset with the database. The invention relates to determining the presence of and/or identifying a polyadenylation site within a sequence of a transcribed gene or variants present in a sample. The method involves assigning to gene fragments gene candidates within a database by comparing signals in the database with the database comprising data representing mRNAs with the polyA sites and/or 'virtual genes' representing a possible polyadenylation site within an actual gene. The method is useful for alternative polyadenylation site within an actual gene. The method is useful for alternative polyadenylation sites within a sequence of a transcribed gene or sequence of transcribed gene variants present or potentially present in a sample, in identifying gene features, particularly in identifying differences between sequence variants that occur in a population of nucleic acid molecules, especially in identifying or discovering polyA site usage or determining polyA site usage in a nucleic acid sample, and gene variants arising from alternative polyA sites. The present sequence represents a double stranded product DNA fragment Lonnerberg P, Oldin M, Linnarsson S, Example; Fig 2; 81pp; English 29-JAN-2002; 2002US-0352245P. (GLOB-) GLOBAL GENOMICS AB WPI; 2003-627619/59 ò 엄 ö The present invention relates to a method for providing a profile of mRNA molecules present in a sample. The method comprises generating two independent patterns characteristic of the population of mRNA molecules expressed in the sample and analysing the patterns using a combinatorial algorithm, comparing gene expression by different or same cell types under different conditions, and identifying genes having a role in various cellular processes. The method is useful for the analysis and identification of transcribed genes, and fingerprinting. The method can be used to identify genes which play a role in determining various cellular processes, including susceptibility to external factors, development, and disease. The present sequence for a PCR primer is used in the production of a single pattern characteristic of a sample, employing a Type II restriction enzyme (i.e. HaeII) in the methods of the Providing mRNA profile, by generating two independent patterns characteristic of sample mRNA population, analyzing patterns, comparing gene expression by cell types under varied conditions, and identifying Gaps Identification of transcribed gene, mRNA profile, gene expression, cellular process, fingerprinting, susceptibility to external factor, development, disease, PCR, primer, ss. ö Length 18; 1; Indels Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other; Score 16.4; DB 1; Pred. No. 4.3e+02; 0; Mismatches Bauren G; Disclosure; Fig 1; 67pp; English. 1735 CAAAAAAAAAAAAAA 1752 18 CGAAAAAAAAAAAAA 1 23-JUL-2001; 2001WO-IB001539 21-JUL-2000; 2000GB-00018016. 21-JUL-2000; 2000US-0219925P. 0.9%; (GLOB-) GLOBAL GENOMICS AB. Local Similarity 94.4 es 17; Conservative

ö Nucleic acid manipulation, mRNA profiling, polymerase chain reaction, electrophoresis, type II restriction enzyme, HaeII; ds. Gaps ; 0 Score 16.4; DB 1; Length 18; Pred. No. 4.3e+02; 0; Mismatches 1; Indels Pihlak A; Nucleotide sequence of a double stranded product DNA. Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other; Metsis A, Ernfors P, Bauren G, 1735 CAAAAAAAAAAAAAA 1752 18 CGAAAAAAAAAAAAA 1 ACF36364 standard; DNA; 18 BP 28-JAN-2003; 2003WO-IB000843. 9-JAN-2002; 2002US-0352215P. Query Match 0.9%; Best Local Similarity 94.4%; Matches 17; Conservative (GLOB-) GLOBAL GENOMICS AB (first entry) WPI; 2003-618365/58 WO2003064691-A2. Linnarsson S, 04-DEC-2003 Montelius A; 07-AUG-2003 Synthetic. ACF36364; RESULT 821 ACF36364/c 

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                                                                                                     The invention relates to producing a population of double-stranded product DNA molecules comprising amplification by a nested PCR method. The method is useful in profiling mRNA transcribed in a system under investigation. The oligonuclectides are used as size standards in electrophoresis, and as internal controls allowing for calculation of relative amounts of material present. The present sequence represents adouble stranded product DNA, which aids in outlining an approach to production of a single pattern characteristic of a sample, employing a
Producing a population of double-stranded product DNA molecules, useful for mRNA profiling, comprises amplification by nested polymerase chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       short interfering nucleic acid; siNA; downregulation; inhibition; mitogen-activated protein kinase; MAP kinase; MAPK, RNA interference; cytostatic; anorectic; antidiabetic; antiinflammatory; antiaathmatic; immunosuppressive; antibacterial; antirheumatic; antiarthritic; antipsoriatic; gastrointestinal; obesity; diabetes; tumour; inflammatory disease; asthma; septic shock; rheumatoid arthritis; psoriasis; inflammatory bowel disease; drug screening;
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:433.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New short interfering nucleic acid, useful e.g. for treatment and diagnosis of cancer, downregulates expression of mitogen-activated protein kinase genes.
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                                                                                                                                                                                                                                                                                                                     Score 16.4; DB 1; Length 18;
Pred. No. 4.3e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genetic engineering; pharmacogenomic; gene mapping; ss
                                                                                                                                                                                                                                                                                         Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                      type II restriction enzyme (HaeII)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-MAR-2002; 2002US-0363124P.
06-JUN-2002; 2002US-036782P.
29-AUG-2002; 2002US-0406784P.
05-SEP-2002; 2002US-0408378P.
09-SRP-2003; 2002US-0409233P.
15-JAN-2003; 2003US-0409239P.
                                                                         Example, Fig 1; 105pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SIRN-) SIRNA THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                    18 CGAAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADE29811 standard; RNA; 19 BP.
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                                                                                                                                                                                                                                                                                                                       Query Match 0.9
Best Local Similarity 94.4
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-FEB-2002;
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The present invention of a mitogen activated protein kinase characterizing interior acts (MAPK) genes by RNA interference. Also described: (1) a method for modulating expression of MAPK genes in cells, tissue explants or conjugates and/or complexes of siNA; (1) kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or complexes of siNA; and (4) vectors that express siNA and cells containing these vectors. MAPK siNAs can expressive, antiabacterial, antirheumatory.

Containtritic, antiporate and gastrointestinal activities. The MAPK siNAs can be used to modulate the expression of MAPK genes, in cells, tissue explants or organisms, e.g. for treating obseity; diabetes types I complicate and or filammatory diseases (asthma, ceptic shock, rheumatoid arthritis, psoriasis and inflammatory bowel disease). They can also be used for drug screening; diagnosis; target identification and validation; genetic engineering; pharmacogenomics; cubilitication and validation; genetic engineering; pharmacogenomics; containing the containing mapping (e.g. of single-nucleotide contained to the procession of MAPK sind which is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
               nucleic acid (siNA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               short interfering nucleic acid, siNA, downregulation; inhibition; mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference; cytostatic; anorectic; antidiabetic; antinflammatory; antiasthmatic; immunosuppressive; antibacterial; antirheumatic; antiarthritic; antipsoriatic; gastrointestinal; obesity; diabetes; tumour; inflammatory disease; asthma; septic shock; hreumatoid arthritis; psoriasis; inflammatory bowel disease; drug screening; genetic engineering; pharmacogenomic; gene mapping; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                             0.9%; Score 16.4; DB 1; Length 19; 94.4%; Pred. No. 4.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19 BP; 1 A; 12 C; 4 G; 0 T; 2 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                  polymorphisms). The present sequence represents in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1119 CGCCGTGGAGAGGAGGC 1136
                   invention describes
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; 2002US-0363124P.
; 2002US-0386782P.
; 2002US-0406784P.
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2003US-0440129P
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 94.4%;
nes 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADE29706 standard; RNA; 19
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30-JUN-1997; RESULT 824 Matches ð 셤

New short interfering nucleic acid, useful e.g. for treatment and diagnosis of cancer, downregulates expression of mitogen-activated protein kinase genes.

Example 3; SEQ ID NO 328; 164pp; English.

The present invention describes a short interfering nucleic acid (siNA) that downregulates expression of a mitogen-activated protein kinase (NAPK) genes by RNA interference. Also described: (1) a method for modulating expression of MAPK genes in cells, tissue explants or capanisms by introduction of siNA; (2) kits for in vitro or in vivo delivery of siNA; and (4) to conjugates and/or complexes of siNA; and (4) conjugates and/or complexes of siNA; and (4) certors that express siNA and cells containing these vectors. MAPK siNAs have cytostatic, amornectic, antidiabetic, antiinflammatory, antisathmatic, immunosuppressive, antibacterial, antirheumatic, antipacriatic, antipacriatic and gastrointestinal activities. The MAPK siNAs can be used to modulate the expression of MAPK genes, in cells, tissue explants or organisms, e.g. for treating obseity; diabetes types I cand II; a wide range of tumours, and inflammatory disease (asthma, septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel disease). They can also be used for drug screening; diagnosis; target cidentification and validation; genetic engineering; pharmacogenomics; studying gene function and gene mapping (e.g. of single-nucleotide processed). They can also be used for drug screening; whatmacogenomics; studying gene function and gene mapping (e.g. of single-nucleotide processed). They can also be used for drug screening where the control of t polymorphisms). The present sequence represents in the exemplification of the present invention.

Sequence 19 BP; 2 A; 4 C; 12 G; 0 T; 1 U; 0 Other;

Score 16.4; DB 1; Length 19; Pred. No. 4.4e+02; 1; Mismatches 1; Indels 1119 CGCCGTGGAGAGGAGGC 1136 1 CGCCGUGGGGAGGAGGCC 18 0.98; 88.98; 16; Conservative Query Match Best Local Similarity

AAV12302 standard; DNA; 20 AAV12302;

BP.

17-JUN-1998 (first entry)

Ribonucleotide reductase R1 3'UTR fragment SEQ ID NO:46.

Ribonucleotide reductase R1; 3'-untranslated region; 3'UTR; tumour; housekeeping gene; identification; modulator; metastasis; neoplastic; papilloma; atherosclerosis; angiogenesis; viral infection; ss.

Homo sapiens

WO9800532-A2

08-JAN-1998.

97WO-CA000454.

96US-0021152P 01-JUL-1996;

(WRIG/) WRIGHT J A. (YOUN/) YOUNG A H.

Wright JA, Young AH;

WPI; 1998-086958/08.

New oligo-nucleotide(s) complementary to untranslated regions of housekeeping genes - are useful in, e.g. identifying modulators of tumour growth/metastasis and inhibiting growth of neoplastic cells.

Claim 4; Page 29; 64pp; English

of ribonuclectide reductase RI. The present invention describes: (1) coligonuclectide reductase RI. The present invention describes: (1) coligonuclectides (ON) comprising at least 7 consecutive nucleotides (IV) coligonuclectides (ON) comprising at least 7 consecutive nucleotides (IV) complementary to ON; (3) ribozymes (Rb) complementary or homologus (AON) complementary to ON; (3) ribozymes (Rb) complementary or homologus to ON, and able to cleave it; (4) DNA sequence encoding ON, OAN and Rb; (6) an antibody (Ab) that binds to ON, AON and Rb; (6) ant probe into the that hybridise to ON, OAN and Rb; (6) ant probe into the chart hybridise to ON, OAN and Rb; (6) ant probe into the chart hybridise to ON, AON, Rb and Ab are used to modulate (especially inhibit) growth of tumour cells (especially neoplastic cells) and to reduce their repactions, e.g. human immunodeficiency virus, and to reduce their repactions, e.g. human immunodeficiency virus, and operatis on herpes (N may further be used: (1) to identify modulators of tumour growth/metastasis; (11) to identify compounds (especially contential antitumour agents) that inhibit or enhance interaction between on and its binding substances; (11) as probes for detecting related sequences, and (iv) to generate Ab, used for detection and quantification of UTR especially for monitoring progress of cancer therapy. SON inhibit the transfer of the content of the colls, particularly where these are The present sequence represents a 3'-untranslated region (3'UTR) fragment resistant to hydroxyurea 

Sequence 20 BP; 17 A; 1 C; 2 G; 0 T; 0 U; 0 Other;

Gaps ö Query Match 0.9%; Score 16.4; DB 1; Length 20; Best Local Similarity 94.4%; Pred. No. 4.6e+02; Matches 17; Conservative 0; Mismatches 1; Indels

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1736 AAAAAAAAAAAAAAA 1753 18 ઠે 임

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Gaps

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RESULT 825

AAX92839/c ID AAX92839 standard; DNA; 20 BP.

AAX92839;

(first entry) 13-SEP-1999 PCR primer used to amplify an ORF of Chlamydia pneumoniae.

Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; PCR primer; ss. 

Chlamydophila pneumoniae. Synthetic

WO9927105-A2

98WO-IB001890. 20-NOV-1998; 03-JUN-1999

97FR-00014673. 98US-0107078P. 04-NOV-1998; 21-NOV-1997;

(GEST ) GENSET

Griffais R;

WPI; 1999-357842/30.

Genome sequence of Chlamydia pneumoniae.

Page 1543; Disclosure; 1912pp; English.

AAX91991-X97517 represent PCR primers used to amplify open reading frames and other nucleic acid sequences from the genome of Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in

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RESULT 828
                                                                                     RESULT 827
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                                                                                                    ABA05916/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is an oligonucleotide provided in a specification relating to the simplified purification of oligonucleotides by liquid chromatography. The process comprises: (a) pouring oligonucleotides by liquid process comprises: (a) pouring oligonucleotides by liquid chromatography column packed with an acid and alkali resistant packing agent, such as polystyrene resin; (b) pouring a mixed developing solvent composed of a buffer made from a volatile salt and a water solumn; (c) pouring an acid, particularly 6-16 v/v% acetic acid, into the column to deprotect the oligonucleotides protected with the hydrophobic group; (d) pouring a mixed developing solvent composed of a buffer made from a volatile salt, particularly 0.05-0.5 N aqueous momonium hydrogencarbonate solution adjusted at pH 8-10, and a water soluble organic solvent at a suitable concentration gradient to elute the soluble organic solvent at a suitable concentration gradient to elute the solution edigonucleotides; and (e) removal of the solvent and the salt
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heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema odosum or pharyngitis. The polypeptides Ancoded by the open reading frames of the C. pneumoniae genome (see ANSISS4- ANSISS) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
                                                                                                                                                                         Gaps
                                                       nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae
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                                                                                                                                         Score 16.4; DB 1; Length 20;
Pred. No. 4.6e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       process for purification of oligonucleotides using liquid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 16.4; DB 1; Length 20;
Pred. No. 4.6e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide purification, liquid chromatography, hydrophobic protective group, deprotection, ds.
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                                                                                                                Sequence 20 BP; 8 A; 3 C; 7 G; 2 T; 0 U; 0 Other;
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0
                                                                                                                                                                                                    137 TCTGGAGTCCCCTTTCC 154
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                                                                                                                                                                                                                                                                                                     AAF99943 standard; DNA; 20 BP
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Best Local Similarity 94.4%;
Matches 17; Conservative (
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Best Local Similarity 94.4
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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The invention relates to diagnosis of hepatitis B virus (HBV) infection stages comprising identification of full length HBV transcripts (I) and truncated HBV transcripts (II) in a serum sample, where the ratio of I:II is indicative of a particular infection stage. The method is useful for diagnosing HBV infection stages and determining the risk for developing hepatocellular carcinoma. The present sequence is that of a HBV diagnostic PCR primer, useful for the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diagnosing hepatitis B virus (HBV) infection stages and determining the risk for hepatocellular carcinoma, comprises identifying full length HBV transcripts and truncated HBV transcripts in a serum sample.
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antiinflammatory steroid, ubiquinone, antiinflammatory; antiallergic;
antiasthmatic, hypotensive, immunosuppressive, cytostatic, gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis B virus; HBV; infection; hepatocellular carcinoma; diagnosis;
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                                                                                                                                                                                                                                                                                                                                   Hepatitis B virus diagnostic PCR primer SEQ ID NO 6.
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                                             2 AAAAAAAAGAAAAAA 19
                                                                                                                                                                            BP
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1736 AAAAAAAAAAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis B virus
                                                                                                                                                                                                                                                                                                                                                                                                                 PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP1152063-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DEKR-) DEUT
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Gaps

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94.48;

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Pharmaceutical composition for treating ailments associated with impaired
antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
                                                                                                                                                                                                            respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 3859; 872pp; English.
                                                                                                                                                     Li Y, Sandrasagra A, K.
Tang L, Shahabuddin S;
                                                                                              23-APR-2002; 2002WO-US013135.
                                                                                                                24-APR-2001; 2001US-0286137P
                                                                                                                                   (EPIG-) EPIGENESIS PHARM INC
                                                                                                                                                                                 WPI; 2003-229219/22.
                                                        WO200285308-A2
                                        Homo sapiens.
                                                                            31-OCT-2002.
                                                                                                                                                                                                                               ubiquinone
                                                                                                                                                              Miller S,
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Katz E, Pabalan J, Aguilar D;

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the intiation codon, coding regaion, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory theoretical activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing bronchoconstriction, lung surfactant in a subject's tissue, or treating bronchoconstriction, lung surfactant in a subject's tissue, or treating bronchoconstriction, note: The sequence date for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 20 BP; 13 A; 2 C; 0 G; 5 T; 0 U; 0 Other;

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Gaps
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0.9%; Score 16.4; DB 1; Length 20;
14.4%; Pred. No. 4.6e+02;
ve 0; Mismatches 1; Indels
              nilarity 94.4%;
Conservative
              Local Similarity
                           17;
 Query Match
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1731 TTTACAAAAAAAAAA 1748 TTTTCAAAAAAAAAA 20 ო .

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ABZ91658 standard; DNA; 20 (first entry) 17-OCT-2003 ABZ91658; RESULT 829 ABZ91658
ID ABZ9
AC ABZ9
XX
OT 17-0
DT 17-0
DE Huma
XX
Huma
KW antii

BP.

Human oligonucleotide sequence.

Human, antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;

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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the intiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an entiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antisathmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing levels of adenosine receptor, producing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Pharmaceutical composition for treating ailments associated with impaired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, antisense; lung dysfunction, nasal airway dysfunction;
antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
antisense gene therapy, respiratory; lung, adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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94.4%; Pred. No. 4.6e+02;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 15 A; 1 C; 0 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, SEQ ID NO 6900; 872pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human PDE4C oligonucleotide sequence.
                                                                                                                                                                                                                                                                                                                            Li Y, Sandrasagra A, Ka
Tang L, Shahabuddin S;
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Conservative
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                                                                                                                          WO200285308-A2
                                                                                    Homo sapiens.
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Miller S,
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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonuclectide antisense to the intitation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an entiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory steroid and ubiquinone. A composition may have a use in antisense gene therapy. The composition may have a preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an arbiect, for reducing levels of or enclosing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject, for treating bronchoconstriction, lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence date for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; antisense; lung dysfunction; nasal airway dysfunction;
antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
antisense gene therapy, respiratory, lung, adenosine sensitivity, adenosine receptor, bronchodilation, bronchoconstriction, lung allergy, lung inflammation, respiratory disease, ds.
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                                                                                                                                                                                                                                                                                                                                                                   Pabalan J, Aguilar D;
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44.4%; Pred. No. 4.6e+02;
ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 1 A; 11 C; 0 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 14429; 872pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                Katz E,
                                                                                                                                                                                                                                                                                                                                                                                   Tang L, Shahabuddin S;
                                                                                                                                                                                                                                                                                                                                                                   Sandrasagra A,
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ID AEZ87759 standard; DNA; 20 BP
XX
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XX
IT-OCT-2003 (first entry)
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DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequency
XX
XX
W Human; antisense; lung dysfunk
XW antishflammatory steroid; ubis
                                                                                                                                                                                                                          23-APR-2002; 2002WO-US013135.
                                                                                                                                                                                                                                                                       24-APR-2001; 2001US-0286137P.
                                                                                                                                                                                                                                                                                                                    (EPIG-) EPIGENESIS PHARM INC
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Best Local Similarity 94.4%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                              Li Y,
                                                                                                                                      WO200285308-A2.
                                                                                           Homo sapiens
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Miller S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ubiquinone.
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institution of the comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an entile lammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therappy. The composition may have a preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapputic respiratory effect of an entill lammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of, or reducing bronchodilation, increasing levels of ubiquinone or lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed or the patent is not represented in the printed or condition.
                                                                                                                                                                                                                                                                                                                                                                                                                             Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel pharmaceutical composition, which has a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
antisense gene therapy, respiratory, lung, adenosine sensitivity, adenosine receptor; bronchodilation, bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
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                                                                                                                                                                                                                                                                                                                             Katz E, Pabalan J, Aguilar D;
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Pred. No. 4.6e+02;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 3001; 872pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baculovirus C2 complex binding site #10.
                                                                                                                                                                                                                                                                                                                             Li Y, Sandrasagra A, Ka
Tang L, Shahabuddin S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168 GCCCACCTGGCTGCCCC 185
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                                                                                                                                                                                                                                               24-APR-2001; 2001US-0286137P
                                                                                                                                                                                                                                                                                       (EPIG-) EPIGENESIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.9%;
Best Local Similarity 94.4%;
Matches 17; Conservative
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(first entry)
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                                                                                                                           40200285308-A2
                                                                                      Homo sapiens
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Stanton VP

98WO-US005419. 97US-0041057P

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This invention describes a novel method for identifying an inhibitor of potentially useful for treatment of cancer, where the inhibitor is active on a gene vital for cell growth or viability, and where the gene is so subject to loss of heterozygosity (LDH) in a cancer. The inhibitor is used for preventing the development of cancer in a patient having a precancerous condition, by administering to the patient a first allele specific inhibitor (ASI) targeted to an allele of a first essential gene present in cells of the precancerous condition, where the normal somatic cells of the patient are heterozygous for the first gene, the inhibitor is active on at least one but less than all allelic forms of the gene or present in a population and targets only one allelic forms present in the comman somatic cells, and the first gene. The products and methods can be used in the diagnosis, prevention and treatment of LOH disorders, e.g. cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic lesions, benight tumours, endometriosis, polycystic Kidney disease, and graft versus host disease. The method can also be used to remove malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
                                                                                                                                                                                                                                                                                              Identifying target genes for allele-specific drugs - used for diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic plaque, dysplastic lesions, endometriosis or graft versus host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human polymorphic sites described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21 BP; 17 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 7; 605pp; English.
                                                                                                                                                                       (VARI-) VARIAGENICS INC
                                                                                                                                                                                                               Housman D, Ledley FD,
                                                                                                                                                                                                                                                         WPI; 1998-521232/44.
  WO9841648-A2.
                                                                                   19-MAR-1998;
                                                                                                                             20-MAR-1997;
    The sequences given in AAQ41767-825 represent sequences which are bound in an electrophoretic mobility shift assay (EMSA) by Myc. The isolated sequences contain the central E box core of CACGTG which binds very CC weakly with Myc homo-oligomers (Cl complex), but more tightly with Myc chacholigomers (Cl complex). The C2 complex requires a 26-29 kD factor in addition to Myc. The additional factor copurifies with Myc and resembles Max protein. A second copurifying 40-50 kD factor has been contained (forming C2 complex). Sites selected by the C2' complex contain the core CAGGTG which bears remarkable homology to a myogenin binding site (see AAQ41763). Oligonucleotides containing the E box can be CC used in the purification of Myc from a mammalian source. See also AAQ4176-861. The isolated target sequences may be used in a method to inhibit c-Myc oncoprotein activity. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prodn. of c-Myc protein from mammalian cells - and detection of c Myc inhibitors for use in cancer therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 0.9%; Score 16.4; DB 1; Length 21; Local Similarity 94.4%; Pred. No. 4.8e+02; les 17; Conservative 0; Mismatches 1; Indels
probe; electrophoretic mobility shift assay; EMSA; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21 BP; 6 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                             /*tag= a /note= "C2 complex binding site"
                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Fig 7a, 101pp, English.
                                                                                                                                                                                                                                                                                                                      91US-00785567
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                                                                                                       12. .17
/*tag=
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                                                                                                                                                                                                                                                                          09-OCT-1992;
                                                                                                                                                                                                                                                                                                                      30-OCT-1991;
                                                                                                   protein_bind
                                                                                                                                                                                         WO9308701-A1
                                                                                                                                                                                                                                   13-MAY-1993.
                                       Synthetic.
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                                                                                                                                                                                                                                                                                                                 cell viability; loss of heterozygosity; precancerous condition; ASI; allele specific inhibitor; somatic cell; diagnosis; prevention; atherosclerotic plaque; premalignant metaplastic lesion; endometriosis; dyplastic lesion; benign tumour; polycystic kidney disease; transplant; graft versus host disease; malignant cell removal; bone marrow; ss.
                                 Gaps
                                                                                                                                                                                                                                                                                                    Polymorphism; human; inhibitor; cancer; treatment; cell growth;
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Score 16.4; DB 1; Length 21;
Pred. No. 4.8e+02;
0; Mismatches 1; Indels
                                                                1736 AAAAAAAAAAAAAAA 1753
                                                                                               1 AAATAAAAAAAAAA 18
                                                                                                                                                                                                                                                                       Human polymorphic region 689.
      . 86.0
                   94.48;
                                                                                                                                                                           AAZ26500 standard; DNA; 21
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                 Best Local Similarity 94.4
Matches 17; Conservative
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Polymorphism; human, inhibitor; cancer; treatment; cell growth; LOH; cell viability; loss of heterozygosity; precancerous condition; ASI; allele specific inhibitor; somatic cell; diagnosis; prevention; atherosclerotic plaque; premalignant metaplastic lesion; endometriosis; dysplastic lesion; benign tumnour; polycystic kidney disease; transplant; graft versus host disease; malignant cell removal; bone marrow; ss.

Homo sapiens

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Gaps ;

1171 AAATGTGCCACGTGCTCC 1188

Matches

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4 AAATGTACCACGTGCTCC 21

AAZ26142 standard; DNA; 21 BP

Human polymorphic region 331.

AAZ26142
ID AAZ2
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30-NOV-1999 (first entry)

AAZ26142;

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(VARI-) VARIAGENICS INC.
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Best Local Similarity
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ID AAX6
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                                                                                                                                                                                                                                                                    This invention describes a novel method for identifying an inhibitor potentially useful for treatment of cancer, where the inhibitor is active on a gene vital for cell growth or viability, and where the gene is ubject to loss of heteroxygosity (LOH) in a cancer. The inhibitor is precancerus condition, by administering to the patient a first allele precancerus condition, by administering to the patient a first allele present in cells of the precancerus condition, where the normal somatic cells of the patient are heteroxygous for the first gene, the inhibitor is active on at least one but less than all allelic forms of the gene present in a population and targets only one allelic forms present in the normal somatic cells, and the first gene. The products and methods can be cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic cells, and the first gene. The products and methods can be cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic cells, and the first gene, premalignant metaplastic or dysplastic cells, and the first gene, premalignant metaplastic or dysplastic cells, and the first gene, premalignant metaplastic or dysplastic cells, and the first gene, premalignant metaplastic or dysplastic cells contours, and methods can be concers, atheroscolerotic plaques, premalignant metaplastic or dysplastic cells.
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                                                                                                                                                                       Identifying target genes for allele-specific drugs - used for diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic plaque, dysplastic lesions, endometriosis or graft versus host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymorphism; human, inhibitor; cancer; treatment; cell growth; LOH; cell viability; loss of heterozygosity; precancerous condition; ASI; allele specific inhibitor; somatic cell; diagnosis; prevention; atherosclerotic plaque; premalignant metaplastic lesion; endometriosis; dysplastic lesion; benign tumour; polycystic kidney disease; transplant; graft versus host disease; malignant cell removal; bone marrow; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          malignant cells from bone marrow transplants. AAZ25812-Z26825 represent
human polymorphic sites described in the method of the invention
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44.4%; Pred. No. 4.8e+02;
ve 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21 BP; 15 A; 2 C; 0 G; 4 T; 0 U; 0 Other;
                                                                                                        Stanton VP;
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98WO-US005419
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                                                                                                    Ledley FD,
                                                                  (VARI-) VARIAGENICS INC
                                                                                                                                      WPI; 1998-521232/44.
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Matches 17; Conserv
                                  20-MAR-1997;
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potentially useful for treatment of cancer, where the inhibitor is active on a gene vital for treatment of cancer, where the inhibitor is active on a gene vital for cell growth or viability, and where the gene is used for preventing the development of cancer in a patient having a precancerous condition, by administering to the patient a first allele present in cells of the precancerous condition, where the normal somatic cells of the patient are heterozygous for the first gene, the inhibitor is active on at least one but less than all allelic form present in the population and targets only one allelic form present in the normal somatic cells of the diagnosis, prevention and treatment of LOH disorders, e.g. cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic lesions, benign tumours, endometriosis, polycycic kidney disease, and graft versus host disease. The method can also be used to remove malignant cells from bone marrow transplants, AAZ25812-226825 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Resistance; tumour development; Marek disease tumour; chicken; system B; system REp-Y; poultry major histocompatibility complex; MHC; class II B-L gene; gene 17.5; gene 12.3; gene B-FIV; class I; genotype; selection; breeding; virue-induced tumour; YF gene; PCR primer; ss.
                                                                                                             Identifying target genes for allele-specific drugs - used for diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic plaque, dysplastic lesions, endometriosis or graft versus host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                       This invention describes a novel method for identifying an inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chicken nucleic acid involved in controlling tumor susceptibility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human polymorphic sites described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR primer used to amplify exon 2 of the YF genes of chicken.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.9%; Score 16.4; DB 1; Length 21;
34.4%; Pred. No. 4.8e+02;
Ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21 BP; 17 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
Stanton VP;
                                                                                                                                                                                                                              Disclosure, Fig 7; 605pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1736 AAAAAAAAAAAAAAA 1753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CNRS ) CNRS CENT NAT RECH SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97FR-00014669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al Similarity 94.4%;
17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AAATAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX60267 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-AUG-1999 (first entry)
  Housman D, Ledley FD,
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The specification describes nucleic acid sequences from genes (or related regions) that encode proteins involved in controlling resistance or susceptibility to development of tumours (e.g. Marek disease tumours) in chickens. The nucleic acid sequences include sequences from gene of systems B or Rfp-Y of the poultry major histocompatibility complex (MHC), other than genes of class II B-L and genes 17.5, 12.3 or B-FIV of class I. The nucleic acid sequences are used to genotype poultry, particularly to select (for breeding) birds resistant to virus-induced tumours. PCR primers AAX60267-68 were used in the course of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21 BP; 1 A; 8 C; 9 G; 3 T; 0 U; 0 Other;
Disclosure; Page 5; 49pp; French
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Gaps
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Score 16.4; DB 1; Length 21;
Pred. No. 4.8e+02;
0; Mismatches 1; Indels
   0.9%;
           94.48;
           Local Similarity 94.4
    Query Match
                      Matches
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CCGCGCCACCCCGGGCC 248 Н 18 CCGCGCCATCCCGGGGCC 231

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AAX18389 standard; DNA; 18 AAX18389

RT-PCR primer of the invention SEQ ID 30. (first entry) 11-MAY-1999

RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

Synthetic.

JP11032765-A.

09-FEB-1999.

97JP-00208312 18-JUL-1997; 97JP-00208312 18-JUL-1997;

(TAKI ) TAKARA SHUZO CO LTD

WPI; 1999-183822/16.

Peptides having at least two new nucleotides - useful as primers in RT-

Example 1; Page 12; 19pp; Japanese.

This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma) k-delta-N3'; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adennine, guanine or cytosine; N = adenine, guanine, cytosine or thymine; amma = thymine; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of repetition of gamma, in which thymine expressed by gamma is composed of 13 or large of a guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene RESULT 8339/C ID AAX18389/C XX AAX11 DT 11-M DX RT-PC XX XY RT-PC XX SYNCI XX YP111-M XX YP111-M XX YP111-M XX YP11-M XX YP11-M XX YP11-M XX YP11-M XX YP11-M XX CT TAK XX

Sequence 18 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 2 Other;

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Gaps

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ch 0.9%; Score 16.2; DB 1; Length 18; 1 Similarity 94.1%; Pred. No. 4.5e+02; 16; Conservative 1; Mismatches 0; Indels
                            Local Similarity
     Query Match
                                                   Matches
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AAV48564-708 represent antisense oligonucleotides directed against the jumb and jumb genes. Of these, only oligonucleotides AAV48655-614
resulted in effective downregulation of negative growth control by Jumb or Jumb, while AAV48615-708 had little effect. The oligonucleotides exemplify the invention. The specification describes oligonucleotides that can each form three hydrogen bonds to cytosine; do not contain four consecutive nucleotides able to form three H-bonds each to four consecutive cytosines; do not contain two sequences of three consecutive nucleotides able to form three H-bonds to three consecutive nucleotides each able to form three H-bonds to three consecutive cytosines, and the ratio between residues able to form two H-bonds each oligonucleotides are used to modulate expression of genes, particularly the genes for p53, ErbB-2, jumb, jumb, TGF-beta I or beta 2 to control proliferation of primary cell cultures (e.g. bone marrow stem, liver or kidney cells, osteoclasts osteoblasts and/or keratinocytes). The oligonucleotides can also be used to analyse function of proteins (by altering their expression or activity) and therapeutically, e.g. in cases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Preparation of antisense oligo:nucleotide(s) which lack long runs of consecutive guanosine or inosine - and have specific ratio of residues able to form two or three hydrogen have greater activity and reduced toxicity, used therapeutically or to modulate growth of cells is
                                                                                                                                                                                                                                                                              junB; junD; antisense oligonucleotide; modulate; gene expression; ss.
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85.7%; Pred. No. 5.1e+02;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21 BP; 0 A; 5 C; 14 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
                                                                                                                                                                                                                                         junB gene antisense oligonucleotide JunB-T-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               348 TCGGGGCCCGCGTGGGTGG 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Fig 5c; 286pp; English
1735 CAAAAAAAAAAAAA 1751
                                                                                                                              AAV48674 standard; DNA; 21 BP
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                       17 BAAAAAAAAAAAAAA 1
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                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JAN-1997;
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Local St.
18;
                                                                                                                                                                                                      15-OCT-1998
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                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                   AAV48674;
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                                                                                           RESULT 838
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Matches
                                                                                                              AAV48674
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us10008789-3.rng

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This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta -N3'; or (X)m5'-(gamma) k-delta-N3'; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, guanine, or cytosine; N = adenine, guanine or thymine; R = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of repetition of gamma, in which thymine expressed by gamma is composed of 13 or lates of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene
                                                                                                                                                                                               Peptides having at least two new nucleotides - useful as primers in RT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens fetal kidney clone AK647 secreted protein gene 3' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.9%; Score 16; DB 1; Length 16; Best Local Similarity 100.0%; Pred. No. 4.4e+02; Matches 16; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16 BP; 0 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                        Disclosure; Page 10; 19pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Secreted protein; fetal kidney; da
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                                                                           97JP-00208312.
                                    97JP-00208312.
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                                                                                                                   (TAKI ) TAKARA SHUZO CO LID
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                                                                                                                                                     WPI; 1999-183822/16.
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                                    18-JUL-1997;
                                                                           18-JUL-1997;
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39-FEB-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention comprises novel rice transposon genes, which are: a non-independent transposon gene, an independent transposon gene, and a transposase gene. The rice genes of the invention are useful for mutation and functional analysis of rice and other plants. The present DNA sequence represents a PCR primer that is used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Independent and non-independent rice transposon and rice transposase genes for functional analysis and mutagenesis in rice and other plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
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                                                                                                                                                                                                         rice; transposon gene; non-independent transposon gene;
independent transposon gene; transposase gene; plant mutation;
plant functional analysis; ss; PCR; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.9%; Score 16.2; DB 1; Length 21;
85.7%; Pred. No. 5.1e+02;
tive 0; Mismatches 3; Indels
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                                                                                                                                                                      Rice transposon gene-related PCR primer #21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NISC-) JAPAN SCI & TECHNOLOGY CORP.
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                                                     ADB74186 standard; DNA; 21 BP
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18-JAN-2002; 2002JP-00099729.
07-JUN-2002; 2002JP-00167345.
12-AUG-2002; 2002JP-00234412.
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                                                                                                                                 (first entry)
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Matches 18, Conservative
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18-JAN-2002; 2
07-JUN-2002; 2
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Gaps

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New polynucleotides encoding secreted human proteins - are derived from foetal kidney or adult retina cDNA libraries, used as, e.g. potential

Disclosure; Page 54; 76pp; English.

vaccines

JP11032765-A

Synthetic

AAX18367/

ઠ 유 Treacy. M;

Gaps

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0; Indels

Length 16;

Score 16; DB 1; Le Pred. No. 4.4e+02;

Match 0.9%; Sco Local Similarity 100.0%; Pr

Query Match

S

Matches

1736 AAAAAAAAAAAAA 1751

1 AAAAAAAAAAAAAA 16

Mismatches

Seguence 16 BP; 16 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

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AACG6068
AACG6068
AC AACG608
AC AACG608
AC AACG600

AC AACG600
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The sequence is that of the 3' end of a sequence encoding a secreted protein from a human fetal kidney clone AK296. Such a sequence is predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, hammatopoiesis regulating activity, tissue growth activity, activin/inhibin activity, chemokineiic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity. It is also stated to be useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes nucleoside derivatives (I) with photolabile protecting groups. (I) are used to synthesize oligonucleotides using the photolithographic nucleic acid chip method, particularly where these are intended for performing enzymatic reactions initiated from a free 3'-hydroxy (especially solid-phase polymerase reactions or ligase reactions, but also reverse transcription, CDNA synthesis etc.), also for hybridization testing, sequencing and in DNA computing. (I) are produced with high selectivity by reaction with a mild acylating agent that has high specificity for the 3'-position, without significant side-reactions (cf. more reactive acylating agents such as chloroformates)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleoside derivatives with photolabile protecting groups, useful in oligonucleotide synthesis, particularly on solid phases, e.g. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA chip; primer; nucleoside derivative; photolabile protecting group; photolithographic nucleic acid chip; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.9%; Score 16; DB 1; Length 16; Best Local Similarity 100.0%; Pred. No. 4.4e+02; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16 BP; 16 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 9; 48pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-APR-1999; 99DE-01015867.
28-JAN-2000; 2000DE-01003631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-679457/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA chip primer #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200061594-A2.
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                                                                                                                                                                                                                                                                              /note= "OTHER = F1(CH2)6-PO-thymine, where F1 is flavine and PO is a phosphate group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Support for hybridization analysis of nucleic acids for sequencing techniques, comprises an array of oligonucleotides having a label where the fluorescence changes follow hybridization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                               Analytical support; genomic sequencing; mutation detection; pharmaceutical development; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dueymes C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.9%; Score 16; DB 1; Length 16; 100.0%; Pred. No. 4.4e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fontecave M, Decout JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                              (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.
                                                                                                                                                                                                                       Location/Qualifiers
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/mod base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 12; 33pp; French.
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                             BP
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                                                                                                                                                                                                                                                                                                                                                                                                                 23-FEB-2000; 2000FR-00002236.
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                             ABA04585 standard; DNA; 16
                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-628265/73.
                                                                                                                   Oligonucleotide #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                     modified base
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                                                                                       15-FEB-2002
                                                                                                                                                                                                                                                                                                                                                        24-AUG-2001
                                                                                                                                                                                          Synthetic
                                                          ABA04585;
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RESULT 843
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Matches
               ABA04585,
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ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore; hybridisation; detection; fluorescence; probe; ss.

Dempcy RO, Afonina IA, Vermeulen NMJ;

WPI; 2001-328656/34

(EPOC-) BPOCH BIOSCIENCES INC.

99US-00428236.

26-OCT-1999;

26-OCT-2000; 2000WO-US029786.

40200131063-A1

Synthetic

**03-MAY-2001.** 

Oligonucleotide portion of ODN-MGB-LF conjugate.

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The present sequence is that of an oligonuclectide (ODN)-winor groove binder (MGF) complex. MGBs bind in a non-intercalating manner to the minor groove of non-single-stranded DNA, RNA or their hybrids. ODN-MGB-LF conjugates of the invention also comprise a latent fluorophore (LF), which binds similarly to the MGB but in an intercalating manner, or lies in the minor groove, or is oriented in some other way to the DNA molecule by MGB, such that it becomes fluorescent (or its fluorescent properties change detectably). The conjugates are used as hybridisation probes and amplification primers for fluorescent detection of specifically PCR, for single-nuclectide mismatch discrimination, target or signal amplification, array-based assays and sequencing, including detection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conjugate of oligonucleotide, minor groove binder and latent fluorophore, useful for detecting specific nucleic acids, e.g. for single-nucleotide mismatch discrimination.
                                                                                                                                ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore; hybridisation; detection; fluorescence; probe; ss.
                                                                                                                                                                                                                                                   /*tag= a
/note= "thymine modified by a minor groove binder (2-
dimethylaminonaphthalene-6- sulfonamide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.9%; Score 16; DB 1; Length 16;
100.0%; Pred. No. 4.4e+02;
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                                                                                                 Oligonucleotide-minor groove binder complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          double-stranded DNA by triplex formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vermeulen NMJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 101; 105pp; English.
                                                                                                                                                                                                                   Location/Qualifiers
 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EPOC-) EPOCH BIOSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                        26-OCT-2000; 2000WO-US029786.
                                                                                                                                                                                                                                                                                                                                                                                                                        99US-00428236
AAF30895 standard; DNA; 16
                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-328656/34
                                                                                                                                                                                                                                                                                                                      WO200131063-A1
                                                                                                                                                                                                                   Key
modified_base
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                                                                 39-JUL-2001
                                                                                                                                                                                                                                                                                                                                                       33-MAY-2001
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                                                                                                                                                                                    Synthetic
                                AAF30895
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The present sequence is that of the oligonucleotide (ODN) component of an ODN-MGB (minor groove binder)-LF (latent fluorophore) conjugate of the invention. MGBs bind in a non-intercalating manner to the minor groove of non-single-stranded DNA, RNA or their hybrids, while a LF binds similarly but in an intercalating manner, or lies in the minor groove, or is criented in some other way to the DNA molecule by MGB, such that it becomes fluorescent (or its fluorescent properties change detectably). The conjugates are used as hybridisation probes and amplification primers for fluorescent detection of specifically hybridising sequences, for analysis or diagnosis, especially (real-time) PCR, for single-nucleotide mismatch discrimination, target or signal amplification, array-based sasays and sequencing, including detection of double-stranded DNA by criplex formation. Many different targets can be detected a single reaction vessel. The present ODN-MGB-LF conjugate was used to demonstrate hybridisation-triggered fluorescence. Upon hybridisation to the complementary target sequence there was an increase in fluorescence complementary target sequence there was an increase in fluorescence complementary target sequence there was an increase in fluorescence emitted by the hybrid increasence emitted by unhybridised (i.e. single-stranded) ODN-MGB-LF, for single-stranded) ODN-MGB-LF, for single-stranded) ODN-MGB-LF, for single-stranded of the fluorescence emitted by unhybridised (i.e. single-stranded) ODN-MGB-LF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conjugate of oligonucleotide, minor groove binder and latent fluorophore, useful for detecting specific nucleic acids, e.g. for single-nucleotide mismatch discrimination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Branched chain compound; nucleic acid synthesis; primer extension; reverse transcription; nucleic acid hybridization; nucleic acid amplification; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 0.9%; Score 16; DB 1; Length 16; Local Similarity 100.0%; Pred. No. 4.4e+02; les 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide used to produce branched chain compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 58; 105pp; English.
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Gaps ö

0; Indels

0; Mismatches

100.08;

Local Similarity 100. 1es 16; Conservative

Best Loca Matches

1736 AAAAAAAAAAAAAA 1751

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AAF30880 standard; DNA; 16 BP

AAF30880/c

09-JUL-2001 (first entry)

AAF30880;

SXXXE

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The specification describes branched compounds containing nucleic acid moieties optionally extended by a polymerase. The branched chain compounds of the invention are used in nucleic acid synthesis reaction, primer extension reaction, reverse transcription reaction of RNA into DNA, nucleic acid hybridization experiment (for identifying sequence of nucleic acid), and nucleic acid amplification experiment (for analysing the expression pattern of genes). The compounds are also used in solid-phase enzymatic reactions. The present sequence was used in the course of the invention to produce branched chain compounds
                                                                                                                                                                                                                                                                                                                                                                                                    Branched compounds useful in e.g. nucleic acid synthesis reaction comprises nucleic acid moieties optionally extended by a polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleotide sequence of oligomer # 1 used to test thermal stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 0.9%; Score 16; DB 1; Length 16; Local Similarity 100.0%; Pred. No. 4.4e+02; No. 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
                                                                                                           '*tag≃ c
'note= "branch present"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein nucleic acid molecule; PNA; ds
                                                                                                                                                  /*tag= b
/note= "COOH attached"
                                                                   a
"COOH attached"
                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 10; 31pp; English.
                                                                                                                                                                                                                                                                                                                                              Schmidt W, Hiller R, Huber M,
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                                                                                                                                                                                                                                                                                                      (LION-) LION BIOSCIENCE AG. (VBCG-) VBC GENOMICS GMBH.
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                                                                   /*tag=
                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-466959/51.
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                                                     modified_base
                                                                                                                                     modified base
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                                                                                             misc_feature
                                                                                                                                                                                          EP1111068-A1
                                                                                                                                                                                                                     27-JUN-2001.
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              Synthetic
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Mueller M;

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This invention relates to oligomuclectide analogues comprising a protein nucleic acid molecule (PNA) monomer. They are used in the detection and separation of nucleic acid molecules and as probes, primers, linkers, adapters and antisense agents on solid supports. Modifications enhance their use as capture and detection probes e.g. by the incorporation of biotin, digoxigenen, radiostopes, fluorescent labels such as lulorescenn and reporter molecules such as alkaline phosphatase. They are also used for enhancing or inhibiting the activity of an enzyme or cellular activity. The compounds are stable to nucleases and proteases, have high affinity, binding specificity and solubility. The polyamide backbone of PNAs is resistant to both nucleases and proteases. PNAs bind nucleic acid molecules with greater affinity than DNA or RNA concentration. The compounds are relatively simple to synthesize and are used in a wide variety of applications. This sequence represents a DNA oligomer which is used to represent the thermal stability of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                       Oligonucleotides analogs useful in detection, separation and purification of nucleic acid molecules, comprise monomers, dimers and oligomers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2'F-ANA antisense oligo #6, to elicit RNase H degradation of target RNA.
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/note= "Bases 8 and 9 are linked by two secouridine
linkers which is represented as S in page 49 and X in
page 57 and Fig 7 and 8 of the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
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1. .16
/*tag= a /*tag= OTHER
/mod base= OTHER
/note= "2'-deoxy-2'-fluoroarabinothymidine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.9%; Score 16; DB 1; Length 16;
100.0%; Pred. No. 4.4e+02;
ive 0; Mismatches 0; Indels
                                                                                                                            Efimov V, Fernandez J, Archdeacon D, Archdeacon Chakhmakhcheau O, Buryakova A, Choob M, Hondorp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                              Example 17; Page 118; 197pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD56451 standard; DNA; 16 BP.
13-MAR-2001; 2001WO-US008111.
                                  14-MAR-2000; 2000US-0189190P.
30-NOV-2000; 2000US-0250334P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oligomers of the invention
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                                                                                          (ACTI-) ACTIVE MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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Gaps

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Detection, single-stranded sensor; detectable fluorescence emission; forensic testing; paternity testing; tissue typing; hereditary disorder; human population genetics; human evolutionary history; cystic fibrosis; human haplotype diversity; Tay-Sachs; sickle-cell anaemia; ss.
                                                                                                                                                                                                                                                                                                                                                                         Oligo-homodeoxyribonucleotide sequence, oligo dT.
                                                                                                                                                                                                                                                                             1736 AAAAAAAAAAAAAA 1751
                                                                                                                                                                                                                                                                                                                              AALS4078 standard; DNA; 16 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-APR-2002; 2002WO-US012176.
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                                                                                                                                                                                                                                                                                          AAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                          (first entry)
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(CHAJ/) CHA J N.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
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08-MAY-2003
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a sample, which comprises: contacting and properties of containing a target polynucleotide with a predetermined single-stranded sensor polynucleotide complementary to the target polynucleotide, in a solution comprising an agent that its a nonaqueous solvent that allows the sensor polynucleotide to produce a detectable fluorescence emission; exciting the sensor polynucleotide, and determining fluorescence emission. The assay is useful for detecting a single or double-stranded target polynucleotide, such as, DNA or RNA in a sample. The assay finds use in a polynucleotide, such as, DNA or RNA in a sample. The assay finds use in a wide variety of different applications includual which was the source of a forensic specimen, in anthropological setting, paternity forensic specimen, in anthropological setting, paternity casting for compatibility between prospective tissue or blood chonors and patients and in screening for hereditary disorders. The method is also useful to study alterations of gene expression in response to a stimulus, disease, drug or medication, and other applications include tharacterisation of human haplotype diversity. The method is useful for detecting polynucleotide sequences from contaminants or pathogens including bacterial, yeast, and viruses to detect single nucleotide polymorphisms, which may be associated with particular alleles or subsets of alleles. The method is useful for detection of mutan between the distance of males or subsets of alleles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorders including cystic fibrosis, Tay-Sachs, and sickle-cell anaemia. This polynucleotide sequence represents an oligonucleotide sequence used in a fluorescence technique of the invention
                                                                                                                                                                                                                                                                                                         The invention relates to a novel assay for detecting a polynucleotide in
                                                               Detecting polynucleotides, for pharmacogenetic testing, comprises contacting a target polynucleotide with a complementary single-stranded sensor polynucleotide and an agent that allows the sensor to fluoresce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleotide sequences associated with increased risk of diseases or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                          Example 1; Page 25; 41pp; English.
   WPI; 2003-103378/09.
                                                                                                                                                                           upon excitation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an acyclic linker-containing oligonucleotide comprising at least one modified deoxyribonucleotide. Oligonucleotides of the invention are useful for preventing or decreasing translation, reverse transcription and/or replication of a target RNA in a system. They are useful for selectively preventing gene expression in a sequence specific manner, for hybridising to complementary RNA such as cellular mRNA or viral RNA, to hybridising to complementary RNA such as cellular mRNA or viral RNA, to hybridise to and induce cleavage of complementary they are also useful therapeutically in formulations or medicaments to prevent or treat a disease characterised by the expression of a particular target RNA. The invention is used in gene therapy. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence is an antisense oligo used to elicit human RNase (ribonuclease) H degradation of target RNA. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                    Novel acyclic linker-containing oligonucleotide useful for preventing decreasing translation, reverse transcription and/or replication of a target RNA in a system, comprises a modified deoxyribonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                      Mangos MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Fig 7; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.08;
                                                                      29-OCT-2002; 2002WO-CA001628
                                                                                                                                     29-OCT-2001; 2001US-0330719P
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Matches 16, Conservative
                                                                                                                                                                                                                                                                      Damha MJ, Viazovkina
                                                                                                                                                                                                                                                                                                                                         WPI; 2003-421516/39.
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Gaps
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                                                                                                                                                                                                             hydroxyproline nucleic acid; HypNA; PNA; peptide nucleic acid; gene expression; respiration; secretion; signalling; ion-channel activity; cell motility; developmental phenotype; tumour regression; hybridisation; ss.
Score 16; DB 1; Length 16; Pred. No. 4.4e+02;
                      0; Indels
                                                                                                                                                                                                                                                                                                                 /*tag= a
/note= "Optional N-terminal acetyl"
        100.0%; Pred. ...
                                                                                                                                                                                         DNA hybridisation oligomer SEQ ID 9.
                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                             1736 AAAAAAAAAAAAAA 1751
                                                                                                                        ADB68519 standard; DNA; 16 BP.
 0.9%;
                                                                 16 AAAAAAAAAAAAA 1
                                                                                                                                                                     04-DEC-2003 (first entry)
                        16; Conservative
            Best Local Similarity
                                                                                                                                                                                                                                                                                                       misc_difference
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                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                              ADB68519;
 Query Match
                        Matches
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21-AUG-2003

Stucky GD;

Cha JN, Morse DE,

07-FEB-2003; 2003WO-US003904.

us10008789-3.rng

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Human flt1 VEGF receptor hammerhead ribozyme substrate #1095.
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                                                                                                                                                                                                                                                                                                                                                                                                      Example 17; Page 233; 240pp; English
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                                                        09-FEB-2002; 2002US-00072975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JUL-1999 (first entry)
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es 16; Conservative
                                                                                                                                                                          Efimov V, Fernandez J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mcswiggen J,
                                                                                                                 (ACTI-) ACTIVE MOTIF
                                                                                                                                                                                                                            WPI; 2003-689653/65.
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AC AAX6

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DE Human

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ВР

Escobedo J;

Stinchcomb D,

96WO-US017480.

96US-00584040. 95US-0005974P

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The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (VEGF). A patient (preferably human) having a fordition associated with the level of the fms-like tyrosine kinase 1 (flc-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour anglogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient. AAXX7155 to AAX75752 represent specific examples of nucleic acid molecules from the present invention
                                                                             mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vascular endothelial growth factor receptor; VBGF receptor; flt-1; flk-1; MSR; hammerhead ribozyme; cleavage; tumour angiogenesis; psorials; rheumatoid arthritis; ocular disease; fms-like tyrosine kinase 1; kinase insert domain containing receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (VEGF). A patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                     Nucleic acid molecule modulating VEGF receptor(a) gene expression or stability – useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient.
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100.0%; Pred. No. 4.6e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                    Claim 4; Page 79; 218pp; English
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96US-00584040.
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WPI; 1997-259017/23.
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11-JAN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel method of inhibiting the expression of one or more genes or RNA transcripts by administering at least one oligonucleotide analogue that includes at least one hydroxyproline nucleic acid (HypNA) monomer to a cell or organism or their extracts. Throligonucleotides of the invention may be used to monitor properties oligonucleotides of the invention may be used to monitor properties channel activity, cell motility, developmental phenotype and tumour regression. Furthermore, they may be utilised to determine the effects of particular genes, as antisense or homologous recombination constructs e.g. for creating animal models of disease and finally, for increasing the activity of some enzymes, such as polymerases. The current sequence is that of the DNA hybridisation oligomer SEQ ID 9 of the invention. This sequence may also comprise a peptide nucleic acid (PNA).
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                                                                                                                                                                                                                                                                                                                                                           Method of inhibiting expression of genes or RNA transcripts, useful for therapy and determining effects of genes, by administering oligomers containing hydroxyproline nucleic acid.
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100.0%; Pred. No. 4.4e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                    Archdeacon D, Archdeachon J,
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Rare expressed gene; analysis; expression; nucleic acid sample;

PCR primer; 88

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Synthetic.

Mus sp.

Murine gene anchor PCR primer SEQ ID NO:3.

(first entry)

31-JAN-2000

AAZ35714;

AAZ35714 standard; DNA; 17 BP.

RESULT 854 AAZ35714/c

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(preferably human) having a condition associated with the level of the fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour anglogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient. AAX67275 to AAX75752 represent specific examples of nucleic acid molecules from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a PCR primer used in the identification of a human pollanosis associated gene. The gene is highly expressed in individuals with high pollen-specific immunoglobulin E (IgE) levels. The invention relates to the nucleotide sequence encoding the pollenosis associated protein, diagnosing pollenosis and screening candidate compounds for treating pollenosis. The gene can be used in diagnosing pollenosis, and screening candidate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pollenosis-associated protein; high pollen-specific immunoglobulin E; IgE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene highly expressed in patients with high cedar pollen-specific IgE
levels, useful for diagnosing pollenosis, and screening candidate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR primer GT15G used in pollenosis associated gene identification.
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                                                                                                                                                                              Query Match 0.9%; Score 16; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 4.6e+02; Matches 16; Conservative 0; Mismatches 0; Indels
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                                                                                                                                               Seguence 17 BP; 0 A; 1 C; 0 G; 0 T; 16 U; 0 Other;
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Lu N, Ogawa K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             compounds for pollenosis treatment
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                                                                                                                                                                                                                                                                                                                                                                              AAA30181 standard; DNA; 17 BP.
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Imai Y,
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Obayashi I,
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The present invention describes a providing a nucleic acid sample comprising: (a) providing a nucleic acid sample comprising: (a) providing a nucleic acid sample comprising: (a) providing a nucleic acid sample; (b) providing and providing one or a portion of sequences, and providing one or a portion of sequence of the nucleic acid sample; (b) mixing and hybridizing the nucleic acid sample with probes; (c) subsequently recovering nucleic acid sample with probes; (c) subsequently recovering nucleic acid sample with probes; (c) substantially complementary to a portion of sequence of the nucleic acid sample having a plurality of kinds of probes having a known sequence of two nucleic acid sample with the corryme or the probe itself; and (iv) subsequently recovering the nucleic acid sample with the probes; (ii) mixing and hybridizing the nuclease activity of an enigmence or the probe itself; and (iv) subsequently recovering the nucleic acid sample having a plurality of species of sequences and oligonucleotides primer having predetermined sequences for synthesizing DNA strands; (II) providing one or a plurality to a portion of a sequence of the nucleic acid sample having such a structure to probe having a known sequence substantially complementary to a portion of a sequence of the nucleic acid sample having such a structure to prevent a polymerase reaction from its 3' end and a nuclease reaction from its 3' end and a nuclease reaction for the samples prepared in (III); and (v) subsequently recovering nucleic acid sample for the analysis of rare expressed caid molecules synthesized in (IV). The method is useful for the acid molecules synthesized in (IV) rhe method is useful for the sequence of sequence represents a pCR primer used in the expressed in the primer and sequence represents a pCR primer securing nucleic acid sample prepared in the primer and sequence represents a pCR primer used in the primer secure or sequence acid sample prepared in the sequence acid sample primer and sequence acid sample sequence acid sam
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Preparation of nucleic acid sample, useful for analysis of rare expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Кіуаша М,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 11; 22pp; English
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Query Match Best Local Matches 1735 CAAAAAAAAAAAAA 1750

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This invention describes novel DNA sequences preferentially expressed in IgA nephropathy patients, and DNA sequences stringently hybridizing to IgA nephropathy patient claims cover diagnostic reagents for IgA nephropathy incorporating the antisense sequences; the treatment of IgA nephropathy using the antisense sequences for mRNA inhibition; proteins associated with IgA nephropathy, containing sequences encoded by the DNA sequences; antibodies recognizing these proteins; the production of the proteins by culture of host cells transformed with DNA encoding them; diagnostic reagents for IgA nephropathy containing the antibodies; and compositions for the treatment of IgA nephropathy which contain the antibodies. The products of the invention can be used for the diagnosis and treatment of IgA nephropathy. This sequence represents a primer used in the isolation and identification of the human IgA nephropathy-associated proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anchored oligo (dT) primer GT15G used for modified differential display.
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                                                                                                                                                                 IgA nephropathy-associated protein; diagnosis; treatment; antisense; human; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA sequences preferentially expressed in IgA nephropathy patients, proteins encoded by them, and antibodies to those proteins.
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Pred. No. 4.6e+02;
0; Mismatches 0; Indels
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                                                                                                                                 Human IgA nephropathy-associated cDNA primer #62.
                                                                                                                                                                                                                                                                                                                                                                                                                  Ishiwata T, Sakurada M, hamuura A;
sawada S, Takei M, Shibata K, Furuya A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 170; 180pp; Japanese.
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AAX82721 Btandard; DNA; 17
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Les 16; Conservative
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                                                                                                                                                                                                                     Homo sapiens.
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Matches
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              Stimulus-regulated nucleic acid; sequence profile; nucleic acid level; differentially expressed nucleic acid; disease state; cancer; autoimmune disease; infectious disease; aging; developmental disorder; proliferative disorder; neurological disorder; toxicity; primer; treatment resistance; differential expression; drug discovery; growth factor; epidermal growth factor; radiation; stress; pathogen; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Measuring expression of low abundance reduced complexity target nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to a stimulus, e.g. a chemical, drug or growth factor (especially epidermal growth factor), radiation, stress or a pathogen. The methods can also be used to determine co-regulated genes that can be potential
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100.0%; Pred. No. 4.6e+02;
ve 0; Mismatches 0; Indels
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98US-0098070P.
99US-0118624P.
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ses 16; Conservative
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                                                                                                                                                                                            W09955913-A2
                                                                                                                                                                                                                                                                     27-APR-1999;
                                                                                                                                                                                                                                                                                                             27-APR-1998;
                                                                                                                                                                                                                                                                                                                                                 04-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                 27-AUG-1998;
                                                                                                                                                                                                                                04-NOV-1999
                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA25449/
g
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99WO-US008547.

.9-APR-1999;

28-OCT-1999

M09954459-A2

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The present invention describes nucleic acids (A) that interact stably with a target sequence and contain at least one phosphoro(di)thioate with a target sequence and contain at least one phosphoro(di)thioate contains a dead of the describerally any catalytic nucleic acid (A') that modulates expression of the oestrogen receptor.

Gene, are used to treat cancer (particularly of breast or endometrium), contain violations associated with levels of oestrogen receptor.

Governlate inhibition of gene expression with alterations in phenotype, correlate inhibition of gene expression with alterations in phenotype, correlate inhibition of gene expression with alterations in phenotype, correlate inhibition of therapeutic targets, and as research reagents (for RNA, in the same way that restriction endomucleases are used with DNA). The combination of therapeutic rargets, and as research casenace to mucleases, binding affinity and/or activity. AAA21503 to AAA24747 represent oestrogen receptor harmerhead ribozyme sequences.

AAA24747 represent oestrogen receptor harmerhead ribozyme sequences.

AAA24748 to AAA25052 represent their corresponding target sequences.

Sequences, and AAA26107 to AAA26211 represent their corresponding target sequences and antisense oligonucleotides used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acids that interact, and optionally cleave, target sequences,
                                                                                                                                                                                                                                                                                           Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
Reynolds M, Zwick M, Jarvis T, Woolf T, Haeberli P;
Matulic-Adamic J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 77; Page 79; 148pp; English.
                                                                                                                                               99WO-US008547.
                                                                                                                                                                                     98US-0082404P.
98US-00103636.
                                                                                                                                                                                                                                                     (RIBO-) RIBOZYME PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 used to treat cancer
                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-013248/01.
                      Homo sapiens.
                                                                                                                                               19-APR-1999;
                                                           W09954459-A2
                                                                                                                                                                                       20-APR-1998;
                                                                                                                                                                                                           23-JUN-1998;
                                                                                                     28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention
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Gaps
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Score 16; DB 1; Length 17; Pred. No. 4.6e+02; 0; Mismatches 0; Indels
    100.08; PL
  Query Match 0.99
Best Local Similarity 100.
Matches 16; Conservative
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1736 AAAAAAAAAAAAAA 1751

17 AAAAAAAAAAAAA 2 ઠ 쉽

AAA25454 Standard; DNA; 17 BP 19-JUL-2000 (first entry) AAA25454; RESULT 858

Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1952

Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage; hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide; gene expression modification; cancer; phosphorothioate; endonuclease; anticancer; breast cancer; endometrium cancer; ss.

WO200065046-A1

Synthetic

Homo sapiens

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with a target sequence and contain at least one phosphoroid;) thioate with a target sequence and contain at least one phosphoroid;) thioate link, having endonuclease activity. (A), and more generally any catalytic nucleic acid (A') that modulates expression of the oestrogen receptor.

Gene, are used to treat cander (particularly of breast or endometrium).

Cor other conditions associated with levels of oestrogen receptor.

Correlate inhibition of gene expression with alterations in phenotype, correlate inhibition of gene expression with alterations in phenotype, particularly for identification of therapeutic targets, and as research reagents (for RNA, in the same way that restriction endomucleases are used with DNA). The combination of modifications in (A) improves the sistance to nucleases, binding affinity and/or activity. AAA22503 to AAA24748 to AAA2592 represent their corresponding target sequences.

Company of AAA2503 represent cestrogen receptor hairpin riboxyme sequences, and AAA26107 to AAA26171 represent their corresponding target sequences.

Company of AAA26107 to AAA26171 represent their riboxyme sequences and antisense oligonucleotides used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                        New nucleic acids that interact, and optionally cleave, target sequences used to treat cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, pollinosis-associated gene 373; IgE; immunoglobulin E; cedar pollen allergy; T-cell; reduced expression; detection; diagnosis; drug screening; allergic disease; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                      present invention describes nucleic acids (A) that interact stably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                 Bellon L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR anchor primer, SEQ ID NO:5, used in human gene 373 isolation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 0.9%; Score 16; DB 1; Length 17; Local Similarity 100.0%; Pred. No. 4.6e+02; hes 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                   Karpeisky A,
Haeberli P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                 Mcswiggen JA,
vis T, Woolf T,
                                                                                                                                                                                                                   Beigelman L, Mcswig
Zwick M, Jarvis T,
                                                                                                                                                                                                                                                                                                                                                                                   Claim 77; Page 79; 148pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1733 TACAAAAAAAAAAA 1748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC64204 standard; DNA; 17 BP
                                                                                                                          98US-0082404P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 TACAAAAAAAAAA 1
                                                                                                                                                                               (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                          WPI; 2000-013248/01.
                                                                                                                                                                                                                                    Reynolds M, Zwick
Matulic-Adamic J;
                                                                                                                                                                                                                 Thompson JD,
                                                                                                                          20-APR-1998;
23-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC64204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 859
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us10008789-3.rng

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The invention relates to the human pollinosis-associated gene 373 which with high cadar pollen-specific IGE (immunoglobulin E) levels. The gene was isolated from T-cells from individuals allergic to cadar pollen using the differential display method. The invention also relates also relates to the protein encoded by pollinosis gene 373; expression constructs and host cells comprising pollinosis-associated gene 373 nucleic acids; pollinosis-associated gene 373 nucleic acids; protein encoded by the gene; methods of detection of pollinosis-associated gene 373 nucleic acids; and a method of diagnosis of allergic diseases via the detection of pollinosis-associated gene 373 nucleic acids; and a method of diagnosis of allergic diseases via the detection of pollinosis-associated gene 373 nucleic acids; acids. The invention additionally encompasses methods of screening drug acids. The invention additionally encompasses methods of screening drug candidates for the treatment of allergic diseases by measuring the expression of pollinosis-associated gene 373 in pollen antigen-stimulated T-cells in the presence of a test compound relative to a control.

T-cells in the presence of a test compound relative to a control.

Condidates for the treatment of allergic diseases and in the screening of drug candidates for the treatment of such diseases. The present sequence represents a PCR primer used in the custom in the general sequence represents a PCR primer used in the isolation of human pollinosis-associated gene 373 cDNA
                                                                                                                                                                                                                                                                                                                                      Pollinosia-associated gene 373 undergoing significantly low expression in subjects with high cedar pollen-specific immunoglobulin-E levels, useful in diagnosis of allergic diseases and screening drug candidates.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 6; Page 70; 80pp; Japanese.
                                                26-APR-2000; 2000WO-JP002730
                                                                                                    99JP-00120489
                                                                                                                                                     (GENO-) GENOX RES INC
                                                                                                                                                                                                      Sugita Y,
Imai Y,
                                                                                                                                                                                                                                                                                        WPI; 2000-687339/67.
                                                                                                       27-APR-1999;
                                                                                                                                                                                                         Nagasu T, S
Obayashi I,
02-NOV-2000
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Gaps °. Score 16; DB 1; Length 17; Pred. No. 4.6e+02; 0; Mismatches 0; Indels Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other; 100.0%; Printer 0; 0.9%; Query Match Best Local Similarity 100.0 Matches 16, Conservative

1735 CAAAAAAAAAAAA 1750 17 CAAAAAAAAAAAA 2 ò 셤

AAC64183 standard; DNA; 17 21-FEB-2001 (first entry) AAC64183; RESULT 860 AAC64183, 

BP

PCR anchor primer, SEQ ID NO:4, used in human gene 419 isolation.

Human; pollinosis-associated gene 419; FAF-1 homologue; Fas-associated factor-1; IgE, Immunoglobulin E; cedar pollen allergy; T-cell; reduced expression; detection; diagnosis; drug screening; allergic disease; PCR primer; 88.

Synthetic

WO200065045-A1

02-NOV-2000

26-APR-2000; 2000WO-JP002729.

99JP-00120490 27-APR-1999;

(GENO-) GENOX RES INC

Gunji S; Kashiwabara T, Oshida T, Obayashi M, Yoshida N, Ogawa K, Matsui K; Sugita Y, Imai Y, Obayashi I, Nagasu T,

WPI; 2000-687338/67.

Gunji S;

Obayashi M,

Kashiwabara T, Oshida T, Obay Yoshida N, Ogawa K, Matsui K;

Pollinosis-associated gene 419 undergoing significantly low expression in subjects with high cedar pollen-specific IgE levels, useful in diagnosis of allergic diseases and screening drug candidates.

Example 6; Page 50; 77pp; Japanese.

The invention relates to the human pollinosis-associated gene 419 which exhibits reduced expression in the T-cells of individuals with high cedar pollen specific IgB (immunoglobulin E) levels. The gene was isolated from collen expecific IgB (immunoglobulin E) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen using the differential display method. Pollinosis-associated gene 419 has homology with the gene encoding human Pas-associated Gactor-1 (PAR-1). The invention also relates to the protein encoded by pollinosis gene 419; expression crelates to the protein encoded by pollinosis gene 419; primers and probes; antibodies against the protein encoded by the gene; method of detection of pollinosis-associated gene 419 pucleic acids; and a method of diagnosis of allergic diseases via the detection of pollinosis-associated gene 419 in the intended of sereening drug candidates for the treatment of allergic methods of screening drug candidates for the treatment of allergic compound relative to a control.Pollinosis-associated gene 419 is useful in the screening of drug candidates control diseases and in the screening of drug candidates (for the treatment of such diseases). The presente requence represents a PCR primer used in the isolation of human pollinosis-associated gene 419 cDNA

Seguence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

.. 0 Score 16; DB 1; Length 17; Pred. No. 4.6e+02; 0; Indels 100.0%; Bred. No. Local Similarity 100. es 16; Conservative Query Match Matches

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RESULT 861 AAC64173

AAC64173 Standard; DNA; 17

BP

AAC64173;

(first entry)

21-FEB-2001

PCR anchor primer, SEQ ID NO:4, used in human gene 513 isolation.

Human, pollinosis-associated gene 513; IgE; immunoglobulin E; cedar pollen allergy; T-cell; reduced expression; detection; diagnosis; drug screening; allergic disease; PCR primer; ss. 

Synthetic

WO200065049-A1

32-NOV-2000.

26-APR-2000; 2000WO-JP002733.

99JP-00120491. 27-APR-1999;

(GENO-) GENOX RES INC

expression in in diagnosis

Example 6; Page 40; 69pp; Japanese.

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Gunji

Obayashi M,

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The invention relates to the human pollinosis-associated gene 513 which exhibits significantly reduced expression in the T-cells of individuals with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen using the differential display method. The invention also relates to methods of detection of pollinosis-associated gene 513 nucleic acids; a method of diagnosis of allergic diseases via the detection of pollinosis-associated composit of allergic diseases via the detection of pollinosis-associated creatment of allergic diseases by measuring the expression of pollinosis for the treatment of allergic disease by measuring the expression of pollinosis associated gene 513 in pollen antigen-stimulated T-cells in the presence of a useful in the diagnosis of allergic diseases and in the screening of drug candidates for the treatment of such diseases and in the screening of crepresents as PCR primer used in the isolation of human pollinosis-
                                                                                                                  Pollinosis-associated gene 513 undergoing significantly low subjects with high cedar pollen-specific IgE levels, useful of allergic diseases and screening drug candidates.
Kashiwabara T, Oshida T, Obay
Yoshida N, Ogawa K, Matsui K;
                                                                                                                                                                                                                            Example 6; Page 39; 46pp; Japanese.
Sugita Y,
Imai Y,
                     Obayashi I,
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Length 17; 0; Indels Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other; 0.9%; Score 16; DB 1; Le 100.0%; Pred. No. 4.6e+02; iive 0; Mismatches 0; Best Local Similarity 100. Matches 16; Conservative Query Match

associated gene 513 cDNA

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AAC64163 standard; DNA; 17 BP AAC64163 RESULT 862 AAC64163, 

(first entry) 21-FEB-2001

PCR anchor primer, SEQ ID NO:4, used in human gene 581 isolation

Human; pollinosis-associated gene 581; IgE; immunoglobulin E; cedar pollen allergy; T-cell; reduced expression; detection; diagnosis; drug screening; allergic disease; PCR primer; ss.

Synthetic

WO200065048-A1.

02-NOV-2000

26-APR-2000; 2000WO-JP002732

99JP-00120492 27-APR-1999;

(GENO-) GENOX RES INC

Gunji S; Obayashi M, Kashiwabara T, Oshida T, Obay Yoshida N, Ogawa K, Matsui K; Nagasu T, Sugita Y, Obayashi I, Imai Y,

WPI; 2000-687341/67.

Pollenosia-associated gene 581 undergoing significantly low expression in subjects with high cedar pollen-specific IgE levels, useful in diagnosis of allergic diseases and screening drug candidates.

The invention relates to the human pollinosis-associated gene 581 which exhibits significantly reduced expression in the T-cells of individuals with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene can select a selection of the invention also relates also relates a solution and pollinosis associated gene 581; to expression constructs and host cells comprising pollinosis-associated gene 581 constructs and host cells comprising pollinosis-associated gene 581 constructs and host cells comprising pollinosis-associated gene 581 mucleic acids; pollinosis-associated gene 581 primers and probes; antibodies against the protein encoded by the gene; methods of dagenosis of allergic diseases via the detection of pollinosis-associated gene 581 mucleic acids. The invention additionally encompasses methods of dagnosis of allergic diseases via the treatment of allergic diseases by measuring the expression of pollinosis-associated gene 581 in pollen antigen stimulated T-cells in the presence of a test compound relative to contice and in the screening of drug candidates for the Treatment of allergic diseases and in the screening of drug candidates for the Treatment of such diseases. The present sequence represents a PCR primer used in the isolation of human pollinosis-associated gene 581 cDNA 

Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Gapa ö 0.9%; Score 16; DB 1; Length 17; 100.0%; Pred. No. 4.6e+02; Indels 100.0%; Prec. ... 16; Conservative Local Similarity Query Match Matches

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1735 CAAAAAAAAAAAAA 1750 17 CAAAAAAAAAAAAAA

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Gaps

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RESULT 863 AAC64215/c

BP AAC64215 standard; DNA; 17 

(first entry)

21-FEB-2001

PCR anchor primer, SEQ ID NO:4, used in human gene 627 isolation

diagnosis; Human, pollinosis-associated gene 627; IgE; immunoglobulin E; cedar pollen allergy; T-cell; reduced expression; detection; drug screening; allergic disease; PCR primer; ss.

Synthetic.

NO200065051-A1

26-APR-2000; 2000WO-JP002735

27-APR-1999;

(GENO-) GENOX RES INC.

Gunji S; Obayashi M, Oshida T, Obay wa K, Matsui K; T, Oshida Ogawa K, Kashiwabara Yoshida N, Sugita Y, , Imai Y, Obayashi I, H Nagasu

WPI; 2000-687344/67.

Pollinosis-associated gene 627 undergoing significantly low expression in subjects with high cedar pollen-specific IgE levels, useful in diagnosis of allergic diseases and screening drug candidates.

Example 6; Page 42; 51pp; Japanese.

The invention relates to the human pollinosis-associated gene 627 which exhibits significantly reduced expression in the T-cells of individuals with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene

(GENO-) GENOX RES INC. (EISA ) EISAI CO LTD. WPI; 2000-687343/67. WO200065050-A1. 27-APR-1999; Nagasu T, Su Obayashi I, 21-FEB-2001 02-NOV-2000 Synthetic. AAC64232; Query Match Yokoi A; Matches AAC64232/C
AAC64232/C
AAC64232/C
AAC64232/C
AAC6A232/C
AAC6A22/C
AAC6A232/C
A ઠે g

ö was isolated from T-cells from individuals allergic to cedar pollen using the differential display method. The invention also relates to methods of detection of pollinosis-associated gene 627 nucleic acids; a method of treatment of allergic diseases via the detection of pollinosis-associated gene 627 nucleic acids; and a method of screening drug candidates for the treatment of allergic disease by measuring the expression of pollinosis-associated gene 627 in pollen antigen-stimulated T-cells in the presence of a test compound relative to a control. Pollinosis-associated gene 627 in gradidates for the treatment of such diseases and in the screening of drug candidates for the treatment of such diseases. The present sequence represents a PCR primer used in the isolation of human pollinosis-Gaps PCR anchor primer, SEQ ID NO:4, used in human gene 795 isolation .. 0.9%; Score 16; DB 1; Length 17; 100.0%; Pred. No. 4.6e+02; ive 0; Mismatches 0; Indels Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other; 1735 CAAAAAAAAAAAAA 1750 17 CAAAAAAAAAAAA 2 AAC64232 standard; DNA; 17 (first entry) Local Similarity 100. nes 16; Conservative

88. Human; pollinosis-associated gene 795; vimentin homologue; 1gE; immunoglobulin E; cedar pollen allergy; T-cell; reduced expression; detection; diagnosis; drug screening; allergic disease; PCR primer;

26-APR-2000; 2000WO-JP002734.

99JP-00120494

Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji , Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;

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Pollinosis-associated gene 795 undergoing significantly low expression in subjects with high cedar pollen-specific IgE levels, useful in diagnosis of allergic diseases and screening drug candidates.

Page 46; Example 6; 73pp; Japanese.

exhibits significantly reduced expression in the T-cells of individuals with high cedar pollen-specific IgE (immunoglobulin B) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen using the differential display method. Pollinosis-associated gene 795 has homology with the human vimentin gene. The invention also relates also relates to the protein encoded by pollinosis gene 795; to expression constructs and host cells comprising pollinosis-associated gene 795 nucleic acids; pollinosis-associated gene 795 nucleic acids; pollinosis-associated gene 795 armers and probes; antibodies against the protein encoded by the gene; methods of detection The invention relates to the human pollinosis-associated gene 795 which

The present invention describes the human pollinosis-associated gene 465 which has a nucleic acid sequence of 3442 base pairs (bp), given in (AAC92291), that undergoes significantly low expression in subjects after pollen scattering, and is useful in the diagnosis of allergic diseases and screening candidate compounds for remedies capable of regulating the response of T cells to the stimulus by an antigen. The gene is useful in the diagnosis of allergic diseases and screening candidate compounds for remedies capable of regulating the response of T cells to the stimulus by an antigen. The present sequence represents a PCR primer which is used in an example from the present invention

Example 6; Page 44; 61pp; Japanese.

Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

ö of pollinosis-associated gene 795 nucleic acids, and a method of diagnosis of allergic diseases via the detection of pollinosis-associated gene 795 nucleic acids. The invention additionally encompasses methods of screening drug candidates for the treatment of allergic disease by measuring the expression of pollinosis-associated gene 795 in pollen antigen-stimulated T-cells in the presence of a test compound relative to a control. Pollinosis-associated gene 795 is useful in the diagnosis of allergic diseases and in the screening of drug candidates for the treatment of such diseases. The present sequence represents a PCR primer used in the isolation of human pollinosis-associated gene 795 cDNA Pollinosis-associated gene 465 undergoing significantly low expression in subjects after Pollen scattering, useful in diagnosis of allergic diseases and screening candidate compounds to regulate response of T cells to antigen stimulus. Gaps Human pollinosis-associated gene 465 related PCR primer SEQ ID NO:4. Gunji Kashiwabara T, Oshida T, Obayashi M, Gunji Yoshida N, Ogawa K, Matsui K, Takahashi E; Human; pollinosis-associated gene 465; pollen scattering; allergy; ö Length 17; 0; Indels Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other; Score 16; DB 1; Lo Pred. No. 4.6e+02; Mismatches 0.9%; Scc... 100.0%; Pred 0; M allergic disease; PCR primer; ss 1735 CAAAAAAAAAAAAA 1750 BP 18-MAY-2000; 2000WO-JP003191. 27-MAY-1999; 99JP-00148784. 17 CAAAAAAAAAAAAA 2 AAC92294/c ID AAC92294 standard; DNA; 17 (first entry) Query Match 0.9 Best Local Similarity 100. Matches 16; Conservative (GENO-) GENOX RES INC (EISA ) EISAI CO LTD. Sugita Y, , Imai Y, WPI; 2001-061528/07. WO200073439-A1. Homo sapiens 22-MAR-2001 07-DEC-2000. AAC92294; Nagasu T, Obayashi Yokoi A; RESULT 865 8888888888888 g ò

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to the human pollinosis-associated gene 787 which exhibits significantly reduced expression in the T-cells of individuals after the pollen-scattering season, relative to expression levels in T-cells before the pollen-scattering season. The gene was isolated from T-cells before the pollen-scattering season. The gene was isolated from T-cells from individuals allergic to pollen using the differential display method. The invention also relates to pollinosis-associated gene 787 prucleic acids; and amethod of diagnosis of allergic diseases via the detection of pollinosis-associated gene 787 nucleic acids. The invention additionally encompasses a method of screening drug candidates for the treatment of allergic disease by measuring the expression of pollinosis-associated gene 787 nucleic acids in the presence of a test compound relative to a control. Pollinosis-associated gene 787 in pollen antigen-stimulated T-cells in the presence of a test compound relative to a control. Pollinosis-associated gene 787 furg candidates for the treatment of such diseases. The present sequence represents a PCR primer used in the isolation of human pollinosis-
                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pollinosis-associated gene 787 undergoing significantly low expression in subjects after pollen scattering, useful in diagnosis of allergic diseases and screening candidate compounds to regulate response of T cells to antigen stimulus.
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kashiwabara T, Oshida T, Obayashi M, Gunji
Yoshida N, Ogawa K, Matsui K, Takahashi E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR anchor primer, SEQ ID NO:4, used in human gene 787 isolation.
                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; pollinosis-associated gene 787; pollen allergy; T-cell; reduced expression; detection; diagnosis; drug screening; allergic disease; PCR primer; ss.
Length 17;
                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
  DB 1; Le . 4.6e+02;
                      ilarity 100.0%; Pred. No. 4.6
Conservative 0; Mismatches
  Score 16;
Pred. No.
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                                                                                                      1735 CAAAAAAAAAAAA 1750
                                                                                                                                                                                                                                                                                      AAC91721 standard; DNA; 17 BP
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0.9%;
                                                                                                                                                    CAAAAAAAAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                               27-MAR-2001 (first entry)
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, Imai Y,
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-DEC-2000
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AAC91721/C
AAC91721/C
AAC91721/C
AAC91721/C
AAC9172-MAR
XX
DT 27-MAR
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AAC91721/C
DT 27-MAR
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A 116-FG
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A 116-FG
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A AC917
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A 116-FG
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A A GENO-PR
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A CGENO-PR
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This invention describes a novel nucleic acid molecule comprising a sequence (I) which undergoes significantly low expression in subjects after pollen scattering, and is useful in disgnosis of allergic diseases and screening candidate compounds for remedies capable of regulating the response of T cells to the stimulus by an antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis; human; PCR primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pollinosis-associated gene 441 which undergoes lower expression in subjects after pollen scattering, useful in diagnosis of allergic diseases and screening candidate compounds to regulate response of T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                    Pollinosis; pollinosis-associated gene 441; allergy; T cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.9%; Score 16; DB 1; Length 17; 00.0%; Pred. No. 4.6e+02;
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Yoshida N, Ogawa K, Matsui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                        Human pollinosis-associated gene 441 primer #3.
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Local Similarity 100.0%; Pred. No. 4.º
                                                                                                                                                                                                                                                                                                                                                                             pollen scattering; antigen; primer; ss.
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1735 CAAAAAAAAAAAAA 1750
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                                         17 CAAAAAAAAAAAA 2
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                                                                                                                                                                                                                                                       20-MAR-2001 (first entry)
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, Imai Y,
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0.9%; Score 16; DB 1; Length 17; 100.0%; Pred. No. 4.6e+02;

100.0%; Pred. ...

Conservative

Local Similarity nes 16; Conserv

Best Loca Matches

Query Match

Homo sapiens.

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The invention provides a method of diagnosis of allergies that involves: assaying the levels of expression of genes B1001, B1466, B1072 or B1151 in T-cells; and comparing them with the level of expression in healthy T-cells. The method is useful for diagnosing allergies, particularly atopic dermatitis. The present sequence represents a PCR primer used for analysis of the expression of the above genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identification of transcribed gene; mRNA profile; gene expression; cellular process; fingerprinting; susceptibility to external factor; development; disease; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5'-PCR primer used to produce single pattern characteristic by FokI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diagnosis of allergies including atopic dermatitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Obayashi I, Matsui K,
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(NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 6; Page 66; 83pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1735 CAAAAAAAAAAAAAA 1750
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                                                                                                                                                                                                                                                                  02-MAR-2000; 2000JP-00061832.
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21-JUL-2000; 2000US-0219925P.
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ABK13941 standard; DNA; 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                Nagasu T, Oshida T,
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                                                                 WO200165259-A1.
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                                                                                                                                  07-SEP-2001
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                                                                The present invention relates to a method for providing a profile of mRNA molecules present in a sample. The method comprises generating two independent patterns characteristic of the population of mRNA molecules expressed in the sample and analysing the patterns using a combinatorial algorithm, comparing gene expression by different or same cell types under different conditions, and identifying genes having a role in identification of transcribed genes, and fingerprinting. The method can be used to identify genes which play a role in determining various cellular processes, including susceptibility to external factors, development, and disease. The present esquence for a PCR primer is used in the production of a single pattern characteristic of a sample, employing a Type IIS restriction enzyme (i.e. FoXI) in the methods of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 stage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, 88; PCR; acetyltransferase, 20-90-05; allergic disease, primer, differential display; eosinophil; antiallergic; atopic dermatitis; GT15G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Examining allergic diseases by differential display of gene showing different expression particularly increased expression in remission in eosinophils of patients, also applicable in screening candidate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tsujimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Acetyltransferase-like protein 20-90-05 PCR primer GT15G.
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100.0%; Pred. No. 4.6e+02;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                        Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENO-) GENOX RES INC.
(NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
(RISA ) EISAI CO LTD.
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                                   Disclosure; Fig 2; 67pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                              16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                        present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sugita Y,
Takahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK49636;
                                                                                                                                                                                                                                                                                                                                                                           Query Match
genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 870
ABK49636/c
                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Gaps

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candidate compounds which that in the eosinophils of a healthy individual

(i.e. differential display). Also included are methods of screening for
candidate compounds which affect the expression level of the gene or the
activity of the protein encoded by the gene (including related proteins
and mutants), the use of probes based on the gene sequence in the
examination of allergic diseases, the use of reporter constructs in the
controlling region of the gene, cells transformed with the vector, an
controlling region of the gene, cells transformed with the vector, an
intendity against the protein and a model animal for allergic diseases
which is a transgenic non-human vertebrate with lowering of expression
intensity of the gene in eosinophils. The method is examining allergic
diseases particularly atopic dermatitis which is also applicable in
screening candidate compounds for remedies. Such method can be performed
in high throughput, at low cost. The present sequence is a differential
display PCR primer for the cDNA encoding the human acetyltransferase-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The specification describes a method for examining allergosis. The method comprises measuring the expression level of the gene given in ABL59037, and comparing it with the expression level of the gene in the eosinophils of a healthy person. The method is used for the examination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence represents a PCR primer, which is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.9%; Score 16; DB 1; Length 17;
100.0%; Pred. No. 4.6e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; allergosis; eosinophil; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleotide sequence of PCR primer GT15G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENO-) GENOX SOYAKU KENKYUSHO KK.
(KOKU-) KOKURITSU SHONI BYOIN INCHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 17; 20pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of a healthy person. The methoc
allergosis. The present sequend
in the course of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1735 CAAAAAAAAAAAAA 1750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAAAAAAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABLS9040 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.99
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-439993/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein 20-90-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Method for examining allergic diseases by differential display of seventeen genes showing different expression particularly significant increase in eosinophils in patients with mild atopic dermatitis, also applicable in screening compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human B1153 expression in allergic disease related PCR primer GT15G.
                                                                                                                                Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .9%; Score 16; DB 1; Length 17;
0.0%; Pred. No. 4.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                    Human allergic disease related PCR primer SEQ ID NO: 20.
                                                                                                                                                                                                                                                                                                                                                                            Nagasu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                            Obayashi M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                GENOX RES INC.
JAPAN GEN NAT CHILDREN'S HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sxample 1; Page 110; 165pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                            Ogawa K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1735 CAAAAAAAAAAAAA 1750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BB
            ABN99831 standard; DNA; 17 BP
                                                                                                                                                                                                                                                                      28-SEP-2001; 2001WO-JP008574.
                                                                                                                                                                                                                                                                                                  13-OCT-2000; 2000JP-00314093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAAAAAAAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAL49950 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                      15-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16; Conservative
                                                                                                                                                                                                                                                                                                                                                                            Sugita Y, Hashida R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          VPI; 2002-372311/40.
                                                                                                                                                                                                            WO200233069-A1.
                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                       25-APR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-DEC-2002
                                                                                                                                                   primer; 88.
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                                          ABN99831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    873
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ABN99831
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0.9%; Score 16; DB 1; Length 17; 100.0%; Pred. No. 4.6e+02; ive 0; Mismatches 0; Indels

16; Conservative

Best Local Similarity

Query Match Matches

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the invention
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                                                                                                                                                                                                                                                                                                                                                              15-JUL-2002
                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-APR-2002.
         Sugita Y,
Takahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sugita Y,
                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                            ABK49758;
                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                 ABK49758/
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                                                                                                                                                                                                                                                                           셤
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                                                                                                                                                                                                                                                         The present invention relates to a method of examining allergic diseases which comprises comparing the expression level of gene B1153 in allergy patients with the expression level in healthy subjects. The method is useful for the treatment, prevention, disagnosis and study of allergic diseases including atopic skin inflammation and aethma. The present sequence is a PCR primer described in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.
        Human; allergy; B1153; differential expression; antiallergic; asthma;
antiasthmatic; antiinflammatory; atopic skin inflammation; PCR; primer;
                                                                                                                                                                                                   Examination of allergic diseases comprises detecting gene B1153 over expressed in T cells of allergy patients for diagnosis treatment and investigation of atopic skin inflammation and asthma.
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                  Tsujimoto G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Allergic disease examination method related anchor primer SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Allergic disease, allergy; antiallergic; intersectin 2; eosinophil; atopic dermatitis; human; PCR; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                    Score 16; DB 1; Length 17; Pred. No. 4.6e+02;
                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                 Nagasu T,
                                                                                                                                                                                                                                                                                                                                  Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                 Sugita Y,
                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENO-) GENOX RES INC.
(NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
(EISA ) EISAI CO LTD.
                                                                                                                                               (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
                                                                                                                                                                                                                                        Example 6; Page 82; 102pp; Japanese.
                                                                                                                                                                 Oshida T,
                                                                                                                                                                                                                                                                                                                                          Query Match 0.9%; Sco
Best Local Similarity 100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                         1735 CAAAAAAAAAAAAA 1750
                                                                                                  21-DEC-2001; 2001WO-JP011286
                                                                                                                    21-DEC-2000; 2000JP-00389476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-OCT-2000; 2000JP-00314093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                 Matsumoto Y, Imai Y,
                                                                                                                                      (GENO-) GENOX RES INC
                                                                                                                                                                                   WPI; 2002-713252/77.
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                                                             WO200250269-A1
                                            Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                27-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-AUG-2002
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                                                                                                                                                                                                                                                                                                                 invention
                                                                                                                                                                                                                                                                                                                                                                                                          11
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The present invention relates to a method for examining allergic diseases with intersectin 2 as an indicator gene, which comprises determining the expression level of the gene in the cosinophils in a patient, and comparing the expression level with that in the cosinophils of a healthy individual. The method is for examining allergic diseases, particularly atopic dermatitis, which is also applicable in screening candidate compounds for remedies. The present sequence is an anchor primer described in the exemplification of
                                                                                                                                                       Method for examining allergic diseases by differential display of intersectin 2 gene showing different expression particularly significant increase in eosinophils in patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Atopic dermatitis; ss; differential display; primer; PCR; eosinophil; allergic disease; antiallergic; dermatological; GT15g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to gene sequences that are differentially expressed in eosinophils from patients with atopic dermatitis in the increment stage as compared with those in the remission stage. These sequences are used in a novel method for examining allergic diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genes showing
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Saito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.9%; Score 16; DB 1; Length 17;
100.0%; Pred. No. 4.6e+02;
tive 0; Mismatches 0; Indels
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Nagasu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human atopic dermatitis cDNA related PCR primer GT15g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nagasu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ļ
Obayashi M,
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INIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
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                                                                                                                                                                                                                                                                                          Example 1; Page 53; 90pp; Japanese.
Ogawa K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ogawa K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1735 CAAAAAAAAAAAAA 1750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 CAAAAAAAAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
Hashida R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hashida R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                          WPI; 2002-372313/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-330097/36.
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vaccines. The present sequence was used to illustrate the invention

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The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ2, MDZ3 is concoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2, MDZ7 is encoded at chromosome 16p21.2 and MDZ12 is encoded at chromosome 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy, or in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic acids and proteins are also useful for disquosing or monitoring a disease caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic acids can also be used as probes to detect and characterize gross acids can also be used as probes to detect and characterize gross useful in constructing microarrays for measuring gene expression. The probes are useful as therapeutic agents for gene therapy or as
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comprising determining the expression levels of these genes and comparing the expression level with that in the eosinophils of a healthy individual. The method of the invention may have antiallergic of dermatclogical activities. The method can be used to diagnose allergic diseases particularly atopic dermatitis, and may also be used to screen candidate compounds for remedies. The method of the invention can be performed in high throughput, at low cost. The present sequence represents the GTLSg PCR primer used to amplify the differentially amplified atopic dermatitis related cDNA sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytostatic; immunostimulant; gene therapy; vaccine; human; zinc finger protein; MDZ3; MDZ4; MDZ12; chromosome 7q22.1; chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer; developmental disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New zinc finger-containing proteins and nucleic acids, useful in
manufacturing a medicament for treating or preventing a disorder
associated with decreased or increased expression or activity of MDZ3,
MDZ4, MDZ7 or MDZ12, e.g. cancer.
                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                 0.9%; Score 16; DB 1; Length 17; 100.0%; Pred. No. 4.6e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                        Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human MDZ7 scanning oligonucleotide SEQ ID 5259.
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                                                                                                                                                                                                                                                                                                                                                                                                  CAAAAAAAAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADB04273 standard; DNA; 17
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Matches 16, Conservative
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ADB04273/c
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proteins and their coding sequences: MD23, MD21, MD212. MD23 is encoded at chromosome 7q22.1, MD24 is encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2, mD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy, or in manufacturing a medicament for treating or preventing a disorder cor in manufacturing a medicament for treating or preventing a disorder. Cor in manufacturing a medicament of expression or activity of MD23, MD24, MD27, or MD212, monitoring a disease caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic acids and proteins are also useful for disquosing or monitoring a disease caused by altered expression of MD23, MD24, MD27, or MD212 genetic locus. The probes are also be used as probes to detect and characterize gross alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are useful in constructing microarrays for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as
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                                                                                                                                                                                                                                                                                                                                                                                                                               Cytostatic; immunostimulant; gene therapy; vaccine; human; zinc finger protein; MDZ3; MDZ4; MDZ12; chromosome 7q22.1; chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer; developmental disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7 or MDZ12, e.g. cancer.
                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the present invention relates to novel human zinc finger-containing
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                                                                  0.9%; Score 16; DB 1; Length 17;
100.0%; Pred. No. 4.6e+02;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 4.6e+02;
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                                 Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                Human MDZ7 scanning oligonucleotide SEQ ID 5257.
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                                                                                                                                                                                                                                                                               ADB04271 standard; DNA; 17 BP
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                                                                 Ouery Match
Best Local Similarity 100.C
Matches 16; Conservative
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Matches 16; Conserva
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The invention relates to determining the presence of and/or identifying a polyadenylation site within a sequence of a transcribed gene or variants present in a sample. The method involves assigning to gene fragments gene candidates within a database by comparing signals in the dataset with the database, the database comprising data representing mRNAs with known colyA sites and/or 'vitutal genes' representing a possible party and/or 'vitutal genes' representing a possible colyA sites and/or vitutal genes' representing a possible colyAdenylation site within an actual gene. The method is useful for determining the presence of and/or identifying a polyadenylation site or sequences of transcribed gene variants present or potentially present or sequence sequence variants that occur in a population of differences between sequence variants that occur in a population of ancleic acid molecules, especially in identifying or discovering polyA site usage or determining polyA site usage in a nucleic acid sample, and gene variants from a first present sequence contributed to the present sequence ariants from a first present sequence contributed to the present c
                                                                                                                                                                                                                                                                                 Determining polyadenylation sites within transcribed gene sequences present in a sample comprises assigning to gene fragments gene candidates within a database by comparing signals in the dataset with the database.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 17;
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                                                                                                                                                                                                   Ernfors P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        represents a double stranded product DNA fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 16; DB 1; Le
Pred. No. 4.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                              Lonnerberg P, Oldin M, Linnarsson S,
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100.0%; Pred
0; M
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                                                                  28-JAN-2003; 2003WO-IB000255.
                                                                                                            29-JAN-2002; 2002US-0352245P
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ID ACF36370 standard; DNA; 17
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es 16; Conserv
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                      07-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid encoding oxalate decarboxylase from Aspergillus phoenices, for degrading oxalic acid, identifying transformed plant cells, and preventing pathogenic disease in plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of a primer used in the invention. The invention relates to a novel nucleic acid (see ABZ70560) encoding Aspergillus phoenices oxalate decarboxylase (APOXD) (see ABP72475). The gene and its encoded protein are useful in degrading oxalate, in diagnostic assays, for protecting plants against disease, and as a
                                                                                                                                                                                                                                                                                                                                 Aspergillus phoenices; oxalate decarboxylase; APOXD; transgenic plant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.9%; Score 16; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 4.6e+02; Matches 16; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PION-) PIONEER HI-BRED INT INC.
AAAAAAAAAAAAAA 1751
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                                                                                                26-JUN-2001; 2001CA-02350328.
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                         04-DEC-2003 (first entry)
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Synthetic

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ACF36345;

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New naturally derived DNA specifically expressed during blastogenesis of a plant, useful for producing a transformed plant and for compulsive expression of a protein.
                                                                                                                                                                  The invention relates to producing a population of double-stranded product DNA molecules comprising amplification by a nested PCK method. The method is useful in profiling mRNA transcribed in a system under investigation. The oligonuclectides are used as size standards in electrophoresis, and as internal controls allowing for calculation of relative amounts of material present. The present sequence represents adouble stranded product DNA, which aids in outlining an approach to production of a single pattern characteristic of a sample, employing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               during plant blastogenesis. The DNA of the invention is useful for producing a transformed plant. Methods of the invention are also useful for compulsive expression of this DNA. Methods of the invention are useful for plant tissue specific expression of genes. Also, the growth stage of a plant can be controlled specifically. The current sequence represents a PCR primer for amplifying a plant blastogenesis specific gene of the invention.
                                                                  Producing a population of double-stranded product DNA molecules, useful for mRNA profiling, comprises amplification by nested polymerase chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR primer for amplifying plant blastogenesis specific gene #SEQ ID 3.
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PCR; primer; ss.
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Pred. No. 4.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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100.0%; Pred
                                                                                                                                                                                                                                                                                                             type II restriction enzyme (FokI)
                                                                                                                                     Example; Fig 2; 105pp; English
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hes 16; Conservative
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                              WPI; 2003-618365/58
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Montelius A;
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                                                                                                   reaction
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ADC84470/c
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Gaps ..

Length 17;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel apoptosis-related DNAs and proteins - for diagnosis, preventing treating diseases associated with apoptosis.
                                                   Gapa
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                      0.9%; Score 16; DB 1; Length 17; 100.0%; Pred. No. 4.6e+02; tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 4.8e+02;
tive 0; Mismatches 0; Indels
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Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                  Nucleotide sequence PCR primer 11
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                                                                                                    17 CAAAAAAAAAAAA 2
                                                                                                                                                                     AAV54174 standard; cDNA; 18
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nes 16; Conservative
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                                                                                                                                                                                                                                                                                                                 Synthetic.
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                         Query Match
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                                                    Matches
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Example 1; Page 49; 70pp; Japanese.
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ID AAZ90641 standard; DNA; 18 BP.
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Best Local Similarity 100.0
Matches 16; Conservative
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Best Local Similarity 100.
Matches 16; Conservative
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AAZ90650/c
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PCR; primer; amplification; apoptosis; antibody; inhibition; ss; immunohistological staining.
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Matches 16; Conservative
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AAV54171/6
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This is the nucleotide sequence of a PCR primer used in the method of the invention, involving the use of novel apoptosis-related DNAs and proteins. The inventions can be used as diagnostic reagents for apoptosis p.g. (monoclonal) antibodies for the protein, as a reagent in immunohistological staining, as a apoptosis inhibitors. It can also be used for treatment of apoptosis-related diseases
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Pred. No. 4.8e+02;
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Pred. No. 4.8e+02;
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The present invention describes a method of producing binary sequence tags from nucleic acid fragments in a sample, involving incubating the sample with cleaving reagents, mixing offest adaptors with the sample, incubating with more cleaving reagents and mixing the sample with adaptors are coupled to binary sequence tags. The method is useful in sequence analysis, including analysis and comparison
                                                                                                                         The invention relates to identification of genes and proteins of adipose tissue relating to obesity, particularly complications of visceral obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis, hyperunicemia and aleep apnea syndrome. The genes (AAZ9061-633) and the proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention and treatment of adipose tissue related diseases. Sequences AAZ90640-51 represent PCR primers amplifying the human adipose tissue genes
                                        A physiologically active protein specifically derived from mammal tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Producing binary sequence tags, useful for analyzing nucleic acid sequence tags, gene expression or gene-expression patterns, involves generating nucleic acid fragments, which are mixed with offset adaptors
                                                                                                                                                                                                                                                                                                                                           / Match 0.9%; Score 16; DB 1; Length 18; Local Similarity 100.0%; Pred. No. 4.8e+02; nes 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Binary encoded sequence tag; BEST; nucleic acid analysis; gene expression; adaptor; PCR primer; 8s.
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                                                                                                                                                                                                                                                                                                       Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 101; 101pp; English.
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                                                                                     Example 2; Page 18; 50pp; Japanese.
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06-APR-2000; 2000US-00544713.
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WPI; 2000-306578/27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to identification of genes and proteins of adipose tissue relating to obesity, particularly complications of visceral obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes (AAZ9661-633) and the proteins (AAV67589-V67600) are used in the genetic diagnosis, prevention and treatment of adipose tissue related diseases. Sequences AAZ90640-51 represent PCR primers amplifying the human adipose tissue genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A physiologically active protein specifically derived from mammal tissue.
                                                                                                                                                                      Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human; arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
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100.0%; Pred. No. 4.8e+02;
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                                                                                                                                duman adipose tissue gene amplifying primer #11
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Matches 16; Conservative 0; Mismatches
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  AAZ90650 standard; DNA; 18
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                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NISB ) JAPAN TOBACCO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NISB ) JAPAN TOBACCO INC
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The present invention relates to a new method for identifying compounds for treating and/or preventing cytomegalovirus (CWV) infection and/or related diseases. The method of the invention comprises contacting a test compound with at least nee of the cellular kinases RICK, RIP, Nck-Interacting kinase, MKK3 and SRRK-2 and detecting any change in kinase activity. The method of the invention can be used to treat and/or prevent CWV infections and related diseases. Oligomucleotides that can detect the specified kinases can also be used for diagnosis of infection. The spreamt nucleic acid sequence represents human CMV reverse transcriptase (RT)-PCR primer TXN that was used in the methods of the invention for preparation of radioactively labelled cDNA probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying agents for treatment or prevention of cytomegalovirus infection, comprises contacting test compound with cellular kinase and detecting change in cellular kinase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cytomegalovirus; HCMV; virucide; cytomegalovirus infection; CMV; cellular kinase; RICK; RIP; Nck-Interacting kinase; MKX3; SRPK-2; reverse transcriptase PCR; RT-PCR; primer; ss.
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                   Pred. No. 4.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                         Human cytomegalovirus (HCMV) RT-PCR primer TXN.
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                                        Mismatches
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100.0%; FIN
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                                                                                                                                 16 AAAAAAAAAAAAA 1
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/label= n
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                                        16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cytomegalovirus
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                Best Local Similarity
Matches 16; Conserv
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The invention relates to novel pyridylpyrimidine derivatives and methods of detecting prion infections and/or prion disease in an individual or in cells. Cells. Cells. Cells involves adding at least one monoclonal or polyclonal antibody, oligonucleotide or pyridylpyrimidine derivative to the sample or in cells, cell cultures and/or pyrimidine derivative to the sample or in cells, cell cultures and/or cell lysates and detecting the activity of at least one human cellular protein kinases (e.g., FGF-RI (also known as flg, Fl-1, Fl-2, b-FGFR), Tk (also known as CCK-2, DDR-2 or EDDR, EC number 2.7.1.112), Abl (also known as CCK-1), PRK), human cellular protein phosphatases such as FTP-SL (Also known as CDK1), PRK), human cellular protein phosphatases such as FTP-SL (Also known as GDK1), PRK), human cellular signal transduction of prions in cells and in the manufacture of pharmaceutical composition for prophylaxis and/or treatment of infectious disease (e.g. Scrapie, chronic wasting disease (CWD), transmissible mink encephalopathy (IMR), or neurodegenerative disease (CWD), bovine spongiform encephalopathy (BSE), variant CJD, Gerstmann-Straussler-Scheinker syndrome (GSS), fatal familial insomnia (FFI), Kuru and Alpers syndrome, especially BSE, CJD, or reuuchdegenerative diseases (e.g., Alzheimer's disease) in humans or ruminants. The present DNA sequence is a primer used to prepare correspondence is a primer used to prepare in the exemplification of the invention
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                                                                                                                                                                                          Human, pyridylpyrimidine derivative, cellular protein kinase, Scrapie, cellular protein phosphatase, cellular signal transduction; prophylaxis; prion infection; chronic wasting disease; CWD; Creutzfeldt-Jacob disease; CUD; transmissible mink encephalopathy; bovine spongiform encephalopathy; TME; BSE; Gerstmann-Straussler-Scheinker syndrome; GSS; Alpers syndrome; fatal familial insomnia; FFI; kuru; neurodegenerative disease; nootropic; Alzheimer's disease; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New pyridylpyrimidine derivatives useful in the treatment or prevention of infectious disease e.g. Kuru syndrome and Creutzfeld-Jacob disease
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                                                                                                                                                     Primer used to prepare radioactively labelled cDNA probes from RNA.
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100.0%; Pred. No. 4.8e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stein-Gerlach M, Salassidis K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAY-2001; 2001EP-00111858.
29-MAY-2001; 2001US-029528P.
13-JUL-2001; 2001US-00117113.
18-JUL-2001; 2001US-0305899P.
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                  AAD52799 standard; DNA; 18
                                                                                                       (first entry)
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Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                         14-MAY-2003
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AAD52799
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0.9%; Score 16; DB 1; Length 18; 100.0%; Pred. No. 4.8e+02; ive 0; Mismatches 0; Indels

1736 AAAAAAAAAAAAA 1751

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16; Conservative

Local Similarity

Query Match Best Loca Matches 16 AAAAAAAAAAAA 1

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The present invention describes a compound (I) of 8 - 50 nucleotides targeted to a nucleic acid molecule (II) encoding tumour necrosis factor (TNF) inducible protein, A20, and which specifically hybridises with and inhibits expression of A20, or a compound (Ia) of 8 - 50 nucleotides with and inhibits expression of A20, or a compound (Ia) of 8 - 50 nucleotides with and huck and antiviral activities. (I) can be used as inhibitors of TNF inducible protein, A20. (I) is useful for inhibiting the expression of A20 in cells or tissues, and for treating an animal having a disease condition associated with A20, e.g. a inflammatory disorder, viral infection and hyperproliferative disorder e.g. cancer. (I) is also useful prophylactically, e.g. to prevent or delay infection, inflammation or tumour formation. (I) is also useful as therapeutic, diagnostic and research reagent, for cuseful as therapeutic, diagnostic and research reagent, for consecution of various members of a biological pathway, and in antisense gene therapy. The present sequence represents an antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense compound useful for preventing or delaying infection, inflammation or tumor formation, hybridizes and inhibits a nucleic acid molecule encoding tumor necrosis factor inducible protein, A20.
                                                                                                                                                                             Human; tumour necrosis factor inducible protein A20; phosphorothioate; antisense modulation; antisense oligonucleotide; antiinflammatory; cytostatic; antiviral; gene therapy; TNF inducible protein A20; inflammatory disorder; viral infection; hyperproliferative disorder; cancer; inflammation; tumour formation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                 /mod_base= OTHER
/note= "2'-methoxyethyl (MOE) nucleotide wings and a
deoxy gap with a phosphorothioate backbone"
                                                                                                                                             Human TNF inducible protein A20 antisense oligonucleotide SEQ ID:47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mod_base= OTHER
/note= "2'-O-methoxyethyl nucleotides"
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/mode= "2'-O-methoxyethyl nucleotides"
15. 20
/*tag= c
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                                    ABL51169 standard; DNA; 20 BP
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                                                                                                          27-JUN-2002 (first entry)
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modified_base
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                                                                                                                                                                                                                                                                                            Homo sapiens.
Synthetic.
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                                                                      ABL51169;
RESULT 891
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The invention relates to diagnosis of hepatitis B virus (HBV) infection stages comprising identification of full length HBV transcripts (I) and truncated HBV transcripts (II) in a serum sample, where the ratio of I:II is indicative of a particular infection stage. The method is useful for happrocation HBV infections atages and determining the risk for developing hepatocallular carcinoma. The present sequence is that of a HBV diagnostic PCR primer, useful for the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diagnosing hepatitis B virus (HBV) infection stages and determining the risk for hepatocellular carcinoma, comprises identifying full length HBV transcripts and truncated HBV transcripts in a serum sample.
                                                                                                                                                                                                                                                                                                                                                                   Hepatitis B virus; HBV; infection; hepatocellular carcinoma; diagnosis;
oligonucleotide for human TNF inducible protein A20, from the present
                                                                                                        Gape
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                                                                        0.9%; Score 16; DB 1; Length 20;
100.0%; Pred. No. 5.2e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                      Hepatitis B virus diagnostic PCR primer SEQ ID NO 5.
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                                          Sequence 20 BP; 6 A; 5 C; 3 G; 6 T; 0 U; 0 Other
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                                                                                                                                                                                                                                             ABA05915 standard; DNA; 20 BP
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                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                  PCR primer; ss.
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                   invention
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                                                                             Query Match
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ABA05915/
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AAD33499

Aguilar D;

Pabalan J,

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Disclosure; Page 14; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AGIL-) AGILENT TECHNOLOGIES INC.
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                                                                                                                                                                                                                                                                                                                                                                        .0-SEP-2001; 2001EP-00307665
                                                                                                                                                                                                                                                                                                                                                                                                                                11-SEP-2000; 2000US-00659173
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                                                                                                                                       Molecular array; probe; ss
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Best Local Similarity 100.0
Matches 16; Conservative
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                                                                                                                                                                                                                                                        EP1186673-A2.
                                                                                                                                                                                                Unidentified.
                             01-JUL-2002
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ABZ86271/C
ID ABZ862
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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation coodon, coding regaion, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an entilnflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of, or reducing sensitivity to adenosine, reducing levels of ung surfactant in a subject, for retaring bronchodilation, increasing levels of ung surfactant in a subject, or treating pronchonstriction, increasing levels of ung surfactant in a subject or treating bronchodilation, increasing levels of ung surfactant in a subject or treating pronchonstriction, increasing levels of ung surfactant in a subject or treating bronchonstriction, increasing levels of ungenty or treating surfactant in a subject or treating bronchonstriction, increasing levels of ungenty or treating surfactant in a subject or treating bronchonstriction, increasing levels of ungenty or dependenty or treating surfactant in a subject or treating surfactant in a subject or treating bronchonstriction, increasing levels of ungenty or treating surfactant in a subject or treating surfactant in a subject or treating bronchonstriction, increasing levels of condition.
                                                                                                                                                                                                                                                                                                                        Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 16; DB 1; Length 20;
Pred. No. 5.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                             Ä,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 15; SEQ ID NO 1513; 872pp; English.
                                                                                                                                                                             Katz
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                                                                                                                                                                          Li Y, Sandrasagra A, K
Tang L, Shahabuddin S;
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100.0%; Pred
0; N
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23-APR-2002; 2002WO-US013135.
                                                       24-APR-2001; 2001US-0286137P.
                                                                                                                  (EPIG-) EPIGENESIS PHARM INC.
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Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                     Miller S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method for calibrating data scanned from a molecular array. The method involves employing calibration probes that generate signals proportional to the total concentrations of labelled target molecules to which the molecular array probes are directed over an entire range of sample solutions and molecular arrays incorporating sets of calibration probes. Method is useful for calibrating different types of signals scanned from a molecular array, or calibrating signals scanned from a molecular array, or calibrating signals scanned from different molecular arrays. The present sequence is poly (A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Calibration of molecular array data by employing calibration probes that generate signals proportional to total concentrations of labeled target molecules, and molecular arrays incorporating sets of calibration probes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                T7T18Apad_PS27-20-0003 probe for calibration of molecular array data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from different molecular arrays. The present sequence is poly (, normalisation probe used in calibration of molecular array data
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Pred. No. 5.2e+02;
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100.0%; Pred. No. ...
... 0; Mismatches
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                     (first entry)
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Gaps

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0; Indels

98JP-00005399. 98JP-00005399,

14-JAN-1998;

14-JAN-1998;

(HITA ) HITACHI LTD

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Homo sapiens.
                                                        07-SEP-2001.
                                                               Fisher PB,
                                         AAH26601;
                                     RESULT 896
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nervous system Query Match Matches Analysis of DNA fragment - comprises addition of known common oligonucleotide, amplification of resultant DNA fragment and analysis and labelling of amplified DNA. which comprises: (i) addition of a known common oligonuclectide sequence to at least one terminal of each DNA fragment; (ii) amplification of the resultant DNA fragment as a primer using a first common primer containing a complementary nuclectide sequence to the above mentioned known common oligonuclectide sequence, a second common primer containing a complementary nucleotide sequence to the prepared known common oligonucleotide sequence optionally having been introduced with complementary nucleotide sequence at a terminal, and a specific primer capable of hybridisation with a DNA fragment containing whole or part of the amplified DNA to find the information of the DNA fragment; in which the specific primer is designed to prepare fragments of the common first and second primers and to give short fragment of the common first and second primers and to give short fragment of amplified DNA and (iv) labelling them to make their differentiation of informations of known and unknown genes readily provides information of whitnown gene and simultaneous monitoring of signals derived from minor genes. Furthermore, labelling of DNAs according to functions of known genes can be performed. AAZ09189-Z09201 represent oligonucleotide primers This invention descibes a novel method for the analysis of a DNA fragment used to illustrate the method of the invention Example 1; Page 12; 17pp; Japanese.

ö Gaps ö Length 21; 0; Indels Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 U; 0 Other; Score 16; DB 1; Le Pred. No. 5.4e+02; 0; Mismatches 0; 0.9%; Scc... 100.0%; Pre Query Match Best Local Similarity 100.0 Matches 16; Conservative

AAH26601 standard; DNA; 21 BP 12-NOV-2001 (first entry)

Mda-7 gene AP-1 and C/EBP binding site flanking sense PCR primer.

Melanoma differentiation associated gene-7; Mda-7; human; promoter; neuroblastoma; astrocytoma; glioblastoma multiforme; cervical cancer; breast cancer; colon cancer; prostate cancer; osteosarcoma; chondrosarcoma; tumour; therapy; PCR primer; electrophoretic mobility shift assay; EMSA; ss.

WO200164921-A1.

28-FEB-2001; 2001WO-US006782

29-FEB-2000; 2000US-00515369.

(UYCO ) UNIV COLUMBIA NEW YORK.

Madireddi MT;

WPI; 2001-565508/63.

Melanoma differentiation associated gene-7 promoter capable for treating cancer comprises directing transcription of heterologous coding sequence encoding tumor suppressor polypeptide positioned downstream, useful for Example 2; Page 70; 132pp; English

The present sequence is that of a sense primer flanking the region corresponding to the putative AP-1 and C/EBP binding sites present between Ndel and Nbel restriction enzyme sites in the human melanoma differentiation associated gene-7 (maa-7) promoter (see AAH26595). The sense primer and an antisense primer (see AAH26602) were used in the PCR amplification of this region of the promoter. The PCR product was used in a electrophoretic mobility shift assay (EMSA) which demonstrated that CUUN/AP-1 and C/EBP-beta transcription factors bind to defined sites within the mda-7 promoter during the process of terminal differentiation constructs in which the mda-7 promoter is operably linked to a coding sequence encoding a tumour suppressor protein. A pharmaceutical composition including the recombinant expression construct is used in a claimed method of treating melanoma, neuroblastoma astrocytoma, glioblastoma multiforme, cervical cancer, breast cancer, colon cancer, processe cancer, osteosarcoma, chondrosarcoma or a cancer of the central

Sequence 21 BP; 3 A; 3 C; 8 G; 7 T; 0 U; 0 Other;

Gape ö 0.9%; Score 16; DB 1; Length 21; 100.0%; Pred. No. 5.4e+02; ive 0; Mismatches 0; Indels 16; Conservative Local Similarity

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8 셤 RESULT 897 ABS97681

ABS97681 standard; DNA; 21 BP

ABS97681;

(first entry) 23-DEC-2002 Histamine N-methyl transferase (HNMT) sequencing Primer #4.

Human; 88; primer; cytochrome P450 Al; CVP4501Al; UGT2B4; MDR1;

KW cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

KW adrenergic receptor betal; ADBRI; arryl hydrocarbon; AHR; MRP3; NRIL2;

Maryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;

KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;

KW cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;

KW cyclooxgenase 2; EPRX2; S-lipoxygenase activating protein; FLAP;

KW glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;

KW MDP-Gluturonosyl transferase 224; UDP-Gluturonosyl transferase 287;

KW DP-Gluturonosyl transferase; UGT2B15; urokinase receptor;

WHIGHOUS resistance 1; lactotransferrin; orphan nuclear receptor;

W multidrug resistance associated protein 3; cancer; prostate;

W multidrug resistance associated protein 3; cancer; prostate;

W multidrug resistance associated protein 3; cancer; prostate;

KW altered drug metabolism; cardiovascular function; colorectal tumour;

KW central nervous system; pulmonary; immunological; sequencing. 

domo sapiens

40200257410-A2

25-JUL-2002.

28-NOV-2001; 2001WO-US044838.

28-NOV-2000; 2000US-00724389.

(DNAS-) DNA SCI LAB INC Hall J; Guida M, 

WPI; 2002-698522/75.

Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for disorder-related traits.

Example 13; Page 124; 714pp; English.

This invention relates to the sequence of an isolated nucleic acid molecule comprising at least one base variation from that of a known human cytochrome P450 Al (CYP4501Al), cytochrome P450 Al (CYP4501Al), cytochrome P450 Al (CYP4501Al), cytochrome P450 Al (CYP4501Al), cytochrome P450 OZEI (CYP4501Al), adrenergic receptor betal (ADBRI), cytochrome P450 OZEI (CYP5501Al), adrenergic receptor betal (ADBRI), cytochrome P450 OZEI (CYP5501Al), adrenergic receptor betal (ADBRI), cytochrome P450 OZEI (CYP55), aryl hydrocarbon receptor nuclear translocator (ARNY), cathepsin S (CTSS), cyclooxegense 2 (CXC2), diazepam binding cransferase (HNMY), RADPH quinone-S-transferase 2 (KNWT), hydralikrah 2) KuK2, nicothamide -N-methyl cransferase (HNMY), RADPH quinone soridoreductase 2 (KNQ2), culfortansferase thermolabile (SYM), UDP-glucuronosyl transferase 2BH (UGT2BI), unclear acedeptor (KNRP3), corphan nuclear receptor (KNRP3), cytophan markers for locating and characterising the genes that care responsible for specific traits within the genome and eventually care responsible for specific traits within the genome and eventually conforting the discorders. The nuclear caid molecules comprising the colymorphic sequences contained in CYP4501A, CYP94501A, CONSTILLING C peripheral nervous system function. The present sequence represents a sequencing primer used to sequence the polymorphic genes of the invention

Sequence 21 BP; 15 A; 3 C; 1 G; 2 T; 0 U; 0 Other;

; 0.9%; Score 16; DB 1; Length 21; 00.0%; Pred. No. 5.4e+02; 0; Indels Best Local Similarity 100.0%; Pred. No. 5.40 Matches 16; Conservative , 0; Mismatches Query Match

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Gaps

8 유

ABS97669 standard; DNA; 21 BP 

23-DEC-2002 (first entry) ABS97669;

Histamine N-methyl transferase (HNMT) PCR Primer #4.

Human; ss; primer; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1; PCR;

cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF; adrenergic receptor beta1; ADBR1, aryl hydrocarbon, AHR; MRD3; NR112; aryl hydrocarbon, AHR; MRD3; NR112; aryl hydrocarbon, AHR; MRD3; NR112; cyclooxgenase 2; COX2; diazepam binding inhibitor; DB1; heematological, epoxide hydroxylase 2; EPHK2; 5-lipoxygenase activating protein; FLAP; glutathione-S-transferase 12; GST12; histeramine-N-methyl transferase; HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT; MADPH quinone oxidoxeductase 2; NOQ2; sulfotransferase thermolabile; STM; UDP-glucuronosyl transferase 287; UDP-glucuronosyl transferase 287; UDP-glucuronosyl transferase 10472B15; urokinase receptor; unlidrug resistence 1; lactotransferrin; orphan nuclear receptor; acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR3; CHMR5; altered drug metabolism; cardiovascular function; colorectal tumour; central nervous system; pulmonary; immunological,

Homo sapiens.

WO200257410-A2.

25-JUL-2002.

28-NOV-2001; 2001WO-US044838.

28-NOV-2000; 2000US-00724389.

(DNAS-) DNA SCI LAB INC.

Guida M, Hall J;

WPI; 2002-698522/75.

Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for disorder-related traits.

Example 13; Page 123; 714pp; English.

This invention relates to the sequence of an isolated nucleic acid molecule comprising at least one base variation from that of a known human cytochrome P450 AJ (CYP4501AI), cytochrome P450 AJ (CYP4501AI), cytochrome P450 AJ (CYP4501AI), adreneyle receptor betal (ADBRI), cytochrome P450 O2EI (CYP4501AI), adreneyle receptor (ADBRI), diagraph binding control of transferase (HNWT), (RAI)Ikkein 2) KLK2, nicothnamide -N-methyl cransferase (HNWT), NADPH quinone Scrience 13 (GST21), histamine-N-methyl cransferase (HNWT), NADPH quinone Scrience 13 (GTS21), up-glucuronosyl transferase 2B7 (UGTSB1), up-glucuronosyl transferase (UGTSB1), up-gluc

us10008789-3.rng

Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.

Cyclin D2 ribozyme binding site #49

40200032765-A2

Mammalia.

04-DEC-2000 (first entry)

AAA84352;

Robbins JM;

Barber JR,

Tritz R, Welch PJ, WPI; 2000-412314/35.

(IMMO-) IMMOSOF INC

98US-0110954P.

06-DEC-1999; 04-DEC-1998;

08-JUN-2000.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method for calibrating data scanned from a molecular array. The method involves employing calibration probes that generate signals proportional to the total concentrations of labelled target molecules to which the molecular array probes are directed over an entire range of sample solutions and molecular arrays incorporating sets of calibration probes. Method is useful for calibrating different types of signals scanned from a molecular array, or calibrating signals scanned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Calibration of molecular array data by employing calibration probes that generate signals proportional to total concentrations of labeled target molecules, and molecular arrays incorporating sets of calibration probes.
haematological function, in CHMR3, CHMR4 or CHMR5 for altered central a peripheral nervous system function. The present sequence represents a primer used to amplify the sequences of the invention
                                                                                                                                                                                                                                                                                             T7T18Apad_PS26-21-0003 probe for calibration of molecular array data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from different molecular arrays. The present sequence is poly (normalisation probe used in calibration of molecular array data
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                                                                        0.9%; Score 16; DB 1; Length 21;
100.0%; Pred. No. 5.4e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21 BP; 16 A; 3 C; 0 G; 2 T; 0 U; 0 Other;
                                                   Sequence 21 BP; 15 A; 3 C; 1 G; 2 T; 0 U; 0 Other;
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100.0%; Pred. No. 5.4e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 14; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AGIL-) AGILENT TECHNOLOGIES INC.
                                                                                                                            1735 CAAAAAAAAAAAA 1750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-SEP-2000; 2000US-00659173
                                                                                                                                                    2 CAAAAAAAAAAAA 17
                                                                                                                                                                                                                   AAD33500 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                      Molecular array; probe; ss
                                                                                                                                                                                                                                                                     01-JUL-2002 (first entry)
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Best Local Similarity 100.º
Matches 16; Conservative
                                                                                       Local Similarity 100.
nes 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                        EP1186673-A2.
                                                                                                                                                                                                                                                                                                                                              Unidentified
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                                                                           Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                       ij
                                                                                                                                                         The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.

Representative examples of ribozyme recognition sites are given in AAA82415 to AAA86787. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in restenosis treatment.
New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1, PCNA and Cyclin B1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                0.9%; Score 15.8; DB 1; Length 19; 89.5%; Pred. No. 5.3e+02; ive 0; Mismatches 2; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19 BP; 5 A; 5 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyclin D2 ribozyme binding site SEQ ID NO:1938.
                                                                                                              Disclosure; Page 75; 109pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1515 TGGCCACATCTTGTGCAAG 1533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGAGCACATCTTGCGCAAG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH59514 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
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Matches
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AAA84352 standard; DNA; 19 BP.

RESULT 900 AAA84352 ID AAA8433

AAAAAAAAAAAA 16

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/note= "at least one (and preferably all) of the backbone subunits are composed of amide units, so that the oligomer consists of the nucleobases attached covalently to a polyamide backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense oligonucleotides which target human ELAM-1 were synthesised in the phosphorothioate form. The oligonucleotides are useful to treat diseases which are modulated by changes in intercellular adhesion molecules. This sequence corresponds to nucleotides 2063-2082 of the 3'-untranslated region of human ELAM-1 coding sequence. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                          Oligo:nucleotide modulation of cell adhesion - used in the treatment of e.g. psoriasis, inflammatory bowel disease or malignant melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide nucleic acid; PNA; intercellular adhesion molecule; ICAM-1; endothelial leukocyte; ELAM-1; vascular; VCAM-1; antiinflammatory; anticancer; antimetastatic; anti-AIDS; anti-rhinoviral; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.9%; Score 15.8; DB 1; Length 20; 89.5%; Pred. No. 5.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide nucleic acid oligomer targetting BLAM-1 3'-UTR.
      /note= "in phosphorothioate form"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 BP; 6 A; 5 C; 9 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 41; Page 62; 101pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             839 CTGCTGGGGTCTCTGGCCC 857
                                                                                                                                                          92US-00939855.
93US-00007997.
93US-00063167.
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*tag= a
                                                                                                                                                                                                                                                                             Bennet CF, Mirabelli CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 89.5
les 17; Conservative
                                                                                                                                                                                                                                       (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                    WPI; 1994-100869/12.
                                              WO9405333-A1
                                                                                                                       27-AUG-1993;
                                                                                                                                                              02-SEP-1992;
                                                                                                                                                                                                17-MAY-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-AUG-1994;
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                                                                                   17-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a ribozyme (1) which cleaves RNA encoding a cytckine involved in inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle dependent kinase, growth factor or a reductase, or administering a nucleic acid molecule (II) comprising a promoter operably linked to a nucleic acid segment encoding (1). (1) can have antipaoriatic, extratolytic and virucide activities, and cleaves RNA encoding (1). (1) can have antipaoriatic, and segment encoding (1). (1) can have antipaoriatic, and gene therapy. (1) and (II) are useful for treating proliferative skin diseases such as psoriasis, atopic dermatitis, actinic keratosis, diseases such as psoriasis, atopic dermatitis, actinic keratosis, also be used for treating proliferative eye diseases such as diabetic retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of prematurity and retinal detachment, and for treating and preventing scarring such, as keloid, adhesion and hypertrophic or hypertrophic burn control of the control o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                              Treating proliferative skin or eye diseases and scarring, using ribozymes that cleave RNA encoding cytokines involved in inflammation, matrix metalloproteinases, growth factors and cell-cycle dependent kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human endothelial leukocyte adhesion molecule; ELAM-1; cell adhesion; modulation; inflammation; psoriasis; malignant melanoma; inhibition; inflammatory bowel disease; antisense oligonucleotide; therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.9%; Score 15.8; DB 1; Length 19; Best Local Similarity 89.5%; Pred. No. 5.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 212; 408pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                 26-OCT-2000; 2000WO-US029500
                                                                                                                                                          99US-0161532P
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(first entry)
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/*tag=
                                                                                                                                                                                                                                 Robbins JM, Tritz R;
                                                                                                                                                                                                                                                                         WPI; 2001-300427/31.
                                                                                                                                                                                            (IMMU-) IMMUSOL INC.
                                      WO200130362-A2
                                                                                                                                                      26-OCT-1999;
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26-SEP-1994
                                                                             03-MAY-2001.
  Synthetic.
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Gaps

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2; Indels

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Query Match
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                                                                                                                                                          New oligomers are claimed which (A) have at least one peptide nucleic acid (PNA) subunit and (B) have a sequence hybridisable to AUG region, coding region, 5-untranslated region or 3'-untranslated region of ICAM-1 or ELAM-1, or hybridisable to AUG region, coding region, 5-untranslated region, exon/intron junction region or 3'-untranslated region of VCAM-1.

The PNAs can be used to target RNA and single stranded DNA (ssDNA) to produce antisense-type gene regulation moieties. Hence they may be used therapeutically for modulating cellular adhesion and thus as antimetastatic agents, anticancer agents, antirhinvoiral agents, anti-1.

AIDS agents and antilinflammantory agents. They may also be useful as diagnostics, e.g. as probes for specific mRNAs. PNA oligomers have high affinity for complementary single stranded DNA. They are also able to form triple helices in which a first PNA strand binds with the resulting double helix or with the first PNA strand. The PNAs possess no significant charge and are water soluble, which facilitates cellular uptake. Further, since they contain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                           New peptide nucleic acid oligomers hybridising to adhesion molecule genes - are stable anti:sense cpds. of high affinity, partic. for treating inflammation, viral infection, cancer etc.
                                                                                                                                                                                                                                                                                                                                                                                    amides of non-biological amino acids, they are biostable and resistant to enzymatic degradation by proteases. The present sequence targets endothelial leukocyte adhesion molecule-1 (BLAM-1) 3'-untranslated region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ICAM-1; endochelial leukocyte adhesion molecule-1; ELAM-1; E-selectin; vascular cell adhesion molecule-1; VCAM-1; white blood cell; brequinar; vascular endothelium; allograft rejection; immunosuppression; rapamycin; anti-lymphocyte serum; monoclonal antibody; cardiac allograft; therapy; renal allograft rejection; donor-specific transplant tolerance; LFA-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense oligonucleotide; human; intracellular adhesion molecule-1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.9%; Score 15.8; DB 1; Length 20;
89.5%; Pred. No. 5.5e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 6 A; 5 C; 9 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense oligonucleotide ISIS 4729.
                                                                                                                                    Claim 10; Page 40; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            839 CTGCTGGGGTCTCTGGCCC 857
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(TEXA ) UNIV TEXAS SYSTEM.
                           Mirabelli CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JAN-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 89.5
Matches 17; Conservative
 (ISIS-) ISIS PHARM INC.
                                                      WPI; 1995-090842/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-1996
                           Bennett CF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13
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antiinflammatory; cytostatic; antiinfectious; infection; inflammation;
detection; antisense therapy; phosphorothiaote; ss.
                                                              Oligo:nucleotide targetted to a nucleic acid sequence encoding ICAM-1, ELAM-1 or VCAM-1 - useful for treating or preventing allo:graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human jun N-terminal kinase kinase-2 antisense oligonucleotide #12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 15.8; DB 1; Length 20
Pred. No. 5.5e+02;
0; Mismatches 2; Indels
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/note= "Phosphorothioate linkages"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 6 A; 5 C; 9 G; 0 T; 0 U; 0 Other;
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                                                                                                                             Example 9; Page 29; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    839 CIGCIGGGICICIGGCCC 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA29827 standard; DNA; 20 BP
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Matches 17; Conservative
Stepkowski SM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monia BP, Cowsert LM;
                               WPI; 1996-268321/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nodified base
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Bennett CF,
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                                                                                              rejection.
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Mon Aug 16 16:46:36 2004

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WPI; 2000-338506/29.
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Antisense compound specifically hybridizing and inhibiting the expression of human Jun N-terminal kinase kinase-2 is useful for treating infection, inflammation and tumor.

Claim 3; Col 40; 31pp; English.

The present invention describes an antisense compound (I) of 8-30 nucleobases, specifically hybridising to, and inhibiting expression of, human jun N-terminal kinase kinase-2 (JKK-2). Also described is a method of inhibiting the expression of human JKK-2 in human cells or tissues, comprising contacting the cells or tissues, with (I), in vitro. (I) has antiinflammatory, cytostatic and antiinfectious activities. (I) is useful for inhibiting the expression of JKK-2 in human cells or tissues and prevents or delays infection, inflammation or tumour formation associated with altered expression of JKK-2 in human sale useful for detecting the levels of JKK-2 in a sample. The present sequence represents a phosphorothioate antisense oligonucleotide for human JKK-2, from the present invention

Sequence 20 BP; 2 A; 12 C; 3 G; 3 T; 0 U; 0 Other;

Gaps ö Length 20; 2; Indels Score 15.8; DB 1; Pred. No. 5.5e+02; 0; Mismatches 0.9%; 89.5%; 17; Conservative Local Similarity Query Match Matches

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997 GGTGGCTGCGGAGAAGATG 1015

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19 Geregeegegaagare 1

AAZ48939 standard; DNA; 20

AAZ48939;

29-MAR-2000 (first entry)

Human ELAM-1 antisense inhibitor, ISIS #4729.

vascular cell adhesion molecule-1; hyperproliferative disorder; VCAM-1; candothelial leukocyte adhesion molecule-1; ELAM-1; skin condition; cancer; viral infection; tumour; diapedesis; graft versus host disease; arthritis; infection; autoimmune disorder; multiple sclerosis; stroke; lyuvenile diabetes mellifus; arthritis; myasthenia gravis; therapy; pemphigus vulgaris; systemic lupus erythematosus; acute myocarditis; cardiovascular disorder; dilated cardiomyopathy; ischemic heart disease; Antisense inhibitor; human; ICAM-1; intercellular adhesion molecule-1; RESULT 906
AAZ48939/C
XX
AAZ489
AC
AAZ489
XX
DT
29-MAR
XX
CACCC
KW
VASCUCC
KW
OCCCC
KW
CCCCC
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OCCCC
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CCCCC
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CCCC
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CCC
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CCCC
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CCC

Homo sapiens

WO9961462-A1

02-DEC-1999

99WO-US011548. 26-MAY-1999;

98US-00085759. 27-MAY-1998;

(ISIS-) ISIS PHARM INC

Bennett CF, Mirabelli CK, Baker BF;

WPI; 2000-072600/06.

New antisense oligonucleotides, used for treating e.g. inflammatory conditions, psoriasis, graft rejection, cancers, infections, cardiovascular disorders or autoimmune disorders.

Example 16; Page 80; 199pp; English

This sequence is an antisense oligonuclectide of the invention. The antisense oligonuclectides are targeted to a nucleic acid encoding a cellular adhesion molecule (ZeM) and is capable of modulating the cepturession of the CAM. They particularly inhibit intercellular adhesion molecule. (ECAM) and is capable of modulating the capable intercellular adhesion molecule. (ECAM.). The antisense endoctides can be used to modulate CAM activity in mediating cell:cell interactions and subsequent cellular and biological responses, ceg. T cell activation, leukocyte transmigration and inflammation. The antisense sequences can be used for modulating the synthesis of a CAM. They can be used for treating an animal suspected of having or being they can be used for treating an inflammation. The condition can insense sequences can be used for treating an inflammatory disease or condition associated with a CAM. Oligonucleotides targeted to ICAM-1 can be used for treating an inflammatory disease or condition e.g. inflammatory bowel disease such as Crohn's disease or condition of the skin, e.g. psoriasis or condition c.g. inflammatory bowel disease such as Crohn's disease or condition of the skin, e.g. psoriasis or cyclotoxic dernatitis, rheumatoid arthritis, allograft rejection, cancer, pneumonia, multiple sclerosis or a viral infection. The ICAM-1 sequences or steducing cyclosporine use in a patient. The oligonucleotides can also be used for reducing corticosteroid use in a patient. The oligonucleotides can also be used for detection and diagnosis. They can also be used for treating e.g. thyperpoid disorders, uncommune forms of arthritis, mysathenia gravis, pemphigus come forms of juvenile diabetes mellitus, mysathenia gravis, pemphigus cyndscardial ischaemia/reperfasion innjury, dialated cardiomyopathy, acute come come come of the \*88888888888888888888888888888888888

Sequence 20 BP; 6 A; 5 C; 9 G; 0 T; 0 U; 0 Other;

Gaps ö Query Match 0.9%; Score 15.8; DB 1; Length 20; Best Local Similarity 89.5%; Pred. No. 5.5e+02; Matches 17; Conservative 0; Mismatches 2; Indels

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839 CTGCTGGGGTCTCTGGCCC 857 Н 19 crecressirioritàsice

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RESULT 907 AAH56368

AAH56368 standard; DNA; 20 BP

AAH56368;

06-SEP-2001 (first entry)

Escherichia coli groE operon antisense oligonucleotide SEQ ID NO:16.

Antisense oligonucleotide; groE; groEL; groES; inhibitor; growth; microorganism: Bscherichia coli; Streptococcus pneumoniae; diagnosis; Streptococcus pyogenes; Staphylococcus aureus; Pseudomonas aeruginosa; antibacterial; antiviral; antiproliferative; antisense therapy; microbial infection; ss.

Sscherichia coli.

WO200136625-A2.

25-MAY-2001.

20-NOV-2000; 2000WO-CA001347.

(GENE-) GENESENSE TECHNOLOGIES INC. 18-NOV-1999; 99US-0166249P.

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Dugourd Wright JA, Young AH,

WPI; 2001-355633/37.

Novel antisense compounds targeting nucleic acid encoding groEL or groES 

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The present invention specifically claims AAH56368 to AAH56832 which are antisense oligonucleotides to nucleotide sequences encoding groE. More generally, antisense compounds (I) comprising antisense oligonucleotides of 5-50 bases targeted to a nucleotide sequence encoding groEL (heat of 5-50 bases targeted to a nucleotide sequence encoding groEL (heat shock protein (HSP)60) (GL) and groES (HSP10) (GS) gene from a microorganism, where the antisense compound is complementary to GL or GS antisensementary to GL or GS is claimed. (I) have antibates there expression of GL or GS, is claimed. (I) have antibates thereby and antibition of expression of groES or groEL. (I) are useful for inhibiting expression of GL or GS in cells or tissues in vitro. (I) are useful for inhibiting the growth of a microorganism, or inhibiting cyloression of GL or GS gene in a microorganism, or inhibiting cyloression of GL or GS gene in a microorganism, (I). (I) are also useful for treating a mammalian pathological condition mediated by the microorganisms which involves identifying a eukaryotic organism is chaving a pathological condition mediated by microorganisms having a condition mediated by microorganisms having a condition mediated by microorganisms with involves identifying a eukaryotic organism is chaving a pathological condition mediated by microorganisms having a condition mediated by microorganisms having a condition mediated by microorganisms having a condition mediated by microorganisms and condition mediated for diagnostics.
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gene of microorganism, which hybridize with and inhibit expression of the genes, useful to inhibit growth of microorganism having the genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapeutics, prophylaxis and as research reagents and Kits, e.g., to prevent or delay microbial infections in humans. They are also useful as molecular weight markers. AMH56362 to AMH56367 and AMH56831 to AAH56884 represent PCR primers for groß sequences which are used in the exemplification of the present invention. AMH56855 to AMH56870 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis; single nucleotide polymorphism; SNP; chromosome 19p13; paternity test; chromosome 5q31-33; forensic test; gene therapy; ds.
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/note= "SNP, optionally insertion or deletion at this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pred. No. 5.5e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exemplification of the present invention. AAH56855 to AJ
groB nucleotide sequence given in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20 BP; 13 A; 0 C; 6 G; 1 T; 0 U; 0 Other;
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                                                                   Claim 3; Page 40; 110pp; English.
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Best Local Similarity 89.5
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour; cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; tumour suppression; tumour reversion; apoptosis; viral resistance; human; viral infection; cell degeneration disease; neurodegeneration; ds; Alzheimer's disease; schizophrenia; immune disease; inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to novel human nucleic acid sequences (1). The present sequence is one such nucleic acid sequence. Expression of (1) are implicated in tumour suppression or reversion and apoptosis and viral
                                                                                                                                     Testing for the presence of polymorphisms associated with inflammatory bowel disease, using a hybridization assay.
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                                                                                                                                                                                                                                                                                                                                                                                                                 0.9%; Score 15.8; DB 1; Length 20;
85.0%; Pred. No. 5.5e+02;
tive 0; Mismatches 3; Indels
                                                                  Siminovitch K;
                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 17 A; 0 C; 2 G; 0 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fumour suppression-related oligonucleotide #1688.
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                                                                  Lander ES, Rioux J,
                WHITEHEAD INST BIOMEDICAL RESELIPSIS BIOTHERAPEUTICS CORP.
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                                                                                                                                                                                         Claim 1; Page 61; 463pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                  Daly M, Hudson TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-610803/66
                                                                                                  WPI; 2001-367874/38
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                (WHED )
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identifying, measuring and/or amplifying nucleic acid sequences, as antisense reagents and for recombinant production of polypeptides (II) polypeptides (II) encoded by (I), vector containing (I), cells containing these vectors and antibodies (Ab) against (II) are all useful for treatment/prevention of viral, tumour and cell degeneration diseases (especially neurodegeneration, such as Alzheimer's disease and schizophrenia). Analysing the expression of (I) is also useful for diagnosis and/or prognosis of such diseases. Transgenic animals carrying (I) are used for studying the actiology of these diseases (also immune and inflammatory diseases). Note: In the present specification, SEQ ID 1 to 2280 are claimed in Claim 1, however only SEQ ID 1 to 2270 are shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hormone-sensitive lipase; antisense oligonucleotide; inhibitor; obesity; phosphorothioate; antidiabetic; anorectic; cytostatic; antisense therapy; abnormal metabolic condition; hyperlipidaemia; type 2 diabetes; cancer; hyperproliferative disorder; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antisense oligonucleotides targeted against nucleic acids encoding hormone-sensitive lipase, useful for treating abnormal metabolic
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human HSL chimeric phosphorothioate oligonucleotide SEQ ID NO:96.
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 resistance. (I) are useful as probes or primers for detecting
                                                                                                                                                                                                                                              Length 20;
                                                                                                                                                                                                                                                                           3; Indels
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/note= "2'-O-methoxyethyl (2'-MOE) wing"
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                                                                                                                                                                                                                Sequence 20 BP; 17 A; 1 C; 1 G; 0 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "phosphorothioate linkages"
                                                                                                                                                                                                                                          Score 15.8; DB 1;
Pred. No. 5.5e+02;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                         1736 AAAAAAAAAAAAAAAAA 1755
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                                                                                                                                                                                                                                              0.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                               ABZ82707 standard; DNA; 20
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/*tag= b
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                                                                                                                                                                                                                                                                           17; Conservative
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                                                                                                                                                                                  in the specification
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                                                                                                                                                                                                                                                             Local Similarity
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Matches
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The present invention describes a compound (I) 8-50 nucleobases in length
                                                                                              targeted to a mucleic acid molecule encoding a hormone-sensitive lipase (HSL) or a splice variant of HSL. The compound specifically hybridises with and inhibits the expression of HSL or a splice variant of HSL, or specifically hybridises with at least an 8-nucleobase portion of an active site on a nucleic acid molecule encoding HSL. (I) have anorectic, antidabetic and cytostatic activities, and can be used in antisense therapy. (I) is useful for treating an animal, particularly human, hyperlipidaemia, type 2 diabetes, a hyperproliferative disorder such as cancer (e.g. pituitary, colorectal, breast, testicular, pulmonary or epithelial cancer). (I) is also useful in modulating blood glucose epithelial particularly plasma or serum glucose levels, in a diabetic animal. The present sequence represents a human hormone-sensitive lipase chimetic phosphorothioate antisense oligonucleotide, which is used in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New oligonucleotide having a sequence complementary to a sequence of ribonucleic acid encoding a heparanase, useful for preparing a composition for treating tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
condition, e.g. hyperlipidemia and obesity, or a hyperproliferative disorder, e.g. cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; heparanase; phosphorothioate; antisense oligonucleotide;
cytostatic; gene therapy; tumour; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human heparanase phosphorothioate oligonucleotide SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                              Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
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                                                                                                                                                                                                                                                                                                                                                                Seguence 20 BP; 4 A; 5 C; 9 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                           Score 15.8; DB 1;
Pred. No. 5.5e+02;
0; Mismatches 2;
                                                  Example 15; Page 89; 167pp; English.
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                                                                                                                                                                                                                                                                                                                               example from the present invention
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/*tag= a
/mod_base= OTHER
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hes 17; Conservat
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modified_base
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WPI; 2003-403142/38.
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11D ADC33
AC ADC33
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rejection, by contacting the allograft with a topical formulation comprising an antisense oligonucleotide targeted to intercellular adhesion molecule-1 (ICAM-1), extracellular adhesion molecule-1 (ICAM-1) or vascular cell adhesion molecule-1 (VCAM-1). The oligonucleotide is useful for inhibiting corneal allograft rejection or for preserving a corneal explant ex vivo, where the explant is human. This sequence corresponds to one of the oligonucleotide of the invention. Sequence 20 BP; 6 A; 5 C; 9 G; 0 T; 0 U; 0 Other; RESULT 913 Matches ADC35554/ 888888888 ઠ 셤 Complementary to a sequence of ribonucleic acid encoding a heparanase.

The oligonuclectide hybridises with the ribonucleic acid under conditions of high stringency and has a sequence comprising 10-40 bp. The citerior control of high stringency and has a sequence comprising 10-40 bp. The citerior control of the heparanase at least one phosphorothicate linkage. Hybridisation of the heparanase, where inhibition of heparanase was a least a 50% reduction in the quality of heparanase means at least a 50% reduction in the quality of heparanase masses. Also described: (1) a method of inhibiting expression of a heparanase in a cell; (2) a composition comprisising the above oligonucleotide in an amount effective to inhibit the expression of compassion of the heparanase in the cell and a carrier; and (3) a method of treating a cumour in a subject comprises administering to the subject and amount of the above oligonucleotide effective to inhibit expression of a heparanase in the subject. Heparanase antisense oligonucleotides have cytostatic the above oligonucleotide effective to inhibit expression of a heparanase in the subject composition for treating tumours. The present sequence represents a human heparanase phosphorothioate antisense oligonucleotide, which is used in the exemplification of the present invention ö Inhibiting corneal allograft rejection, by contacting an allograft with a formulation having an oligonucleotide targeted to intercellular adhesion molecule-1, extracellular adhesion molecule-1 or vascular cell adhesion 88; primer; immunosuppressive; antisense therapy; corneal allograft rejection; intercellular adhesion molecule-1; ICAM-1; extracellular adhesion molecule-1; BLAM-1; vascular cell adhesion molecule-1; VCAM-1; corneal explant. Gaps The present invention describes an oligonucleotide having a sequence The invention relates to a method of inhibiting corneal allograft ö 0.9%; Score 15.8; DB 1; Length 20; 89.5%; Pred. No. 5.5e+02; tive 0; Mismatches 2; Indels Sequence 20 BP; 1 A; 8 C; 6 G; 5 T; 0 U; 0 Other; Example 13; SEQ ID NO 57; 106pp; English. Human ELAM-1 targeted primer #18. 166 GGGCCCACCTGGCTGCCCC 184 Example; Page 25; 48pp; English GGGCTCACCTGGCTGCTCC 20 16-OCT-2002; 2002WO-US033236 18-OCT-2001; 2001US-00982262 ADC39031 standard; DNA; 20 Bennett CF, Mirabelli CK; (first entry) Query Match Best Local Similarity 89.5 Matches 17; Conservative (ISIS-) ISIS PHARM INC molecule-1

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                                                                                                                                                                                                                                Antisense; ss; human; CD81; TAPA-1; tetraspanin; viral infection; cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial; virucide; antiparasitic; inflammatory disorder; parasitic infection; bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel compound hybridizing with nucleic acid molecule encoding CD81 and inhibiting the expression of CD81, useful for treating infections and disease associated with expression of CD81 such as inflammation disorder.
                                                                                                                                                                                                                                                                                                                                                                /note= "Phosphorothioate backbone and all cytidines are -methyl cytidines"
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a compound (antisense oligonucleotide) hybridising with the eighth nucleobase portion of an active site on
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  Length 20;
                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "2'-methoxyethyl nucleotide"
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Score 15.8; DB 1;
Pred. No. 5.5e+02;
0; Mismatches 2;
                                                                                                                                                                                                           Human CD81/TAPA-1 antisense oligonucleotide #14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; SEQ ID NO 26; 55pp; English
                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                     base= OTHER
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/ Match 0.9%;
Local Similarity 89.5%;
les 17; Conservative (
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                                                                                                                                     ADC35554 standard; DNA; 20
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modified_base
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                                                                                                                                                             ADC35554;
                                                 839
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  Query Match
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and inhibiting the expression of CD81. Also included is a composition comprising the antisense oligomorlectide and a carrier or a diluent. The antisense oligomorlectide and a carrier or a diluent. The antisense oligomorlectide is useful for inhibiting the expression of CD81 in cells or tissues. The antisense oligomorlectide is also useful for treating infections preferably viral, bacterial and parasitic and disease such as inflammatory discorders and autonimmune disorders. The disease or condition is characterised by chemical dependency (e.g. cocaine addiction). The present sequence is a CD81 antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes a novel method for identifying an inhibitor on a gene vital for call growth or viability, and where the inhibitor is active on a gene vital for cell growth or viability, and where the gene is subject to loss of heterozygostty (Loff) in a cancer. The inhibitor is used for preventing the development of cancer in a patient having a precancerous condition, by administering to the patient a first allele specific inhibitor (ASI) targeted to an allele of a first essential gene present in cells of the precancerous condition, where the normal somatic cells of the patient are heterozygous for the first gene, the inhibitor is active on at least one but less than all allelic forms of the gene present in a population and targets only one allelic forms of the gene normal somatic cells, and the first gene. The products and methods can be
  nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polymorphism; human, inhibitor; cancer; treatment; cell growth; LOH; cell viability; loss of heterozygosity; precancerous condition; ASI; allele specific inhibitor; somatic cell; diagnosis; prevention; atherosclerotic plaque; premalignant metaplastic lesion; endometriosis; dysplastic lesion; benign tumour; polycystic kidney disease; transplant; graft versus host disease; malignant cell removal; bone marrow; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying target genes for allele-specific drugs - used for diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic plaque, dysplastic lesions, endometriosis or graft versus host disease.
                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                             Length 20;
                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                     Sequence 20 BP; 4 A; 8 C; 6 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                           Score 15.8; DB 1;
Pred. No. 5.5e+02;
0; Mismatches 2;
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                                                                                                                                                                                         oligonuclectide of the invention.

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89.5%;
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nes 17; Conservative
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used in the diagnosis, prevention and treatment of LOH disorders, e.g. cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic lesions, benign tumours, endometriosis, polycystic kidney disease, and graft versus host disease. The method can also be used to remove malignant cells from bone marrow transplants. AAZ25812-Z26825 represent human polymorphic sites described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel biallelic markers used to construct a high density disequilibrium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human biallelic marker downstream amplification primer SEQ ID NO:10471.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome, biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; amplification; single nucleotide polymorphism; SNP; PCR primer;
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                                                                                                                                                                         0.9%; Score 15.8; DB 1; Length 21;
llarity 89.5%; Pred. No. 5.7e+02;
Conservative 0; Mismatches 2; Indels
                                                                                                                                       Sequence 21 BP; 2 A; 6 C; 5 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chumakov I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Page 2463; 2745pp; English.
                                                                                                                                                                                                                                                     459 GAGCACCACGCTGGCCAAA 477
                                                                                                                                                                                                                                                                                         19 GAGCACTACGCTGGCAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                         BP
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98US-0109732P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-IB000822,
                                                                                                                                                                                                                                                                                                                                                                                         AAZ76115 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cohen D, Blumenfeld M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              map of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-013267/01
                                                                                                                                                                                             Local Similarity
les 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnosis; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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23-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-OCT-1999
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Matches
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Sequence 21 BP; 11 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

present invention

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This oligo(T) synthetic oligonuclectide was used for first strand cDNA synthesis from total RNA isolated from either logarithmically growing or quiescent 1011/2 mouse fibroblast cells. It was also used with an arbitarary d(N10) primer in PCR. The PCR products were used in a differential display to identify the mSARP1 gene (see AAV19112) that codes for novel murine secreted apoposis-related protein mSARP1 (see AAV39113-15) and polypeptides to SARP polynuclectides (see also AAV19113-15) and polypeptides (see also AAW37815-17), antibodies specific for SARP, and use of such polynuclectides and antibodies in disponent and therapeutic methods, and methods for treating diseases related to the regulation of SARP expression in tissue and body fluid samples, including
                                                                                                                                                                                                                                                                                                                                                                                                 New secreted apoptosis-related proteins - useful for modulating apoptosis, particularly for treatment of prostatic or breast cancer, also
mouse; prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.9%; Score 15.6; DB 1; Length 17; 88.2%; Pred. No. 5.2e+02; . tive 1; Mismatches 1; Indels
Secreted apoptosis-related protein; SARP; mSARP1; mouse breast cancer; diagnosis; gene therapy; PCR; primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RT-PCR primer of the invention SEQ ID 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                          or diagnosis and monitoring of disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 30; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1735 CAAAAAAAAAAAAAA 1751
                                                                                                                                                                                                                                                                               (LXRB-) LXR BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX18371 standard; DNA; 17 BP
                                                                                                                                                                                                                      96US-0026603P.
96US-0028363P.
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                                                                                                                                                                                                                                                                                                                     Jmansky S, Melkonyan H;
                                                                                                                                                                                                                                                                                                                                                            IPI; 1998-230704/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                               24-SEP-1997;
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11-OCT-1996;
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                                                             Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Locus-specific, separate amplification of exon 2, exon 3, and/or exon 4 of human leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles using defined primer sets, useful for subtyping or typing of HLA Class I alleles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a method for the locus-specific, separate amplification of exon 2, exon 3, and/or exon 4 of human leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles. The method is useful for subtyping or typing of HLA, class 1 alleles. The present sequence is an amplification primer used in the method
                                                             Gaps
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0.9%; Score 15.8; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 5.7e+02;
Matches 17; Conservative 1; Mismatches 3; Indels
                      Length 21;
                                                                                                                                                                                                                                                                                                                                                            Forward primer #26 used for amplification of HLA-A exon 3.
                                                           2, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21 BP; 3 A; 10 C; 7 G; 0 T; 0 U; 1 Other;
                    Score 15.8; DB 1;
Pred. No. 5.7e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                 HLA-A; HLA-B; HLA-C; typing; primer; human; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 CCCCGAAGCAGCCGCAGCCCG 202
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                                                                                                289 GICAATITITGCCCCTIC 307
                                                                                                                                       Grcaarrrricccrcrrrc 1
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99US-0138614P.
                    Query Match 0.9%;
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                        AAC80155 standard; DNA; 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INNO-) INNOGENETICS NV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
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                                                                                                                                                                                                                                                                               AAC80155;
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RESULT 917

8 셤 AAV19118/ 1D AAV1 XX AC AAV1 XX DT 28-AI XX XX XX

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This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)*A-delta-N3'; where X = a labelled compound and/or nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, guanine or cytosine; N = adenine, guanine or thymine; A = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene
                                                                                                        Peptides having at least two new nucleotides - useful as primers in RT-
                                                                                                                                                                                                                                                                                                  Disclosure, Page 11; 19pp; Japanese
WPI; 1999-183822/16
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Gaps ö ch 0.9%; Score 15.4; DB 1; Length 17; I Similarity 94.1%; Pred. No. 5.5e+02; 16; Conservative 0; Mismatches 1; Indels Sequence 17 BP; 1 A; 0 C; 0 G; 16 T; 0 U; 0 Other; Local Similarity sednences Query Match Matches

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1734 ACAAAAAAAAAAAA 1750 17 ATAAAAAAAAAAAAA ð 셤

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AAX18370 standard; DNA; 17
        (first entry)
         11-MAY-1999
                    Synthetic.
     AAX18370;
AAX18370,
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BP

RT-PCR primer of the invention SEQ ID 11.

RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

JP11032765-A

97JP-00208312. 18-JUL-1997; 09-FEB-1999.

97JP-00208312. (TAKI ) TAKARA SHUZO CO LTD 18-JUL-1997;

WPI; 1999-183822/16

Peptides having at least two new nucleotides - useful as primers in RT-

with a target sequence and contain a teast one phosphoro(di)thioate link, having endomuclease activity. (A), and more generally any catalytic nucleic acid (A') that modulates expression of the oestrogen receptor gene, are used to treat cancer (particularly of breast or endometrium), in vivo or by transforming cells ex vivo and implanting treated cells, or for other conditions associated with levels of oestrogen receptor. Because of the high selectivity for targeted RNA, (A) can also be used to carrelate inhibition of gene expression with alterations in phenotype, particularly for identification of therapeutic targets, and as research reagents (for RNA, in the same way that restriction endomucleases are used with DNA). The combination of modifications in (A) improves

resistance to nucleases, binding affinity and/or activity. AAA23503 to AAA24747 represent oestrogen receptor hammerhead riboxyme sequences, and AAA24748 to AAA2592 represent their corresponding target sequences.

AAA2593 to AAA26105 represent oestrogen receptor hairpin riboxyme sequences, and AAA26107 to AAA2618 represent their corresponding target sequences. AAA2619 to AAA26171 represent their corresponding target sequences. AAA2619 to AAA26171 represent their sequences and antisense oligonucleotides used in the exemplification of the present

invention

New nucleic acids that interact, and optionally cleave, target sequences, used to treat cancer.

WPI; 2000-013248/01. Matulic-Adamic J; Thompson JD, Reynolds M,

Bellon L;

Karpeisky A, Haeberli P;

Beigelman L, Mcswiggen JA, Zwick M, Jarvis T, Woolf T,

The present invention describes nucleic acids (A) that interact stably

Claim 77; Page 79; 148pp; English.

Disclosure; Page 11; 19pp; Japanese.

This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, gamma = thymine; N = adenine, guanine, cytosine or thymine; gamma = thymine; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-FCR and determination of base sequences. The new

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sequences allow for reproductive and highly efficient analysis of gene
                                                                                                                                                                                                    Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1954
                                                                                                                                                                                                                    Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage; hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide; gene expression modification; cancer; phosphorothioate; endonuclease; anticancer; breast cancer; endometrium cancer; ss.
                                                               Gaps
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0
                                           0.9%; Score 15.4; DB 1; Length 17; 94.1%; Pred. No. 5.5e+02; ive 0; Mismatches 1; Indels
                         0 G; 15 T; 0 U; 0 Other;
                                                                               1732 TTACAAAAAAAAAAA 1748
                                                                                                                                        456/c
AAA25456 standard; DNA; 17 BP.
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98US-00103636.
                                                                                               17 TTAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                   (RIBO-) RIBOZYME PHARM INC.
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                                                                                                                                                                                  19-JUL-2000 (first entry)
                                                     1 Similarity 94.1 16; Conservative
                           Sequence 17 BP; 2 A;
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                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                       19-APR-1999;
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                                            Query Match
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with a target sequence and contain at least one phosphoro(di)thioate link, having endonuclease activity. (A), and more generally any catalytic nucleic acid (A') that modulates expression of the oestrogen receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene, are used to treat cancer (particularly of breast or endometrium), in vivo or by transforming cells ex vivo and implanting treated cells, or for other conditions associated with levels of cestrogen receptor.

Because of the high selectivity for targeted RNA, (A) can also be used to correlate inhibition of gene expression with alterations in phenotype, particularly for identification of therapeutic targets, and as research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acids that interact, and optionally cleave, target sequences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reagents (for RNA, in the same way that restriction endonucleases are used with DNA). The combination of modifications in (A) improves resistance to nucleases, binding affinity and/or activity. AAA23503 to AAA24747 represent cestrogen receptor hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their corresponding target sequences. AAA25993 to AAA26105 represent coefficient receptor hairpin ribozyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention describes nucleic acids (A) that interact stably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
                                                                                                                                                                                                                                                                                                                                                                    Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1953.
                                                                                                                                                                                                                                                                                                                                                                                                  hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide; gene expression modification; cancer; phosphorothioate; endonuclease; anticancer; breast cancer; endonuclease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antisense oligonucleotides used in the exemplification of the present
                                   0.9%; Score 15.4; DB 1; Length 17;
14.1%; Pred. No. 5.5e+02;
ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beigelman L, Mcswiggen JA, Karpeisky A,
Zwick M, Jarvis T, Woolf T, Haeberli P;
Sequence 17 BP; 2 A; 1 C; 1 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17 BP; 2 A; 0 C; 1 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequences, and AAA26107 to AAA26218 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 77; Page 79; 148pp; English
                                                                                                               1730 GITTACAAAAAAAA 1746
                                                                                                                                                                                                                                                   AAA25455 standard; DNA; 17 BP
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98US-00103636.
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                                                                                                                                                   GTATACAAAAAAAAA 1
                                                       Local Similarity 94.1%;
les 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                               19-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               used to treat cancer.
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Reynolds M, Zwick
Matulic-Adamic J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                         AAA25455;
                                       Query Match
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Bellon L;

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with a target sequence and contain at least one phosphoro(di)thioate

link, having endonuclease activity. (A), and more generally any catalytic

nucleic acid (A) that modulates expression of the osetrogen receptor

gene, are used to treat cancer (particularly of breast or endometrium),

in vivo or by transforming cells ex vivo and implanting treated cells, or

for other conditions associated with levels of osetrogen receptor.

Because of the high selectivity for targeted RNA, (A) can also be used to

correlate inhibition of gene expression with alterations in phenotype,

particularly for identification of therapeutic targets, and as research

reagents (for RNA, in the same way that restriction endonucleases are

used with DNA). The combination of modifications in (A) improves

tesistance to nucleases, binding affinity and/or activity. AAA23503 to

AAA24748 to AAA2592 represent their corresponding target sequences.

AAA25931 to AAA2592 represent their corresponding target sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acids that interact, and optionally cleave, target sequences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequences, and AAA26107 to AAA26218 represent their corresponding target sequences. AAA26219 to AAA26271 represent other ribozyme sequences and antisense oligonucleotides used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention describes nucleic acids (A) that interact stably
                                                                                                                                                                                                                                                                                                                      Destrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1955
                                                                                                                                                                                                                                                                                                                                                                        hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
gene expression modification; cancer; phosphorothioate; endonuclease;
anticancer; breast cancer; endometrium cancer; ss.
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bellon L;
                                      ö
                                                                                                                                                                                                                                                                                                                                                           Destrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
 Length 17;
                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Karpeisky A,
Haeberli P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17 BP; 2 A; 1 C; 1 G; 13 T; 0 U; 0 Other;
Score 15.4; DB 1;
Pred. No. 5.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beigelman L, Mcswiggen JA,
wick M, Jarvis T, Woolf T,
 ch 0.9%; Score 15.4; I Similarity 94.1%; Pred. No. 5.5e 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 77; Page 80; 148pp; English
                                                                       1731 TTTACAAAAAAAAA 1747
                                                                                                                                                                                                         Hb.
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                                                                                                                                                                                                       AAA25457 standard; DNA; 17
                                                                                                            17 TATACAAAAAAAAA
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                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zwick M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used to treat cancer
                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matulic-Adamic J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-APR-1999;
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23-JUN-1998;
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                                                                                                                                                                                                                                                                               19-JUL-2000
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 Query Match
Best Local S:
Matches 16
                                                                                                                                                                                                                                              AAA25457;
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0.9%; Score 15.4; DB 1; Length 17;

Query Match

their corresponding target

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                 Gaps
                 ..
Pred. No. 5.5e+02;
                0; Mismatches
      94.1%;
               16; Conservative
        Best Local Similarity
              Matches
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1729 AGTTTACAAAAAAAA 1745 17 AGTATACAAAAAAAA 1 ઠે 셤

ABK02364 standard; RNA; 17

ABK02364;

12-MAR-2002 (first entry)

Human NOGO Amberzyme #36.

Human; 88; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; DO20; neurice growth inhibitor gene; NOGO; hammerhead ribozyme; DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; Jymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCI; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; ampotrophic lateral sclerosis; ALS; Parkinson's disease; ataxia; Huntingcon's disease; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

sapiens Ношо

Synthetic.

WO200159103-A2.

16-AUG-2001.

09-FEB-2001; 2001WO-US004273.

11-FEB-2000; 2000US-0181797P. 28-FEB-2000; 2000US-0185516P. 06-MAR-2000; 2000US-0187128P.

(RIBO-) RIBOZYME PHARM INC. (BLAT/) BLATT L. BLATT L. MCSWIGGEN J. (MCSM/)

CHOWRIRA B M. CHOM/)

Chowrira BM; Blatt L, Mcswiggen J,

WPI; 2001-607195/69.

and Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, central nervous system injury.

Claim 88; Page 131; 200pp; English.

The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NOGO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNAzyme) an Inozyme (an endolytic nucleic acids (e.g. a ribozyme or a DNAzyme) an NCH motif), a G-cleaver (cleaving RNA with a NRN motif) pran amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg^2+. Eurthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targetting nucleic acid may be used to RESULT 3.

AND ABER COLD 3.

A

treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular nonHodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
Leukaemia, Hiv (human immunodeficiency virus) associated NHL, mantle-cell
lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
immune thrombocytopaemia, and inflammatory arthropathy. The NOGOcrafetting nucleic acid is used to cleave RNA of the NOGO ene in the
presence of a divalent cation that is preferably Mg^2+. Furthermore, the
nucleic acid may be contacted with a cell to reduce NOGO activity of the
cell and treat a patient having a condition associated with the level of
NOGO. The treatment may further comprise the use of one or more
therapies. In particular, the NOGO-tragetting nucleic acid may be used to
treat central nervous system (CNS) injury and cerebrovascular accident
(CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (MS),
parkinson's disease, attaxia, Huntington's disease, Creutzfeldt-Jakob, disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NOGO expression. The present sequence is an amberzyme molecule of the invention 

Seguence 17 BP; 7 A; 0 C; 10 G; 0 T; 0 U; 0 Other;

Gaps ö 0.9%; Score 15.4; DB 1; Length 17; 94.1%; Pred. No. 5.5e+02; Ive 0; Mismatches 1; Indels 94.1%; 16; Conservative Local Similarity Query Match Best Loca Matches

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861 AGGAAGAGGAAGAGGAG 877 1 AGGAGGAGGAAGAGGAG

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RESULT 924

ABA91530 standard; DNA; 17 BP ABA91530/

ABA91530;

(first entry) 23-APR-2002

DNA-RNA-DNA oligonucleotide AGT02014 used to test RNase H cleavage.

DNA-RNA hybrid; RNase H; nucleic acid detection; ss.

Synthetic

Location/Qualifiers /\*tag= a /label= RNA misc\_RNA 

WO200206531-A2

24-JAN-2002.

12-JUL-2001; 2001WO-US022166

14-JUL-2000; 2000US-00616761. 30-MAR-2001; 2001US-00823647.

(GENE-) APPLIED GENE TECHNOLOGIES INC.

Dattagupta N;

WPI; 2002-171819/22.

Probes for detecting target nucleotide sequence in sample, has sequence that forms hairpin structure having a double-stranded segment and singlestranded loop collectively forming region complementary to target sequence

3xample 4; Page 49; 72pp; English.

The present sequence is that of DNA-RNA-DNA hybrid oligonucleotide · AGT02014. This is one of a set of oligonucleotides (see ABA91527-30) used

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to assess the minimum number of ribonucleotides in DNA-RNA chimeric oligonucleotides required for Rhase H cleavage. Each oligonucleotide of the get had a different number of ribonucleotides, 1 in the present case. The oligonucleotides were mixed with target DNA oligonucleotide AGT02009 (See ABA91531) and incubated with Rhase H (5 U/ml) at 37 degrees C for 30 minutes. The results showed that 4 ribonucleotides were the minimum number for RNA cleavage. The invention provides probes for nucleic acid hybridisation. The probes form a hairpin structure comprising a doublestranded stem and a single-stranded loop, and are capable of both intramolecular and intermolecular hybridisation. The double-stranded stem may comprise a methylphosphonate DNA, RNA hybrid that is resistant to RNAse H cleavage. When the probe hybridisation that is resistant to strand in the DNA, RNA duplex becomes sensitive to RNAse H treatment and can be removed. Arrays and methods for nucleic acid hybridisation using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the probes are provided
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Sequence 17 BP; 1 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

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Gaps
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Score 15.4; DB 1; Length 17;
Pred. No. 5.5e+02;
0; Mismatches 1; Indels
  0.9%;
              Local Similarity 94.1
168 16; Conservative
     Query Match
                             Matches
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ABK18820 standard; RNA; 17 BP. RESULT 925 ABK18820

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09-APR-2002 (first entry)
 ABK18820;
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Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic; ophthalmological; antidarthritic; antipsoriatic; virucide; osteopathic; vulnerary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis; tumour angiogenesis; diabetic retinopathy; macular degeneration; neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris; angiofibroma of tuberous sclerosis; port-wine setain; wound healing; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss; Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme; Human ERG DNAzyme target sequence Seq ID No 1467.

Homo sapiens. amberzyme.

WO200188124-A2.

22-NOV-2001.

16-MAY-2001; 2001WO-US015866.

16-MAY-2000; 2000US-00572021

(RIBO-) RIBOZYME PHARM INC. (GLAX ) GLAXO GROUP LTD.

Mclaughlin F, Mcswiggen JA, Jarvis T, Von Carlowitz I, WPI; 2002-082995/11.

Randi AM;

useful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome. Novel polynucleotide which down regulates expression of Ets-related useful for treating cancer. disheria wattannon treating

Claim 4; Page 92; 149pp; English.

The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for treating conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,

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tumour angiogenesis, diabetic retinopathy, macular degeneration, neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca vulgarie, angiofibroma of tuberrous sclerosis, port-wine stains, Sturge Weber syndrome, Nippel-Trenaunay-Weber syndrome, Oaler-Weber-rendu syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for creating a patient having a condition associated with the level of ERG, by contacting cells of the patient with (I) under conditions suitable for the treatment. The method comprises the use of one or more therapies the treatment. The method comprises the use of one or more therapies or under conditions suitable for the treatment. Leukaemia or tumour angiogenesis is treated by administering (I) to the patient in conjunction with one or more of other therapies such as radiation or chemotherapy treatment. (I) is useful for reducing ERG activity in a cell, by contacting the cell with (I). (I) is useful for cleaving RNA of ERG gene, by contacting (I) with RNA, in the presence of a divalent cation such as Mg2+. (I) is useful for diagnosis of conditions and diseases related to the expression of ERG, and as diagnostic tool to examine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically targeting genes that share homology with ERG gene or ERG fusion genes. ARK1354-ABK22719 represent nucleic acide, including antisense and enzymatic nucleic acide, including antisense and enzymatic nucleic acide, including antisense and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequential consensus region-directed amplification; gene expression; disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligo-AT PCR primer #2 used to illustrate the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.9%; Score 15.4; DB 1; Length 17;
18.2%; Pred. No. 5.5e+02;
ve 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17 BP; 2 A; 12 C; 2 G; 0 T; 1 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                               related PCR primers of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           268 GCACTCCAGCCCCACCC 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GCCCUCCAGCCCCACCC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD44151 standard; DNA; 17 BP.
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97US-0108152P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 88.2
nes 15, Conservative
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Gillies G; Fillmore H, Broaddus W, WPI; 2002-412824/44.

Example, Fig 1D, 19pp; English.

Sequential consensus region-directed amplification for sorting mixture DNAs into 2 or more subsets or distinguishing gene expression patterns 2 samples, useful for disease diagnosis and gene analysis.

The invention relates to a method of sequential consensus region-directed amplification for sorting a mixture of DNAs into 2 or more subsets or

Gaps

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1; Indels

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The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MDZ3, MDZ4, MDZ12, MDZ21. MDZ3 is cancoded at chromosome 7422.1, MDZ4 is encoded at chromosome 6721.3-22.2, MDZ7 is encoded at chromosome 1601.2 and MDZ12 is encoded at chromosome 1602.2 and MDZ12 is encoded at chromosome 1602.2 and MDZ1, mDZ2, and MDZ12 is encoded at chromosome 1502.2 and MDZ1, mDZ2, and MDZ12 is encoded at chromosome 1502.2 associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ4, MDZ7, or MDZ12, encoder at sease acides and proteins are also useful for diagnoshing or monitoring a disease acide can also be used as probes to detect and characterize gross alterations in MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic acides can also be used as probes to detect and characterize gross alterations in MDZ3, MDZ7, or MDZ12 genetic locus. The probes are proteins are useful as therapeutic agents for gene therapy or as proteins are useful as therapeutic agents for gene therapy or as
distinguishing gene expression patterns in 2 samples. The methods, kits and oligonuclectides are useful for sorting a mixture of DNAs into 2 or more subsets or distinguishing gene expression patterns in 2 samples e.g. for disease diagnosis and gene analysis. The present sequence is oligo AT PCR primer used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytostatic; immunostimulant; gene therapy; vaccine; human; zinc finger protein; MD23; MD27; MD21; chromosome 7q22.1; chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer; developmental disorder; ss.
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                                                                                                                                                                                                                                                                                                             0.9%; Score 15.4; DB 1; Length 17; 94.1%; Pred. No. 5.5e+02;
                                                                                                                                                                                                                                 Sequence 17 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human MDZ7 scanning oligonucleotide SEQ ID 5255.
                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1736 AAAAAAAAAAAAAA 1752
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                                                                                                                                                                                                                                                                                                                                                94.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                            16; Conservative
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                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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ADB04269/AX
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ADB04269/AX
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ADB0
DT 20-N
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Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

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The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is concoded at chromosome 6p21.3-22.2, MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome concoder in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MD23. MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic acids and also be used as probes to detect and characterize gross alterations in MD23, MD24, MD212 genetic locus. The probes are useful as therapeutic agents for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as vaccines. The present sequence was used to illustrate the invention.
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                                                                                                                                                                                                                                                                                                                                             Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MDZ3; MDZ4; MDZ12; chromosome 7q22.1;
chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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16; Conservative 0; Mismatches 1; Indels
0.9%; Score 15.4; DB 1; Length 17; 94.1%; Pred. No. 5.5e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                           Human MDZ7 scanning oligonucleotide SEQ ID 5256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 8; SEQ ID NO 5256; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MDZ4, MDZ7 or MDZ12, e.g. cancer.
                                                                         1736 AAAAAAAAAAAAAA 1752
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                                                                                                                                                                                                     ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUL-2002; 2002EP-00016874.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shannon M, Gu Y, Nguyen C;
                                                                                              17 AAAAAAAAAAAAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                   developmental disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 AAAAAAAAAAAAAGA
                                                                                                                                                                                                     ADB04270 standard; DNA; 17
                                                                                                                                                                                                                                                                         (first entry)
                                       16, Conservative
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ses 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-423107/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AEOM-) AEOMICA INC
                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP1281758-A2.
                                                                                                                                                                                                                                                                           20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-FEB-2003.
                                                                                                                                                                                                                                         ADB04270;
                    Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
 Query Match
                                                                                                                                                                 928
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RESULT 929

ACC63788/

us10008789-3.rng

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The oligomer was designed to target human TNF receptor mRNA beginning at nucleotide 2354 and to covalently cross-link to the target via the N4N4-ethanocytosine group. See also AAQ20108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New sequence-specific non-photo-activated crosslinking agents - bind to
the major groove of duplex DNA and are esp. useful for treating latent
infections e.g. HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             deoxyribonucleic acid; major groove; ethanoamino group;
tumour necrosis factor; receptor; messenger RNA; aziridinylcytosine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-linking oligomer 942 to target human TNF Receptor mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 0.9%; Score 15.4; DB 1; Length 18; 1 Similarity 94.1%; Pred. No. 5.7e+02; 16; Conservative 0; Mismatches 1; Indels
                                                                                                            /mod_base= OTHER
/note= "N-methyl-8-oxo-2'-deoxyadenine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= b
/mod_base= OTHER
/note= "N4N4-ethanocytosine"
                                                                                                                                                                               /mod_base= OTHER
/note= "N4N4-ethanocytosine"
                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; Page 27; 42pp; English.
                                                                                       *tag= a
mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1736 AAAAAAAAAAAAAA 1752
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                                                                                                                                                                                                                                                                                                                                                    90US-00529346.
91US-00640654.
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                                                                                                                                                                                                                                                                                                                 90US-00529346
                                                                                                                                                              *tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matteucci MD, Krawczyk S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                              (GILE-) GILEAD SCIE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cross-linking group; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1992-007480/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                      Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified_base
                                                                                                                                               modified base
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                                                                                                                                                                                                                                                                                                                 35-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                      5-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                       14-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1992
                                                                                                                                                                                                                                         WO9118997-A
                                                                                                                                                                                                                                                                              12-DEC-1991
                 Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ20108,
SXCCCXXSXTTTTTTTTXBXXBXXBXXBXXBXTTTTTTTTTXSXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACC68806), which are associated with tumour suppression, tumour reversion, apoptosis and virus resistance. The oligonucleotides are useful as (1) as probes and primers for detecting, identifying, quantifying and/or amplifying nucleic acid, e.g. as one component of gene chip; in vitro as (anti)sense reagents; and (2) for production of recombinant polypeptides. The oligonucleotides are useful for preparation of pharmaccuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.
                                                                                                                                                                                                 Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine; tumour suppression; tumour reversion; apoptosis; virus resistance; viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
                                                                                                                                                              Murine oligonucleotide associated with tumour supression, SEQ ID 1035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                deoxyribonucleic acid; major groove; ethanoamino group;
tumour necrosis factor; receptor; messenger RNA; aziridinylcytosine;
cross-linking group; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to murine oligonucleotides (ACC62754-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-linking oligomer 943 to target human TNF Receptor mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.9%; Score 15.4; DB 1; Length 17; 94.1%; Pred. No. 5.5e+02; ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17 BP; 2 A; 7 C; 3 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 152; 738pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tuijnder M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118
                                                    ACC63788 standard; DNA; 17 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR ENGINES LAB
                                                                                                                                                                                                                                                                                                                                                                                                            17-SEP-2002; 2002WO-IB004210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-SEP-2001; 2001FR-00011979.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGAAGGCCAGAGGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ20109 standard; DNA; 18
                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Telerman A, Amson R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-333167/31.
                                                                                                                                                                                                                                                           schizophrenia; ss.
                                                                                                                                                                                                                                                                                                                                WO2003025176-A2
                                                                                                                                                                                                                                                                                                Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1992
                                                                                                                         01-JUL-2003
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                                                                                       ACC63788
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RESULT 930

δ 셤 AAQ20109/ 1D AAQ2 AC AAQ2 XX D1-A DT 01-A XX GEOX XW CUMO KW CUMO KW CYOMO

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Gaps

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Milligan J;

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The synthetic oligomer is capable of forming a triplex at physiological pH with a purine rich target sequence by coupling into the major groove of the duplex. The specific target sequence of this oligomer is the human tumour necrosis factor receptor mRNA beginning at nucleotide 2354 contg, a purine rich sequence concd. on one strand of the duplex. The oligomer, and others like it are useful in diagnosis and therapy of diseases characterised by specific DNA duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant tumours and inflammation. The triple helices form under mild conditions thus assays may be carried out without subjecting the test specimen to harsh conditions. See also AAQ25452-25501 and AAQ30226-448. (Updated on 25-MAR-2003 to correct PD field.) (Updated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Target; human tumour necrosis factor receptor mRNA; AIDS; triplex; HIV; hepatitis; malignancy; inflammation; ds.
                                                                                                                                               New oligomers contg. modified bases - which form a triplex with G-C doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis, herpes malignancy and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.9%; Score 15.4; DB 1; Length 18;
94.1%; Pred. No. 5.7e+02;
Ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Krawczyk S, Matteucci MD, Milligan J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Purine rich HUMNFR target duplex sequence.
                                                                                   Matteucci MD,
                                                                                                                                                                                                                  Claim 12; Page 72; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1736 AAAAAAAAAAAAAA 1752
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91US-00643382.
91US-00683420.
91US-00686544.
91US-00686546.
 91US-00686547.
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               91US-00766733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ilarity 94.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ25501 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 AAAAAAAAAAGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
(first entry)
                                                                                 Krawczyk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GILE-) GILEAD SCI INC
                                                  SCI INC
                                                                                                                  WPI; 1992-217083/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 16; Conserv
                                                (GILE-) GILEAD
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17-APR-1991;
27-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-NOV-1991;
                                                                                   Froehler B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Froehler B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
07-DEC-1992
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08-APR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Matches
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 셤
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                                                                                                                                                                                                                                                                                                                                                                  The oligomer was designed to target human TNF receptor mRNA beginning at nucleotide 2354 and to covalently cross-link to the target via the N4N4-ethanocytosine group. See also AAQ20109
                                                                                                                                                                                                                                                              New sequence-specific non-photo-activated crosslinking agents - bind to the major groove of duplex DNA and are esp. useful for treating latent infections e.g. HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human tumour necrosis factor receptor mRNA, AIDS, modified, HIV, RSV, HPV, malignancy; hepatitis; inflammation, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mod_base= OTHER
/note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligomer TNFR941 for forming triplex with HUMNFR target duplex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.9%; Score 15.4; DB 1; Length 18; Best Local Similarity 94.1%; Pred. No. 5.7e+02; Matches 16; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18 BP; 0 A; 2 C; 0 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                     Example 4; Page 27; 42pp; English.
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/mod_base= m5c
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91US-00643382.
91US-00683420.
91US-00686544.
91US-00686546.
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                                                                                   90US-00529346.
                                                                                                                   90US-00529346.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ30446 standard; DNA; 18
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                                                                                                                                                                                                   Matteucci MD, Krawczyk S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
(first entry)
                                                                                                                                                                    (GILE-) GILEAD SCIE INC.
                                                                                                                                                                                                                                    WPI; 1992-007480/01.
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18-JAN-1991;
08-APR-1991;
17-APR-1991;
17-APR-1991;
                                                                                                                  25-MAY-1990;
14-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-NOV-1991;
                                                                                   25-MAY-1990;
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07-DEC-1992
                 WO9118997-A.
                                                  12-DEC-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ30446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ30446/c
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The synthetic oligomer is capable of forming a triplex at physiological pH with a purine rich target sequence by coupling into the major groove of the duptex. The specific target sequence of this oligomer is the human tumour necrosis factor receptor mRNA beginning at nucleotide 2354 contg. a purine rich sequence concd. on one strand of the duplex. The oligomer, and others like it are useful in diagnosis and therapy of diseases characterised by specific DNA duplex targets. e.g. HPV, HER, HIV, heparattis B, herpes, malignant tumours and inflammation. The triple bubjecting the test specimen to harsh conditions. See also AAQ25452-25501 and AAQ30226-447. (Updated on 25-MAR-2003 to correct PD field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human tumour necrosis factor receptor mRNA; AIDS; modified; HIV; RSV; HPV; malignancy; hepatitis; inflammation; 88.
                                                                                                                          New oligomers contg. modified bases - which form a triplex with G-C doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis, herpes malignancy and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligomer TNFR942 for forming triplex with HUMNFR target duplex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . Match 0.9%; Score 15.4; DB 1; Length 18; Local Similarity 94.1%; Pred. No. 5.7e+02;
                                                               Matteucci MD, Milligan J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mod_base= OTHER
/note= "OTHER= N4 N4 ethanocytosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                           Claim 12; Page 72; 77pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1736 AAAAAAAAAAAAAA 1752
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91US-00683420.
91US-00686544.
 91US-00766733.
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                                                               Froehler B, Krawczyk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16; Conservative
                          (GILE-) GILEAD SCI INC.
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                                                                                             WPI; 1992-217083/26
   27-SEP-1991;
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modified_base
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08-APR-1991;
17-APR-1991;
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                                                                                                                       The sequence depicts a HUMNFR (tumour necrosis factor receptor) mRNA sequence beginning at nuclectide 2354. The sequence is a viral duplex sequence contg. a purine-rich region concentrated on one chain of the duplex. The sequence may be prepd. by standard DNA synthesis. The HUMNFR duplex sequence is used as a target for novel oligomers which are capable of forming a triplex at physiological pH by coupling into the major groove of the DNA duplex. Three such oligomers TNFR 941-32 are capable of forming a triplex with this sequence. The oligomers are used in the treatment of inflammation. Similar oligomers may be used to target viral DNA duplexes specific for HIV, herpes and other viruses. The triple helices form under mild conditions thus assays may be carried out without inhibit gene expression, as verified by in vitro systems. See also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human tumour necrosis factor receptor mRNA; AIDS; modified; HIV; RSV; HPV; malignancy; hepatitis; inflammation; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                              New oligomers contg. modified bases - which form a triplex with G-C doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis, herpes malignancy and inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                    0.9%; Score 15.4; DB 1; Length 18; 94.1%; Pred. No. 5.7e+02; tive 0; Mismatches 1; Indels
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/mod_base= OTHER
/note= "N6 methyl-8-oxo-2' deoxyadenine"
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/note= "OTHER= N4 N4 ethanocytosine"
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                                                                                               Claim 11; Page 64; 77pp; English
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91US-00643382.
91US-00683420.
91US-00686544.
91US-00686546.
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(first entry)
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Best Local Similarity 94.19
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WPI; 1992-217083/26.
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modified_base
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17-APR-1991;
17-APR-1991;
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07-DEC-1992
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Matteucci MD, Milligan J;

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The synthetic oligomer is capable of forming a triplex at physiological pH with a purine rich target sequence by coupling into the major groove of the duplex. The specific target sequence of this oligomer is the human tumour necrosis factor receptor mRNA beginning at nucleotide 2354 contg. a purine rich sequence concd. on one strand of the duplex. The oligomer, and others like it are useful in diagnosis and therapy of diseases characterised by specific DNA duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant tumours and inflammation. The triple helices form under mild conditions thus assays may be carried out without subjecting the test specimen to harsh conditions. See also AAQ25452-25501 and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.) (Updated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or treating diseases associated with apoptosis.
                                                                                                                                                                                                                                                                                                                         New oligomers contg. modified bases - which form a triplex with G-C doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR; primer; amplification; apoptosis; antibody; inhibition; ss; immunohistological staining.
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                                                                                                                                                                                                                                                                                                                                                                                         herpes malignancy and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12; Page 72; 77pp; English
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                              91US-00686547.
91US-00766733.
91US-00686546
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                                                                                                                         GILE-) GILEAD SCI INC
                                                                                                                                                                                         Froehler B, Krawczyk
                                                                                                                                                                                                                                                         WPI; 1992-217083/26
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Best Local Similarity
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17-APR-1991;
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AAV54170/C
AAV54170/C
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        This is the nucleotide sequence of a PCR primer used in the method of the invention, involving the use of novel apoptosis-related DNAs and proteins. The inventions can be used as diagnostic reagents for apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent in immunohistological staining, as apoptosis inhibitors. It can also be used for treatment of apoptosis-related diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is the nucleotide sequence of a PCR primer used in the method of the invention, involving the use of novel apoptosis-related DNAs and proteins. The inventions can be used as diagnostic reagents for apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent in immunohistological staining, as apoptosis inhibitors. It can also be used for treatment of apoptosis-related diseases
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                                                                                                                                                    0.9%; Score 15.4; DB 1; Length 18; larity 94.1%; Pred. No. 5.7e+02; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.9%; Score 15.4; DB 1; Length 18;
14.1%; Pred. No. 5.7e+02;
ve 0; Mismatches 1; Indels
                                                                                                                        Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
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Best Local Similarity 94.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR; primer; amplification; immunohistological staining
                                                                                                                                                                                                                                                 18 СТАААААААААААА
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                                                                                                                                                                   Local Similarity
les 16; Conserv
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Length 18; 1; Indels

Score 15.4; DB 1; Pred. No. 5.7e+02; 0; Mismatches 1;

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0.9%;

RESULT 938 AAV54169/c

Example 1; Page 49; 70pp; Japanese

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This is the nucleotide sequence of a PCR primer used in the method of the invention, involving the use of novel apoptosis-related DNAs and proteins. The inventions can be used as diagnostic reagents for apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent in immunohistological staining, as apoptosis inhibitors. It can also be used
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                                                                                                              Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or treating diseases associated with apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
                                                                                                                                                                                                                                                                                                                                                                               0.9%; Score 15.4; DB 1; Length 18; 94.1%; Pred. No. 5.7e+02;
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                                                                                                                                                                                                                                                                                                         for treatment of apoptosis-related diseases
                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                       Example 1; Page 50; 70pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide sequence PCR primer 4.
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 (KYOW ) KYOWA HAKKO KOGYO KK
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                                                                                                                                                                                                                                                                                                                                                                                                 94.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV54167 standard; cDNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunohistological staining
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                                                                            WPI; 1998-495844/42
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                                   Sakaki Y,
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AAV54167/
 SXCCCCCCXSXTTXSXTXSX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is the nucleotide sequence of a PCR primer used in the method of the invention, involving the use of novel apoptosis-related DNAs and proteins. The inventions can be used as diagnostic reagents for apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent in immunohistological staining, as apoptosis inhibitors. It can also be used
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                                                                                                                                                   PCR; primer; amplification; apoptosis; antibody; inhibition; ss; immunohistological staining.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for treatment of apoptosis-related diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 49; 70pp; Japanese.
                                                                                                                Mucleotide sequence PCR primer 6.
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AAV54169 standard; cDNA; 18 BP
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Matches 16; Conservative
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AAV54172/ RESULT

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Gaps

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AAZ90642 standard; DNA; 18 BP.

RESULT 942 AAZ90642/c

AAZ90642;

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The present sequence represents a probe used to isolate human bone morphogenetic protein-16 (BMP-16) cDNA. Human BMP-16 is a homologue of a murine protein celled nodal, which is expressed in the mouse node during castrulation. BMP-16 cDNA is isolated from a human genomic library screened with a probe derived from the nodal DNA sequence. The BMP-16 proteins can induce the formation of bone, cartilage or other connective tissue. They can be used for treating bone, cartilage or other connective tissues and wounds. They can also increase neuronal, astrocytic and glial cell survival and therefore be useful in transplantation and treatment of call survival and therefore be useful in transplantation and treatment of conditions exhibiting a decrease in neuronal survival and repair. They can also exhibit properties, and effects on cells including induction of chemoattractant properties, and effects on cells including induction of collagen synthesis, fibrosis, differentiation responses, cell adhesion, migration and extracellular matrices. These properties make the proteins potential agents for wound healing, reduction of fibrosis and reduction of scar and responses in a reduction of scar and responses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated bone morphogenetic protein-16 - used to develop products for inducing formation of bone, cartilage and other connective tissue, particularly for wound healing and tissue repair.
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                            Human, bone morphogenetic protein-16; BMP-16; murine protein, nodal; formation; bone; cartilage; treatment; wound healing; reduction; fibrosis; scar tissue formation; probe; ss.
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Sequence 18 BP; 2 A; 4 C; 8 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                           Probe used to isolate cDNA encoding human BMP-16.
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                                                                                                                                                                                                                                                                                     04-AUG-1998 (first entry)
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                                       16; Conservative
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                 Best Local Similarity
Matches 16; Conserv
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The invention relates to identification of genes and proteins of adipose itsease relating to obesity, particularly complications of visceral obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis, hyperuricemia and sleep apnes ayndrome. The genes (AAZ90631-633) and the proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention and treatment of adipose tissue related diseases. Sequences AAZ90640-51 represent PCR primers amplifying the human adipose tissue genes
                                                                                                                                                                                                                                                                                                                                                   A physiologically active protein specifically derived from mammal tissue.
                                                                                                  Adipose tissue, obesity, diabetes; hyperlipemia, hypertension, human, arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
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44.1%; Pred. No. 5.7e+02;
ve 0; Mismatches 1; Indels
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                                                                        Human adipose tissue gene amplifying primer #3.
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hes 16; Conservative
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                                                                                                                                               Homo sapiens.
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                                           13-JUN-2000
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Matches
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Score 15.4; DB 1; Length 18; Pred. No. 5.7e+02; 0; Mismatches 1; Indels

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16; Conservative

Local Similarity

Query Match Matches

0.9%;

1479 CTCTGAGGGCGAGTGTC 1495 crercacceccacrere 17

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1735 CAAAAAAAAAAAAAA 1751
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                                                                                                                              The invention relates to identification of genes and proteins of adipose tissue relating to obesity, particularly complications of visceral obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis, hyperuricemia and sleep apnes syndrome. The genes (AAZ90631-633) and the proteins (AAX67589-X67600) are used in the genetic diagnosis, prevention and treatment of adipose tissue related diseases. Sequences AAZ90640-51 represent PCR primers amplifying the human adipose tissue genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A physiologically active protein specifically derived from mammal tissue.
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                                                                              A physiologically active protein specifically derived from mammal tissue.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human; arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
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4.1%; Pred. No. 5.7e+02;
ve 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human adipose tissue gene amplifying primer #1
                                                                                                       Example 2; Page 18; 50pp; Japanese
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 98JP-00225228
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Conservative
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Best Local Similarity 94.1
Matches 16; Conservative
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nes 16; Conserv
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23-JUL-1998;
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tissue relating to obesity, particularly complications of visceral obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis, hyperunicemia and sleep apnea syndrome. The genes (AAZ90631-633) and the proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention and treatment of adipose tissue related diseases. Sequences AAZ90640-51
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                                                                                                                                                                                                                                                                                                                             Adipose tissue, obesity, diabetes; hyperlipemia; hypertension, human; arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       represent PCR primers amplifying the human adipose tissue genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.9%; Score 15.4; DB 1; Length 18;
94.1%; Pred. No. 5.7e+02;
ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human adipose tissue gene amplifying primer #4.
                                                                                                                                                                                                                                                                               Human adipose tissue gene amplifying primer #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 18; 50pp; Japanese.
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                                                                                                                                                                                                                               13-JUN-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-306578/27.
                                                                                                                          AAZ90645 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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The present invention relates to a coding sequence with a heterologous futron for treating diseases. The invention is also useful for obtaining a transgenic plant having increased resistance to an external stress such as herbicide, a pathogen or pest or an unfavourable environmental factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue relating to obesity, particularly complications of visceral obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis, hyperticemia and sleep apnea syndrome. The genes (AAZ90631-633) and the proteins (AAY67598-X67600) are used in the genetic diagnosis, prevention and treatment of adipose tissue related diseases. Sequences AAZ90640-51 represent PCR primers amplifying the human adipose tissue genes
                                                                                                                                                                                                                                                                                                                      A physiologically active protein specifically derived from mammal tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to identification of genes and proteins of adipose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotides having a heterologous intron, useful for manufacturing medicaments for treating human and animal diseases, by stable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18 BP; 1 A; 0 C; 1 G; 16 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 15.4; DB 1;
Pred. No. 5.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer eGFP2 used to modify eGFP coding region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page 18; 50pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disease; intron; plant; animal; ds.
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                                                               98JP-00225228
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                                                            23-JUL-1998;
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08-FEB-2000,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A method for DNA analysis based on a complementary extension reaction using a DNA polymerase, comprises a combination of fragment walking and MNA sequencing. DNA fragments are formed by digestion of DNA with a restriction enzyme and the targeted DNA sequence can be determined directly from the digested DNA fragments. By exploring the overlapping sequence of the determined base sequence, the overall base sequence of a lengthy DNA can be determined with low redundancy without cloning or subcloning. In addition, the method can be done with commercially available universal primers or with fewer primers than required in existing methods. AAT73291-92 are primers used in determination of the
                                                                                                                                                                                                                                                                                              primer; PCR; polymerase chain reaction; sequencing; walking;
complementary extension reaction; low redundancy; universal primer; ss.
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                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pUC19 sequence. Primer extension was carried out using 16 primers AAT73293
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Pred. No. 6.18+02;
0; Mismatches 1; Indels
0.9%; Score 15.4; DB 1; Length 19;
14.1%; Pred. No. 5.9e+02;
ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 0 A; 2 C; 1 G; 15 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                 Primer for pUC19 DNA amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 23; 50pp; English.
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ID AAT73291 standard; DNA; 20 BP.
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96JP-00013634.
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                94.18;
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AAT73293 standard; DNA; 20
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                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kambara H, Okano K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HITA ) HITACHI LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-205424/19.
                Local Similarity
les 16; Conserv
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                                                                                                                                                                                                                                   12-DEC-1997
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                                                                                                                                                                                                                                                                                                                                           Synthetic.
 Query Match
Best Local Si
Matches 16;
                                                                                                                                                                                                    AAT73293;
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Length 18; 1; Indels

AAT73291;

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Efficient sequencing of long DNA by fragment walking - with simultaneous sequencing of restriction enzyme fragment and adjacent region of intact DNA, avoids the need for cloning and requires fewer primers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; heavy chain; sequencing primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Humanised anti-Fas antibody heavy chain primer, SEQ ID NO:94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 0.9%; Score 15.4; DB 1; Length 20; Local Similarity 94.1%; Pred. No. 6.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
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                                                                                                                                                                        (HITA ) HITACHI LTD.
                                                                                                                                                                                                                                                              WPI; 1997-205424/19.
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                                                             17-SEP-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-SEP-1999;
                                                                                                        18-SEP-1995;
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24-NOV-2000
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           09-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Efficient sequencing of long DNA by fragment walking - with simultaneous sequencing of restriction enzyme fragment and adjacent region of intact DNA, avoids the need for cloning and requires fewer primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A method for DNA analysis based on a complementary extension reaction using a DNA polymerase, comprises a combination of fragment walking and DNA sequencing. DNA fragments are formed by digestion of DNA with a restriction enzyme and the targeted DNA sequence can be determined directly from the digested DNA fragments. By exploring the overlapping sequence of the determined base sequence, the overlapping sequence of the determined with low redundancy without cloning or subcloning. In addition, the method can be done with commercially available universal primers or with fewer primers than required in existing methods. AT73291-92 are primers used in determination of the purch as a purch sequence out using 16 primers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer; PCR; polymerase chain reaction; sequencing; walking;
complementary extension reaction; low redundancy; universal primer; ss.
                                                                                                                                                 primer; PCR; polymerase chain reaction; sequencing; walking; complementary extension reaction; low redundancy; universal primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.9%; Score 15.4; DB 1; Length 20; 94.1%; Pred. No. 6.1e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 1 A; 2 C; 3 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer 2 for pUC19 DNA amplification.
                                                                                                        Primer 1 for pUC19 DNA amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 11; 50pp; English.
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                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-DEC-1997 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Okano K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HITA ) HITACHI LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-205424/19.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                    17-SEP-1996;
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30-JAN-1996;
                                                               12-DEC-1997
                                                                                                                                                                                                                                                              EP767240-A2
                                                                                                                                                                                                                                                                                                         09-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kambara H,
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Gaps

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98JP-00276883.

30-SEP-1998;

EP767240-A2

AAT73292

RESULT 950 AAT73292,

셤 ઠ

Matches

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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFB7A, or a humanised version of HFB7A containing identical CDFS (complementarity determining regions) to antibody HFB7A. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, actory, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephitis, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephitis, rejection. The present sequence represents a humanised HFB7A-derived antires antibody heavy chain sequencing primer used in an exemplification of the invention. (Updated on 15-SEP-2003 to standardise OS field)
                                                                                                                                                                              Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-Fas antibody; monoclonal antibody HFB7A; FERM-BP-5828; murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoincule disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AlDS; graft rejection; heavy chain; sequencing primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Humanised anti-Fas antibody heavy chain primer, SEQ ID NO:98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 5 A; 0 C; 11 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                       Example 15; Page 49; 139pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 TTAGGGGGGAAGAGAA 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA72168 standard; DNA; 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                 (SANY ) SANKYO CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
                                                                                                       WPI; 2000-485645/43.
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les 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JP2000169393-A.
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Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-SEP-1999;
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24-NOV-2000
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                                                                                                                                                                                                                                                    antibody.
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AAA72168/C
XX
AC AAA7210
XX
DT 15-SEP
DT 24-NOV.
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XX
C ALLI-F:
XW ALLI-F:
XW ALCI-F:
XW C CALCION
XW C CALCION
XX C CALCIO
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BP.

Gaps

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1; Indels

0.9%; Score 15.4; DB 1; Length 20; 44.1%; Pred. No. 6.1e+02; ve 0; Mismatches 1; Indels

94.1%;

Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas

98JP-00276883

30-SEP-1998;

(SANY ) SANKYO CO LTD.

WPI; 2000-485645/43.

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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFB7A, or a humanised version of HFB7A containing identical CDRs (complementarity determining regions) to antibody HFB7A. Via its interaction with Fas, the antibody of the invention may therefore be used in the treatment or prevention of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephitis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. The present sequencing primer used in an exemplification of the antibody heavy chain sequencing primer used in an exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to the use of a compound comprising an amino acid sequence His-Phe-Arg-Trp (HFRW) in the manufacture of a medicament and/or an agonist of melanocortin receptor type 3 (MC3-R) where the compound is not adrenocorticotrophic hormone (ACTH) 1-39. The compounds are used to inhibit neutrophil chemoattractant production, polymorphomuclear cell (PMN) accumulation or reduction/treatment of inflammation. Especially,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Medicament; agonist; melanocortin receptor type 3; ACTH; PMN; MC3-R; adreancocritocrophic hormone; neutrophil chemoattractant; antigout; polymorphonuclear cell; septic shock; skin disorder; antiarthritic; melanocortin receptor; anti-inflammatory; antiasmatic; PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibition of neutrophil chemoattractant production, inhibition of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polymorphonuclear cell accumulation or reduction/treatment of inflammation using compounds comprising the peptide sequence HFRW
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                                                                                                                                                                                                                                                                                                                                       -Fas antibody heavy chain sequencing primer used in an exemplif
the invention. (Updated on 15-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                       0.9%; Score 15.4; DB 1; Length 20;
44.1%; Pred. No. 6.1e+02;
ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine melanocortin receptor MC3-R amplifying primer.
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 4 A; 11 C; 0 G; 5 T; 0 U; 0 Other;
                                         Example 15; Page 49; 139pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Getting S, Flower R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 8; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HARV-) HARVEY RES LTD WILLIAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 TTAGGGGGGAAGAGAA 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 Similarity 94.1%;
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZS7075 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 TTTGGGGGGAAGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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Matches 16; Conserv
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  antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, anti-allergic, anti-arthritic, antiviral, antirheumatic, nephrotropic, inmunosuppressive, thyronimetic, antirheumatic, nephrotropic, antiinfertility, neuroprotective, antiatreriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems.
these compounds are agonists of the MC3-R. The inflammatory response/disease is selected from gout, gouty arthritis, rheumatoid arthritis, asthma, reperfusion injury or damage, stroke, myocardial infarction, septic shock, or a skin disorder. Sequences AAZ57073-80 represent PCR primers used for amplifying murine melanocortin receptors
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takahashi T;
                                                                                                                                                              0.9%; Score 15.4; DB 1; Length 20; 94.1%; Pred. No. 6.1e+02; ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humanised HFE7A designed heavy chain DNA primer #5.
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                                                                                                                          Sequence 20 BP; 0 A; 7 C; 4 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example reference 15; Page 137; 263pp; English.
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                                                                                                                                                                                                                                               1689 CTGTCTTCTCTCC 1705
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                                                                                                                                                                                                                                                                                                                                                                                           AAA11602 standard; DNA; 20 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-AUG-2000 (first entry)
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                                                                                                                                                                                                         16; Conservative
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                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA11602;
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inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, Goodpasture syndrome, Crohn's multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, atteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they minic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents primer used in the construction of a humanised anti-Fas antibody HFE7A ö Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; dernatiological; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; aterility; myasthenia gravis; multiple sclerosis; basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection; New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems. Gaps ö Takahashi T; 0.9%; Score 15.4; DB 1; Length 20; 94.1%; Pred. No. 6.1e+02; lve 0; Mismatches 1; Indels Humanised HFE7A designed heavy chain DNA primer #9. Sequence 20 BP; 5 A; 0 C; 11 G; 4 T; 0 U; 0 Other; Tamaki I, Serizawa N, Haruyama H, Nakahara K, 21 TTAGGGGGGAAGAGAA 37 3 TTTGGGGGGAAGAGAA 19 AAA11606 standard; DNA; 20 BP 99EP-00307711. 94.18; 98JP-00276881 98JP-00276882 (first entry) 16; Conservative (SANY ) SANKYO CO LID. Local Similarity WPI; 2000-258930/23. 39-SEP-1999; 30-SEP-1998; 08-AUG-2000 05-APR-2000. 3P990663-A2 primer; ss. Synthetic. invention AAA11606; Query Match RESULT 955 Matches AAA11606/ ð 셤 

Example reference 15; Page 138; 263pp; English. Query Match Matches Š g

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The superior is described a novel numanized anti-Fras antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cells with an abnormal Fas/Fas ligand system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-arterior, anti-arthritic, anti-inflammatory, anti-arthritic, anti-arthritic, anti-inflammatory, anti-arthritic, anti-arthritic, anti-inflammatory, anti-arteriors anti-arthritic, anti-arthritic, anti-inflammatory, anti-arthritic, anti-inflammatory, anti-arteriors anti-arteriors cardiant and hepatropic activity. (I) induce anti-arteriors of ligand binding (I) are used to treat and/or prevent chiesases associated with the Fas/Fas ligand system, especially systemic diseases associated with the Fas/Fas ligand system, especially systemic contents, has himmoto disease, remarcious or hypoplastic canomia, Addison's disease, solorgen's syndrome, pernicious or hypoplastic canomia, Addison's disease, solorgen's syndrome, pernicious or hypoplastic canomia, Addison's disease, solorgen's syndrome, pernicious or hypoplastic canomia, Addison's disease, solorgen's syndrome, sterility, myasthenia gravia, canomia, Addison's disease, solorgen's disease, solorgen's short anti-arteriors and transplant rejection. (I) selectively induced abettes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepaticis (fulminant, chronic, viral CC inhibit apoptosis in normal cells but selectively induce it in abnormal cells appeaded models. (I) act on the active site of Fas, i.e. they mimic cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic cells. They bind to both human anti-murine antibody these conformation of a human anti-murine antibody areasons. This sequence represents conformation and the active site of fas antibody h
This invention describes a novel humanized anti-Fas antibody-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention
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Score 15.4; DB 1; Length 20; Pred. No. 6.1e+02; 0; Mismatches 1; Indels Sequence 20 BP; 4 A; 11 C; 0 G; 5 T; 0 U; 0 Other; ö 0.9%; Local Similarity 94.1%; hes 16; Conservative (

ABL48724 standard; DNA; 20 30-APR-2002 (first entry) ABL48724;

BP.

Humanised anti-Fas antibody related PCR primer SEQ ID NO 62.

heavy chain; apoptosis; antiallergic; immunosuppressive; apoptotic; autoimmune disease; allergy; atopy; PCR primer; ss. Human; mouse; Fas/Fas ligand system; Fas; antibody; light chain;

Synthetic.

JP2001342149-A.

11-DEC-2001.

28-MAR-2001; 2001JP-00093243.

29-MAR-2000; 2000JP-00091144.

(SANY ) SANKYO CO LTD.

Drug for preventing or treating e.g. autoimmune disease or allergy, comprises humanized anti-Fas antibody. WPI; 2002-145114/19.

ö The invention relates to a preventive or treating agent for diseases caused by abnormality in the Fas/Fas ligand system containing, as the active component, an antibody having a light chain subunit and a heavy chain subunit and an activity of combining specifically with mammalian Fas and an activity of inducing apoptosis in a cell expressing Fas. The agent has antiallergic, immunosuppressive and apoptotic activity and is used for preventing and treating autoimmune diseases, allergy, atopy and others. The present sequence is that of a PCR primer useful in the construction of anti-Pas antibodies of the invention Gaps ö 0.9%; Score 15.4; DB 1; Length 20; 94.1%; Pred. No. 6.1e+02; ive 0; Mismatches 1; Indels Example 14 (preparatory); Раде 32; 154pp; Japaneве. Sequence 20 BP; 5 A; 0 C; 11 G; 4 T; 0 U; 0 Other; 21 TTAGGGGGGAAGAGAA 37 3 TTTGGGGGAAGAGGAA 19 ABL48728 standard; DNA; 20 BP. 94.18; Local Similarity 94.1 les 16; Conservative Query Match ABL48728; Best Loca Matches RESULT 957 ABL48728/c \$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac{1}{2}\$\frac ઠે 셤

Human; mouse; Fas/Fas ligand system; Fas; antibody; light chain; heavy chain; apoptosis; antiallergic; immunosuppressive; apoptotic; autoimmune disease; allergy; atopy; PCR primer; ss.

Humanised anti-Fas antibody related PCR primer SEQ ID NO 66.

(first entry)

30-APR-2002

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Gaps

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JP2001342149-A.

11-DEC-2001

28-MAR-2001; 2001JP-00093243.

29-MAR-2000; 2000JP-00091144.

(SANY ) SANKYO CO LTD

WPI; 2002-145114/19.

Drug for preventing or treating e.g. autoimmune disease or allergy, comprises humanized anti-Fas antibody.

Example 14 (preparatory); Page 32; 154pp; Japanese.

Fas and an activity of inducing apoptosis in a cell expressing Fas. The agent has antiallergic, immunosuppressive and apoptotic activity and is used for preventing and treating autoimmune diseases, allergy, atopy and others. The present sequence is that of a PCR primer useful in the construction of anti-Fas antibodies of the invention The invention relates to a preventive or treating agent for diseases caused by abnormality in the Fasd/Fas ligand system containing, as the active component, an antibody having a light chain subunit and a heavy chain subunit and an activity of combining specifically with mammalian

Sequence 20 BP; 4 A; 11 C; 0 G; 5 T; 0 U; 0 Other;

Gaps . 0 Query Match 0.9%; Score 15.4; DB 1; Length 20; Best Local Similarity 94.1%; Pred. No. 6.1e+02; Matches 16; Conservative 0; Mismatches 1; Indels

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**ABA05917** 

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The invention relates to a preventive or treating agent for diseases caused by abnormality in Fas/Fas ligand system containing as the active component an antibody having as the light chain subunit a polypeptide containing residues 1-218 of one of 3, 239 residue amino acid sequences, or residues 1-451 of one of 3, 470 residue amino acid sequences, all fully defined in the specification and having an activity of combining specifically with mammalian Fas and an activity of inducing apoptosis in a cell expressing Fas. The agent has immunosuppressive and antialergic activity and is used for preventing and treating autoimmune diseases, allergy, atopy and others. The present sequence is that of a PCR primer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drug containing humanized anti-Fas antibody, used for preventing and treating autoimmune diseases, allergy, and atopy.
                                                                                                                                                                                                                                                                              Drug containing humanized anti-Fas antibody, used for preventing and treating autoimmune diseases, allergy, and atopy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;
light chain subunit; apoptosis; immunosuppressive; antiallergic;
autoimmune disease; allergy; atopic; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.9%; Score 15.4; DB 1; Length 20;
34.1%; Pred. No. 6.1e+02;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Humanised anti-Fas antibody related PCR primer SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 5 A; 0 C; 11 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                             Example 4 (Preparatory); Page 23; 194pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 TTAGGGGGAAGAGAA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTGGGGGGAAGAGGAA 19
                                                                                                                      28-MAR-2001; 2001JP-00093106.
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                                                                                                                                                              29-MAR-2000; 2000JP-00090918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 Similarity 94.1%;
16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful to the invention
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                                                                                                                                                                                                                                            WPI; 2002-145113/19.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JP2001342148-A.
                                          JP2001342148-A.
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                                                                                11-DEC-2001
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diagnosing hepatitis B virus (HBV) infection stages and determining the risk for hepatocellular carcinoma, comprises identifying full length HBV transcripts and truncated HBV transcripts in a serum sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to diagnosis of hepatitis B virus (HBV) infection stages comprising identification of full length HBV transcripts (I) and truncated HBV transcripts (II) in a serum sample, where the ratio of I:I is indicative of a particular infection stage. The method is useful for diagnosing HBV infection stages and determining the risk for developing hepatocellular carcinoma. The present sequence is that of a HBV diagnostic PCR primer, useful for the invention
                                                                                                                                                                                                                                                                                                       Hepatitis B virus, HBV, infection, hepatocellular carcinoma, diagnosis, PCR primer; ss.
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light chain subunit; apoptosis; immunosuppressive; antiallergic;
autoimmune disease; allergy; atopic; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.9%; Score 15.4; DB 1; Length 20;
44.1%; Pred. No. 6.1e+02;
ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                   Hepatitis B virus diagnostic PCR primer SEQ ID NO 7.
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    TTAGGGGGGAAGAGGAA 37
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                                          TTTGGGGGGAAGAGAA
                                                                                                                                           ABA05917 standard; DNA; 20
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                                                                                                                                                                                                                           (first entry)
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Hes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Koike K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-068256/10.
                                                                                                                                                                                                                                                                                                                                                                     Hepatitis B virus.
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                                                                                                                                                                                                                                                                                                                                                                                                               EP1152063-A1
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    21
                                          18
                                                                                                                                                                                   ABA05917;
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Matches
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ABL45981

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Gaps

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WO200285308-A2 31-OCT-2002. Matches ò 셤

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The invention relates to a preventive or treating agent for diseases caused by abnormality in Fas/Fas ligand system containing as the active component an antibody having as the light chain subunit a polymeptide containing residues 1-218 of one of 3, 39 residue amino acid sequences, or residues 1-451 of one of 3, 470 residue amino acid sequences, all fully defined in the specification and having an activity of combining specifically with mammalian Fas and an activity of inducing apoptosis in a cell expressing Fas. The agent has immunosuppressive and antiallargic activity and is used for preventing and treating autoimmune diseases, allegy, atopy and others. The present sequence is that of a PCR primer,
                                                                                                                                                                                                                                                                                                                                                                                                Length 20;
Example 5 (Preparatory); Page 25; 194pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 4 A; 11 C; 0 G; S T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                              Score 15.4; DB 1;
Pred. No. 6.1e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                0.9%;
                                                                                                                                                                                                                                                                                                  to the invention
                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                           allergy,
useful to
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ö 1; Indels ö ~ 18 TTTGGGGGGAAGAGAA 21 TTAGGGGGGAAGAGAA 16; Conservative

ABZ89489 standard; DNA; 20 17-OCT-2003 (first entry) ABZ89489;

BP

antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; Human; antisense; lung dysfunction; nasal airway dysfunction; lung inflammation; respiratory disease; ds. Human oligonucleotide sequence

Homo sapiens.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC

Katz E, Pabalan J, Aguilar D; Li Y, Sandrasagra A, Ka Tang L, Shahabuddin S; Nyce JW, I Miller S,

WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

Disclosure; SEQ ID NO 4731; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention

immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO has antiinflammatory, antiallergic, antiasthmatic, hypotensive, ftp.wipo.int/pub/published\_pct\_sequences 

Sequence 20 BP; 16 A; 2 C; 0 G; 2 T; 0 U; 0 Other;

Gaps ö Similarity 94.1%; Pred. No. 6.1e+02; 16; Conservative 0; Mismatches 1; Indels 16; Query Match Local Matches

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Gaps

RESULT 962 ABZ99051

ВР ABZ99051 standard; DNA; 20 (first entry) 17-OCT-2003 ABZ99051;

Human PDE4C oligonucleotide sequence.

Human, antisense, lung dysfunction, nasal airway dysfunction, antiinflammatory; antiallergic; antiathammatory, antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds 

sapiens. Homo

WO200285308-A2.

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC.

Pabalan J, Aguilar D; Katz E, ŝ ii Y, Sandrasagra A, Tang L, Shahabuddin Li Y, Miller S, Nyce JW,

WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

Disclosure; SEQ ID NO 14293; 872pp; English.

composition, which has a The invention relates to a novel pharmaceutical composition, which has first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention

Gaps

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immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung allargies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides the protein and coding sequences of a Class II cytokine receptor, designated LICR-2. Two splice variants of this sequence are given. The nucleic acid molecules, proteins and methods are useful for treating autoimmune diseases such as multiple sclerosis, inflammatory bowel disease, rheumatoid arthritis, type I and type II diabetes, allergies and asthma. The present sequence is a PCR primer used to isolate the human IL-22BP gene, also known as LICR-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New LICR-2 nucleic acid molecule encoding a cytokine receptor useful f
treating autoimmune diseases such as multiple sclerosis, inflammatory
bowel disease, rheumatoid arthritis, type I and type II diabetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; IL-22BP; chromosome 1; LICR-2; STAT activation; Class II; cytokine receptor; nootropic; antiinflammatory; antiirheumatic; antiarthritic; antidiabetic; antiallergic; antiathmatic; diabetes; autoimmune disease; multiple sclerosis; inflammatory bowel disease;
       antiallergic, antiasthmatic, hypotensive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.9%; Score 15.4; DB 1; Length 20; 94.1%; Pred. No. 6.1e+02; ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rheumatoid arthritis; allergy; asthma; PCR; primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20 BP; 2 A; 1 C; 2 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 20 BP; 4 A; 6 C; 9 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human IL-22BP coding sequence PCR primer #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Page 4; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1735 CAAAAAAAAAAAAAA 1751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 CAAAAAAGAAAAAAA 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-DEC-2001; 2001US-00026106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACF04183 standard; DNA; 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 94.1
Matches 16; Conservative
   antiinflammatory,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              allergies and asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-587107/55.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta and; or (X)m5'-(gamma) k-delta-N3'; owere X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, guanine or cytosine; N = adenine, guanine or thymine; famma = thymine; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1;3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptides having at least two new nucleotides – useful as primers in RT-
                                                                                                                                                                                                                                                                                        RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
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93.8%; Pred. No. 5.8e+02;
ive 1; Mismatches 0; Indels
                               1; Indels
Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;
Score 15.4; DB 1;
Pred. No. 6.1e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                           RT-PCR primer of the invention SEQ ID 29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 12; 19pp; Japanese.
                                                          155 AGGCCATGTCGGGGCCC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1735 CAAAAAAAAAAAAA 1750
                                                                                   AGGCCATGGCGGGCCC 18
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                                                                                                                                                                 AAX18388 standard; DNA; 17 BP
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ch 0.9%;
l Similarity 94.1%;
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TAKI ) TAKARA SHUZO CO LTD
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                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-183822/16
 Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                18-JUL-1997;
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                                                                                                                                                                                                                                                                                                                       Synthetic.
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ID AAS1
XX
AC AAS1
XX
DT 18-DI
XX
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The invention relates to a probe set for gene expression arrays to provide common equivalent signalling per probe and global amplification of the set. The probe set has a pool of modified cDNA probes, each probe having a central target specific segment copied from a portion of a single mRNA transcript and a universal linker (a WRAP-Probe) located on one or both terminal ends. The universal linker has reporter binding eites to join common reporters to the probes and primer binding sites to copy and amplify the probe. The probes and reporters are useful in diagnostic or drug discovery assays for a wide range of biomedical cappanes, including detection of nucleic acids and gene expression profiles in human diagnostics, forensics and genomic analysis. The methods are useful for amplifying and identifying any unknown DNA fragment and also for improving sensitivity with tissue microarrays or kny arrays. The methods improve the quantification of gene expression and allow highly improved detection of rare transcripts or very small samples. This sequence represents a poly-T primer used in the
                                         WRAP-Probe; gene expression array; global amplification; RNA array; ss; tissue microarray; drug discovery assay; reporter binding site; forensic; diagnostic; genomic analysis; universal linker; poly-T primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel probe sets with common universal linkers at one or both ends (WRAP probes) for gene expression arrays to provide global amplification of probe set and to provide common equivalent signaling regardless of
Modified Poly-T Primer #1 used in construction of probe sets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 88; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                          (GENE-) GENETAG TECHNOLOGY INC
                                                                                                                                                                                                                                                                       09-MAR-2001; 2001WO-US007508.
                                                                                                                                                                                                                                                                                                              09-MAR-2000; 2000US-0187982P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             construction of probe sets
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-596845/67
                                                                                                                                                                               WO200166802-A1
                                                                                                                                                                                                                           13-SEP-2001
                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                      Shafer DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             length.
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Gaps

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Query Match 0.9%; Score 15.2; DB 1; Length 20; Best Local Similarity 85.0%; Pred. No. 6.5e+02; Matches 17; Conservative 0; Mismatches 3; Indels

1000, GGCTGCGGAGAGATGTGGT 1019 1 GTCTGCGGAGATGATTTGGT 20

Matches

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Sequence 20 BP; 3 A; 2 C; 8 G; 7 T; 0 U; 0 Other;

samples

Detection of type C hepatitis virus - using one step DNA polymerase chain reaction with mixed primer set.

92JP-00168226 92JP-00168226,

04-JUN-1992; 04-JUN-1992;

21-DEC-1993,

JP05337000-A.

Claim 2; Page 2; 7pp; Japanese

WPI; 1994-037380/05.

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(SAYA/) SAYAMA

The primers (AAQ55811-841) are used to detect various types of hepatitis of virus. The primers are made from oligo DNA fragments selected from specific hepatitis C virus subtypes. The primers can be used to in a one step PCR reaction which can determine the subtypes of a large number of

ö Gaps ö 0.9%; Score 15.2; DB 1; Length 17; 93.8%; Pred. No. 5.8e+02; tive 1; Mismatches 0; Indels HCV detection primer (DNA type 4 SS3). 1735 CAAAAAAAAAAAAA 1750 AAQ55833 standard; DNA; 20 21-JUL-1994 (first entry) ВААААААААААА 15; Conservative Best Local Similarity Matches 15; Conserv 16 AAQ55833;

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HCV; hepatitis C virus; detection; primer; PCR; mixer primer set; polymerase chain reaction; DNA polymerase; ss.

Synthetic

ģ Sequences were determined from the ends of chromosome 11-specific cosmids by automated sequencing without intermediate subcloning. A sample of 371 Sequencing complex genomes, present as fragments in a cosmid library - b sequencing end-specific nuclectides of each clone then correlating with spatial relationship of cosmid, esp. for mammalian chromosomes. sequence sampled mapping; genomic analysis; complex genome mapping; cosmid library; chromosome 11; sequence tagged site; STS analysis; ss. Chromosome 11 (locus D11S1113) STS primer cSRL-4b4-tA. (SALK ) SALK INST BIOLOGICAL STUDIES. Example 4; Page 73; 128pp; English. BP 94WO-US006810. 93US-00078471 93US-00117952 AAQ82253 standard; DNA; 20 (revised)
(first entry) Smith MW; WPI; 1995-036508/05. .5-JUN-1994; 5-JUN-1993; 25-MAR-2003 07-SEP-1995 WO9429486-A1 07-SEP-1993; Synthetic. Evans GA, AAQ82253; RESULT 967 

and

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Anti-sense polynucleotide complementary to VEGF sequence - inhibit growth factor expression and are used for diagnosis and treatment of cancer and
DNA sequence fragments were determined and of these, 277 were suitable for STS primer prediction by computer analysis (using the "Primer" program available from E.Lander, MIT). The STSs and cosmids were mapped by in situ hybridisation, sometic cell hybrid analysis or both. Using this method, 370 STSs specific for human chromosome 11 were generated an most of them were regionally mapped. This procedure illustrates a novel method for sequencing complex, genomes, designated "sequence sampled mapping". The sequence sampled mapping method is useful for the completion of high density sequence-based maps, and ultimately, for the complete sequencing of genomic DNA directly from cosmid clones. See AAQ82001-082706 for STS primers. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vascular endothelial growth factor; VEGF; antisense oligonucleotide;
therapy; abnormal angiogenesis; cancer; rheumatoid arthritis; diabetes;
                                                                                                                                                                                                                                                        Gaps
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0
                                                                                                                                                                                                                        Score 15.2; DB 1; Length 20;
Pred. No. 6.5e+02;
                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                            Seguence 20 BP; 2 A; 9 C; 2 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence #1 used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matsuda Y,
                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 45; 66pp; Japanese.
                                                                                                                                                                                                                                                                                   914 CAGAGGATGAGCTGGATAGG 933
                                                                                                                                                                                                                                                                                                       CAGAAGGTGAGCTGGAAAGG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tanaka Y,
                                                                                                                                                                                                                                                                                                                                                                                    AAT10129 standard; DNA; 20 BP
                                                                                                                                                                                                                         0.98;
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94JP-00311130.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-068870/07.
                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Uchida K,
                                                                                                                                                                                                                                                                                                                                                                                                                   AAT10129;
                                                                                                                                                               field.)
                                                                                                                                                                                                                                                                                                                                                           RESULT 968
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AAT10129 and AAT10130 represent oligonucleotides used within the invention. These sequences were used to determine the antisense oligonucleotides of the invention (see AAT10121-T10128). These sequences are antisense oligonucleotides complementary to at least 8 consecutive nucleotides of the vascular endothelial growth factor (VEGF) gene (see AAT10120). These antisense sequences inhibit the expression of VEGF to below 30% of normal expression. The antisense oligonucleotides may be used in diagnosis and treatment of diseases involving VEGF expression and associated abnormal angiogenesis, such as cancer, rheumatoid arthritis

Seguence 20 BP; 17 A; 3 C; 0 G; 0 T; 0 U; 0 Other;

and diabetes

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primers shown in AAT1844-55 were used for reverse transcriptase-
polymerase chain reaction (RT-PCR) analysis of interleukin-1-beta
converting enzyme (ICE) -/- mice, to show that they do not express full-
length ICE mRNA transcripts. Using a 5' primer specific for exon 2 and a
series of 3' primers specific for each consecutive exon upto exon 10,
colly transcripts contgo. exons 2-5 were detected in ICE -/- animals. A 5'
primers specific for the neomycin gene and a series of 3' primers specific
for the neomycin gene and a series of 4'- animals.
Continies specific for the neomycin gene and a series of 4'- animals.
Continies specific for the neogene detected a transcript in ICE +/- and -/-
but not +/+ animals. The results of RT-PCR analyses and Northern
hybridisation confirmed that homozygous disruption of the ICE gene
cresults in an absence of detectable full-length ICE mRNA transcripts in
the ICE -/- mice. ICE deficient mice are useful as positive controls to
evaluate the efficacy of ICE inhibitors and to identify disease
conditions that can be treated with ICE inhibitors. Transgenic non-human
animals having functionally disrupted endogenous ICE genes but which has
been reconstituted with human ICE gene can be used to identify agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transgenic animal with disrupted interleukin-1-beta converting enzyme - used to identify ICE inhibitors or disease conditions treatable with ICE inhibitors.
                                                                                                                                                                                                                                                                                                                                                CE, interleukin-1-beta converting enzyme; inhibitor; transgenic; mice;
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                       ö
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85.0%; Pred. No. 6.5e+02;
iive 0; Mismatches 3; Indels
 Length 20;
                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                 functional disruption; primer; RT-PCR; analysis; reverse transcriptase-polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Paskind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 7 A; 4 C; 8 G; 1 T; 0 U; 0 Other;
Score 15.2; DB 1;
Pred. No. 6.5e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Banerjee S,
                                                                         1736 AAAAAAAAAAAAAAAAA 1755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Page 19; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             820 CCAGGGCCAAAGAGGAAGC 839
                                                                                                            1 AAAAAACAAAAACAACAAA 20
                                                                                                                                                                                                    ВЪ.
                                                                                                                                                                                                                                                                                                             5' primer based on ICE exon 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95WO-US012837.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Allen H,
 0.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-00323490
                                                                                                                                                                                                    AAT18444 standard; DNA; 20
                                                                                                                                                                                                                                                                         10-DEC-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 85.0
Matches 17; Conservative
                                         17; Conservative
   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-222010/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seshadri T, Li P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BADI ) BASF AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9612025-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                        AAT18444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQuery Match
                                                                                                                                                                    RESULT 969
                                         Matches
                                                                                                                                                                                   AAT18444
ID AAT3
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1 CCTGAGGGCAAAGAGGAAGC 20

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AAT97419;

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A method has been developed for detecting the presence of a target site (TS), of at least one nucleotide (nt) in a nucleic acid (NA). The method comprises (a) forming an oligonuclectide (ON), consisting of two fluorophores (F1, F2) each covalently linked to separate nt, bound to TS; and (b) detecting fluorescence energy transfer (FET) between F1 and F2 when ON is released from TS. The present sequence represents a synthetic polynuclectide used in an example of the present invention. The method is used to diagnose hereditary and other diseases; to determine infectious agents; in tissue typing for histocompatibility; in forensic identification and paternity testing, and in monitoring the genetic make up of plants and animals. Specifically it is used to detect single nt polymorphisms. The method provides inexpensive, simple, accurate and automatable nucleic acid analyses
                                                                                                                                                                                                                                                                                                                                                                       Detection; target site; nucleic acid; fluorophore; labelled; fluorescent; inherited disease; tissue typing; PCR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting target site in nucleic acid by forming a fluorophore-labelled oligonucleotide at the site - and detecting fluorescent energy following denaturation, used e.g. to detect inherited diseases, in tissue typing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.9%; Score 15.2; DB 1; Length 20;
85.0%; Pred. No. 6.5e+02;
vative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                        Oligomer 814102 Common probe from WO9722719 Example 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/note= "Labelled with fluorescein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 5 A; 0 C; 2 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1729 AGTTTACAAAAAAAAAAA 1748
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                       AAT97431/C

ID AAT97431/C

AAT97431/C

AAT97431/C

AAT97431/C

AAT97431;

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AAT97431;

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AAT97431;

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AAT97431;

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Oligomer s14102 Common probe for the fine typic for the fine for fine for the fine for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96WO-US020379
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AAT97419/c
ID AAT974
XX
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RESULT 970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
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A method has been developed for detecting the presence of a target site (TS), of at least one nucleotide (nt) in a nucleic acid (NA). The method comprises: (a) forming an oligonucleotide (ON), consisting of two fluorophores (F1, F2) each covalently linked to separate nt, bound to TS; and (b) detecting fluorescence energy transfer (FET) between F1 and F2 when ON is released from TS. The present sequence represents a synthetic polynucleotide used in an example of the present invention. The method is used to diagnose hereditary and other diseases; to determine infectious agents; in tissue typing for histocompatibility; in forensic identification and paternity testing, and in monitoring the genetic make up of plants and animals Specifically it is used to detect single nt polymorphisms. The method provides inexpensive, simple, accurate and automatable nucleic acid analyses
                                                                                                Detection, target site, nucleic acid, fluorophore, labelled, fluorescent, inherited disease, tissue typing, PCR, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting target site in nucleic acid by forming a fluorophore-labelled oligonuclectide at the site - and detecting fluorescent energy following denaturation, used e.g. to detect inherited diseases, in tissue typing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Microorganism inhibitor; antisense; nuclease resistant; treatment; ribonucleotide reductase; secA gene; pathological condition; R1 subunit; antimicrobial agent; crop protection; primer; R2 subunit; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.9%; Score 15.2; DB 1; Length 20;
85.0%; Pred. No. 6.5e+02;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 5 A; 0 C; 2 G; 13 T; 0 U; 0 Other;
                                                              Donor Sequence oligomer from WO9722719 Example 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E. coli K12 R1 antisense oligonucleotide 59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1729 AGTTTACAAAAAAAAAAA 1748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 6; Page 46; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 ATTTTACAAAAATAAACAA 1
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                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         al Similarity 85.0
17; Conservative
                                                                                                                                                                                                                                                                                                                         (UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-341707/31.
                                                                                                                                                                                                                                                                                                                                                           Chen X;
                                                                                                                                                                                     WO9722719-A1
                                                                                                                                                                                                                                                       17-DEC-1996;
                                                                                                                                                                                                                                                                                         18-DEC-1995;
                                14-APR-1998
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                                                                                                                                                                                                                     26-JUN-1997.
                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX38359;
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Best Local S
                                                                                                                                                                                                                                                                                                                                                           Kwok P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 972
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Gaps

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Escherichia coli.

Synthetic

Mon Aug 16 16:46:36 2004

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-NUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Valenzuela
                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                           AAZ43822;
                                                                                                                                                                                           Query Match
                                                                                                                                                          probes
                                                                                                                                                                                                                                                                         974
                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                  AAZ43822
                                                                                                                                                                                                                                                                         RESULT
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                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                  X38552) which are nuclease resistant, and comprises about 3-50 nucleotides complementary to the ribonucleotide reductase gene or the secA gene of a microorganism. The antisense oligonucleotides are used to treat mammalian pathological conditions mediated by microorganisms. The oligonucleotides are particularly useful as antimicrobial agents in crop
                                                                                                                                                                                                                                                                                                                                                                                                                                 TANGO 125; T125; alternative splice variant; EGF domain; antibody; secreted protein; agonist; antagonist; predictive medicine; treatment; forensic biology; PCR primer; ss.
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polynuclectides and polypeptides used to modulate a variety of cellular processes.
                                                                                                                                                                         This invention describes novel antisense oligonucleotides (AAX38301-
                                                                                                                                ဌ
                                                                                                                                - useful
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                                                                                                                                                                                                                                                             0.9%; Score 15.2; DB 1; Length 20; 85.0%; Pred. No. 6.5e+02; ative 0; Mismatches 3; Indels
                                                                                                                              RR or SecA genes
                                                                                                                                                                                                                                                                                                                                                                                                                 Primer used for amplifying human TANGO 125 (T125) gene.
                                                                                                                                                                                                                                              Seguence 20 BP; 5 A; 4 C; 8 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
                                                                                                                              New oligonucleotides complementary to
                                                                                                                                                        Disclosure; Page 18; 103pp; English,
                                                                           (GENE-) GENESENSE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                  1204 CGGATCCTGCGGCTATGGG 1223
                                                                                              Dugourd D;
                                                                                                                                        Inhibit growth of microorganisms
                                                                                                                                                                                                                                                                                                                  cedarcaaaceeecrareee 20
                                                                                                                                                                                                                                                                                                                                                             AAZ37137 standard; cDNA; 20 BP.
                                          98WO-CA000666
                                                           97US-0052160P
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99US-00298531
                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                 17; Conservative
                                                                                             Young AH,
                                                                                                             WPI; 1999-120874/10.
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                                                                                                                                                                                                                                                                         Best Local Similarity
        WO9902673-A2
                                          10-JUL-1998;
                                                           10-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9954437-A2
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23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Holtzman DA;
                         21-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-OCT-1999
                                                                                              Wright JA,
                                                                                                                                                                                                                                                                                                                                                                               AAZ37137;
                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                          RESULT 973
AAZ37137/C
                                                                                                                                                                                                                                                                                 Matches
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PCR primers AA237136-237137 are used to amplify the TANGO 125 (T125) gene PCR primers AA237136-237137 are used to amplify the TANGO 125 (T125) gene (AA237131). The T125 procein has two epidermal growth factor (EGF)-like domains at amino acids 107-134 and 141-176 and is predicted to have a molecular weight of approximately 30kD. T125 is predicted to have a caretaclar weight of approximately 30kD. T125 is predicted to have no transmembrane domains and appears to be a secreted protein. There are three alternatively spliced forms of T125: T125b and T125c and T125c (AA237132-237135). The sequences of all variants of T125 are used in the invention to create antibodise which selectively bind to T125. The T125 polypeptide is used to modulate a variety of cellular processes. It can broduce antibodies, and to identify T125 antagonists and agonists. The T125 polymucleotides, polypeptides, homologues and antibodies can be used to recenting assays; predictive medicine; and methods of treatment of the separation associated disorders. The T125 polymucleotides can be used to express the protein; to detect T125 mRNA; to detect genetic alterations in the T125 gene; in forensic biology; and as a source of primers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted protein; treatment; nutritional activity; cytokine;
cell prollferation; cell differentiation; hematopoleals regulation;
tissue growth; activin; inhibin; chemotactic; chemokinetic; hemostatic;
thrombolytic; anti-inflammatory; invasion suppressor; tumor inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20 BP; 2 A; 9 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15.2; DB 1;
Pred. No. 6.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human fetal brain cDNA clone vc10_1 DNA probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       на11 Ј,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
Disclosure; Page 22; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hoffman H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        681 GGCACAGCCAGTGAGGGGCT 700
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98US-0088994P.
98US-0089278P.
98US-0091647P.
98US-0097639P.
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Local Similarity 85.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALPH-) ALPHAGENE INC.
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Disclosure, Page 267; 282pp, English.

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This invention describes novel human secreted proteins which are encoded by polynucleotides obtained from fetal brain, adult skin, adult thymus and adult acrta cDNA libraries. The adult thymus and adult acrta cDNA libraries. The polynucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, hematopoisesis regulating activity, chemotactic/chemokinetic activity, hemostatic and thrombolytic activity, chemotactic/chemokinetic activity, hemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumor invasion suppressor activity, and tumor inhibition activity. The polynucleotides are also stated to be useful for gene therapy. AAZ43809-represented in AAX43777-z43808 which encode the secreted proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liver glycogen phosphorylase; PYGL gene; human; chromosome 14; 1,4-alpha-D-glucan:orthophosphate alpha-D-glucosyltransferase; HGLPa; glycogenolysis; carbohydrate metabolism; blood glucose homeostasis; expression inhibition; hypoglycaemic; type II diabetes; non insulin-dependent; antisense; phosphorothioate; ss.
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nes 17; Conservative
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/\*tag= a /note= "Phosphorothioate linkages"

99US-00357071. 99US-00357071. Claim 3; Col 39; 33pp; English

glycogen phosphorylase.

Monia BP, Cowsert LM; WPI; 2000-270346/23.

Location/Qualifiers

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0.9%; Score 15.2; DB 1; Length 20; 85.0%; Pred. No. 6.5e+02; tive 0; Mismatches 3; Indels

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Sequences Analysis and the september of the antiense controlled the sequences of the sequen
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                           Sequences AAA14008-A14047 represent phosphorothioate antisense
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphorylase expression, such as type II diabetes
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98US-0109732P.
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Best Local Similarity 85.0
Matches 17; Conservative
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            AAZ65654 to AAZ69578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ7440 represent amplification primers for the biallelic markers. The biallelic markers of the invention bave a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and disgnostic methods, as well as the characteriation of the differential efficacious responses to and side effects from the differential efficacious responses to and side effects from him secting on a disease as well as other treatment.

N. B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3056, 3157, 3237, 3297 and 3367, are not actually given a sequence in the Sequence Listing from the
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.9%; Score 15.2; DB 1; Length 20; Best Local Similarity 85.0%; Pred. No. 6.5e+02; Matches 17; Conservative 0; Mismatches 3; Indels
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ID AAZ75831 standard; DNA; 20
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                                                                                                                                                                                                                                                                                                           present invention
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Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and disgnostic methods, as well as the characterisation of the differential efficacious responses to and side effects from pharmaceutical agents acting on a disease as well as other treatment. N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and 3367, are not actually given a sequence in the Sequence Listing from the
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                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                           Length 20;
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                                                                                                                                                                                                                                                                                            Sequence 20 BP; 2 A; 2 C; 9 G; 7 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                           Score 15.2; DB 1;
Pred. No. 6.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HLA-A; HLA-B; HLA-C; typing; primer; human; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC80118 standard; DNA; 20
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Best Local Similarity 85.v.
Best Local 17; Conservative
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                                                                                                                                                                                                                                 present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC80118;
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The present invention describes an anti-CD14 antibody, which has a function of inhibiting the binding of CD14 to the Toll-like receptor (TLR). The anti-CD14 antibody can specifically recognise the epitope containing the domain from numbers 269-315 in human CD14 of the sequence in AAG68127 or a part of it. Anti-CD14 antibody has antibacterial, haemosepaive, antipyretic, hypertensive, immunostimulant, haemostatic and vasotropic activities. The antibody together with other polypeptides are applicable in drugs for treating bacterial infection as well as sepsis, fever, hypotension, leukopenia, thrombosenia, shock and multi-organ failure. AAG68127 to AAG68137 and AAI71230 to AAI71295 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-CD14 antibody or its fragment inhibiting the binding of CD14 to Toll -like receptor, applicable in drugs for treating bacterial infection as well as sepsis, fever, hypotension, leukopenia, thrombopenia and shock.
                                                                                                                                                                                                                                                                                                                                                           TLR/CD14 binding inhibitor; antibacterial; immunosuppressive; antippretic; hypertensive; immunostimulant; haemostatic; vasotropic; bacterial infection; sepsis; fever; hypotension; leukopaenia; thrombopaenia; shock; multi-organ failure; ss.
                                                                                                                                                                                                                                                                                                                                receptor; TLR; CD14; antibody; anti-CD14 antibody;
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Pred. No. 6.5e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                           Human Toll like receptor 4 PCR sense primer 1 SEQ ID NO:7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCTGTCTTCTCTCCA 1706
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22-NOV-2000; 2000JP-00356719.
28-MAR-2001; 2001US-00806158.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOCH ) MOCHIDA PHARM CO LID.
                                                          AAI71234 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF28352 standard; DNA; 20
                                                                                                                                                                                             23-JAN-2002 (first entry)
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nes 17; Conservative
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                                                                                                                                                                                                                                                                                                                         Human; Toll like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA oligomer #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200172993-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                           AAI71234;
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RESULT 979
                           AAI71234/k
XX AAI71234/k
XX AAI71
XXX AAI77
XXX AAI77
XXX HUMBI
XXW HUMBI
XXW AND LIFR
XXW AND LIFR
XXX HOWO
XXX HOW

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The present sequence was used to demonstrate the ability of deoxynucleic 5-Methythiourea (DNMT) compounds to form triplexes with DNA oligomers. An increase in the Content of the oligos resulted in a large decrease in binding. This experiment was performed as an example of a method for preparing oligomucleotides comprising a backbone of alkyl or alkoxy thiourea linkages. The method is useful for preparing oligomucleotides for use in antisense or antigene herapy, to inhibit production of proteins associated with genetic diseases, cardiovacular, inflammatory of monurcellular diseases, and for antiviral therapy, e.g. to treat thuman immunodeficiency virus, human-cytomegalovirus, influenza and herpes infections. The compounds are also useful as diagnostic reagence to detect the presence or absence of the target DNA or RNA sequences to which they specifically bind and by antagonising the normal biological activity of a target protein, they can be used in the manipulation of tissue e.g. tissue differentiation, both in vivo and in ex vivo tissue cultures. The method provides an efficient and rapid solid-phase method for the synthesis of thiourea and S-methylthiourea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
Deoxynucleic S-Methythiourea; DNmt; antisense therapy; cardiovascular disease; inflammatory disease; neurocellular disease; antiviral therapy; human immunodeficiency virus; human-cytomegalovirus; influenza; herpes; infection; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Preparing novel deoxynucleic alkyl thiourea oligonucleotide for use in antisense therapy, by synthesizing oligonucleotides comprising backbone of alkyl or alkoxy thiourea linkages in solution or on solid phase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recognition system; screening; identification; pharmaceutical; toxin; plant protection agent; toxin; venom; carcinogen; venom; teratogen; herbicide; fungicide; pesticide; beta-actin; human; ss.
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85.0%; Pred. No. 6.5e+02;
tive 0; Mismatches 3; Indels
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98US-0111800P.
99US-00347443.
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17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                    Bruice TC;
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02-JUL-1999;
                                                                                              Unidentified
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AAC82913/c
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Matches
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Homo sapiens

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Example 1; Page 4; 13pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                               ABK50429;
                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                       RESULT 983
                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                   ABK50429
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                                                                                                                                                                                                         This invention describes a novel recognition system comprising at least 1 recognition unit bound to a support, each recognition unit comprising a region A with a defined structure adjacent to a region B with a randomized structure. The recognition system is useful for screening, identifying, or characterizing at least 1 component of a sample, especially nucleic acids and/or proteins, and for screening for and/or identifying cellular or synthetic binding partners, preferably proteins, peptides, nucleic acids, chemical agents, preferably organic compounds, pharmaceuticals, plant protection agents, toxins, venoms, carcinogens, teratogens, herbicides, fungicides or pesticides
                                                                                                                                                  Recognition system, e.g. for identifying nucleic acids, comprises at least one recognition unit comprising a region with a defined structure adjacent to a region with a randomized structure.
                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                             0.9%; Score 15.2; DB 1; Length 20;
85.0%; Pred. No. 6.5e+02;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A process for purification of oligonucleotides using liquid chromatography.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide purification, liquid chromatography, hydrophobic protective group, deprotection, ds.
                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 2 A; 0 C; 2 G; 16 T; 0 U; 0 Other;
                                                                                      (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
                                                                                                          Burgstaller P;
                                                                                                                                                                                                                                                                                                                                                                                     1734 ACAAAAAAAAAAAAAA 1753
                                                                                                                                                                                                                                                                                                                                                                                                     ACAACTTAAAAAAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic oligonucleotide #15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF99949 standard; DNA; 20 BP
                                                99DE-01023966.
                                                                   99DE-01023966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99JP-00154974
                                                                                                                                                                                          Example, Fig 1, 8pp, German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                      Local Similarity 85.0
nes 17; Conservative
                                                                                                           Boekenkamp D, Hoppe H,
                                                                                                                               WPI; 2001-050938/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-268251/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP2000342265-A.
         DE19923966-A1
                                                25-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-JUL-2001
                            30-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                         20
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The present sequence is an oligonucleotide provided in a specification relating to the simplified purification of oligonucleotides by liquid chromatography. The process comprises: (a) pouring oligonucleotides by liquid chromatography column packed with an optective group into a liquid chromatography column packed with an optective cresistant packing agent, such as polystyrene resin; (b) pouring a mixed developing solvent composed of a buffer made from a volatile salt and a water soluble organic solvent at a suitable concentration gradient into the column; (c) pouring an aixed from a volatilarly c.0.16 v/# acetic acid, into the column to deprotect the oligonucleotides protected with the hydroghobic group; (d) pouring a mixed developing solvent composed of a buffer made from a volatile salt, particularly 0.05-0.5 N aqueous ammonium hydrogencarbonate solution adjusted at pH 8-10, and a water soluble organic solvent at a suitable concentration gradient to elute the deprotected oligonucleotides; and (e) removal of the solvent and the salt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cephalosporin C-acetyl hydrolase; CPC-AH; cephalosporin C; CPC; primer; cahB; 7-aminocephalosporanic acid; ss; PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to production of Acremonium chrysogenum cephalosporin C-acetyl hydrolase (CPC-AH) and its utilisation in the synthesis of deacetylated derivatives of cephalosporin C (CPC) and the inactivation of the gene for increasing production of cephalosporin. Derivatives and/or their synthesis intermediates can be synthesised by growing a microbial host transformed with a DNA sequence that includes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Velasco Alvarez J, Gutierrez Martin S, Casqueiro Blanco FJ;
Campoy Garcia S, Fierro Fierro F, Barredo Fuente JL, Diez Garcia B;
Martin Martin JF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acremonium chrysogenum cephalosporin C (CPC) gene cahB PCR primer #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .Match 0.9%; Score 15.2; DB 1; Length 20; Local Similarity 85.0%; Pred. No. 6.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1736 AAAAAAAAAAAAAAAAAA 1755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Page 55; 64pp; Spanish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from the eluted oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 AAAATAAAACAAAAGAAAA 1
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The present sequence is that of oligonucleotide AGT02025, which contains a single mismatch with a target DNA oligonucleotide (see ABA91531). It is one of a set of oligonucleotides (see ABA91532-37) containing mismatch(se) to the target DNA that were tested in a hybridisation/RNase H cleavage assay. The results showed that 2 mismatches between the target and the probe ablated RNase H cleavage. The effect of one mismatch site was less than that of two mismatch sites, and showed a polarity effect, with weaker inhibition shown in assays with AGT02021 than in assays using an oligonucleotide in which the mismatch was at an adjacent position. Oligonucleotides in which the mismatch was go or Crather than A showed similar inhibition of RNase H cleavage. The invention provides probes for nucleic acid hybridisation. The probes form a hairpin structure
the cahB gene encoding A. chrysogenum CPC-AH, under conditions where it is either expressed or inactivated. The genes and proteins are used for removal of acetyl groups, especially from the 3'-carbon of CPC or from 7-aminocephalosporanic acid, to give deacetylated products useful as intermediates for cephalosporin antiblotics. Inactivation of the gene that expresses CPC increases production of cephalosporins by A. chrysogenum. This sequence represents a PCR primer used to clone the cahB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             that forms hairpin structure having a double-stranded segment and single-
stranded loop collectively forming region complementary to target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probes for detecting target nucleotide sequence in sample, has sequence
                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                       Score 15.2; DB 1; Length 20;
Pred. No. 6.5e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA oligonucleotide AGT02025 used to test RNase H cleavage
                                                                                                                                                                       Sequence 20 BP; 1 A; 8 C; 4 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/note= "mismatch to target DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid detection; probe; mismatch; ss
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                                                                                                                                      gene encoding A. chrysogenum CPC-AH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                 1462 TGTGGGCTGCTGCTCCTC 1481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 5; Page 50; 72pp; English.
                                                                                                                                                                                                                                                                                                            1 TGCGTGCTGCTACTCTCCTC 20
                                                                                                                                                                                                                                                                                                                                                                                                                       BP
                                                                                                                                                                                                       0.9%;
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30-MAR-2001; 2001US-00823647.
                                                                                                                                                                                                                                                                                                                                                                                                                      ABA91537 standard, DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-APR-2002 (first entry)
                                                                                                                                                                                                                            Local Similarity 85.0 nes 17; Conservative
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comprising a double-stranded stem and a single-stranded loop, and are capable of both intramolecular and intermolecular hybridisation. The double-stranded stem may comprise a methylphosphonate DNA:RNA hybrid that is resistant to RNase H cleavage. When the probe hybridises with a target DNA, the RNA strand in the DNA:RNA duplex becomes sensitive to RNase H treatment and can be removed. Arrays and methods for nucleic acid hybridisation using the probes are provided
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an anti-CD14 antibody which can specifically recognise an epitope containing a part of a domain with not less than 8 amino acids in human CD14 in the region from positions 269-315 in a fully defined sequence of 356 amino acids as given in the specification. The antibody is useful in drug compositions for treating sepsis and for screening remedies for sepsis. This polynucleotide sequence represents anti-CD14 related oligonucleotide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-CD14 monoclonal antibody which inhibits CD14/T lymphocyte receptor binding by specifically recognizing epitope in human CD14 domain to prevent interaction and suppress cell activation, useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunosuppressive; antibacterial; anti-CD14 antibody; epitope; sepsis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-CD14 monoclonal antibody related oligonucleotide #1.
                                                                                                                                                Sequence 20 BP; 17 A; 0 C; 0 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1687 TGCTGTCTTCTCTCCA 1706
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                                                                                                                                                                                                                                                                                           1 AAAAAAATTATAAAAA 20
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AAL41013 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-OCT-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human CD14; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified.
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Matches
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synthesis; polynucleotide array; protecting group;

Oligonucleotide synthesis method related DNA #9.

Oligonucleotide oxidation; 88.

EP1176151-A1.

Synthetic.

30-JAN-2002.

Caruthers M;

Dellinger DJ, Perbost MGM, Betley JR,

WPI; 2002-156732/21

(AGIL-) AGILENT TECHNOLOGIES INC.

28-JUL-2000; 2000US-00627249 27-JUL-2001; 2001EP-00118360

us10008789-3.rng

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The present invention relates to antisense oligonucleotides and methods for modulating the expression of human or mouse casein kinase 2-alpha prime. The antisense oligonucleotides are useful for inhibiting the expression of casein kinase 2-alpha prime. Such diseases with aberrant expression of casein kinase 2-alpha prime. Such diseases include diabetes mellitus, and hyperproliferative disorders (particularly cancers e.g. breast cancer, prostate cancer, or liver cancer). The antisense compounds are also useful for diagnostics, therapeutics, prophylaxis, e.g. to prevent or delay infection, inflammation or tumnour formation, as research reagents and kits, and in distinguishing between functions of various members of a biological pathway. ABS67940-ABS67917 represent human or mouse casein kinase 2-alpha prime antisense oligonucleotides which comprise a phosphorothioate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antisense oligonucleotides targeted to nucleic acid encoding casein kinase 2-alpha prime, useful for diagnosing and/or treating a disease or condition associated with expression of casein kinase 2-alpha prime.
                                                                                                                                                                                         Human, casein kinase 2-alpha prime; diabetes mellitus; hyperproliferative disorder; breast cancer; prostate cancer; liver cancer; inflection; inflammation; tumour formation; cytostatic; antidiabetic; antiinflammatory; antimicrobial; phosphorothioate;
                                                                                                                                                      Human casein kinase 2-alpha prime antisense oligonucleotide #14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.9%; Score 15.2; DB 1; Length 20;
35.0%; Pred. No. 6.5e+02;
lve 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wyatt JR;
                                      ABS67915 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-2002; 2002WO-US002772.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-FEB-2001; 2001US-00780173
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                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                           antisense therapy, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mckay R, Freier SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-627539/67.
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ses 17; Conserv
                                                                                                                                                                                                                                                                                                                                                      40200262951-A2.
                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                  29-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                             15-AUG-2002
                                                                             ABS67915
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RESULT 986
ABS67915
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The present invention relates to a method for the synthesis of a polynucleotide which involves coupling a second nucleoside to a first nucleoside through a phosphite linkage, where the second nucleoside has a non-carbonate protecting group protecting a hydroxyl, and exposing the product to a composition which concurrently oxidizes the phosphite formed to a phosphate and deprotects the protected hydroxyl of the second nucleoside. The method is useful for synthesizing the polynucleotides, for carrying out either 3' to 5' or 5' to 3' synthesis and for fabricating an addressable array of polynucleotides on a substrate. The present sequence is an oligonucleotide produced to demonstrate the method
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                Synthesis of polynucleotide useful during fabrication of an array involves coupling nucleoside phosphoramidite and a solid-supported nucleoside and treating the product with an oxidation/deprotection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 0 A; 10 C; 0 G; 10 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 17; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 GGGGAAGAGAAAAAAA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 GGGGGGGGAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               composition.
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Matches
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Gaps

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857 CTGCAGGAAGAGGAAGAGGA 876

Conservative

Best Loca Matches

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AAL45130 standard; DNA; 20

RESULT 987 AAL45130/c

AAL45130;

12222EX

24-MAY-2002 (first entry)

20 GGCACAGGCCATGAGGGGCT

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US2002028508-A1
                                             Holtzman DA,
                      23-APR-1998;
22-JUN-1998;
29-JUL-1998;
    Unidentified.
                                 29-JUL-1999;
            07-MAR-2002
                    23-APR-1998;
                             23-APR-1999
                               22-JUN-1999
primer; 88
                                                            disorders.
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Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                   Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiinflammatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodiation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nyce JW, Li Y, Sandrasagra A, K
Miller S, Tang L, Shahabuddin S;
                                                                                                                                                                                    Human oligonucleotide sequence
                        ABZ87221 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-APR-2002; 2002WO-US013135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-APR-2001; 2001US-0286137P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EPIG-) EPIGENESIS PHARM INC
                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200285308-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                               17-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ubiquinone.
                                                                             ABZ87221;
ABZ87221/
                                                    The invention relates to nucleic acids encoding a variety of proteins human T139 (TANGO-139), T125 (TANGO-125), T110 (TANGO-110), murine T175 (TANGO-125), human T139 (TANGO-139), T125 (TANGO-125), T110 (TANGO-110), murine T175 (TANGO-125), human T135 or murine WDNM-2, having diagnostic, preventive, therapeutic and other uses. Polypeptide of the invention has the ability to modulate cell-cell interactions, hematopoiesis and the ability to modulate clotting. Polypeptide and polynucleotide of the invention are useful for diagnosing and treating disorder characterised by their aberrant expression or activity. The artibodies are useful as modulating agents in regulating a variety of cellular processes e.g. cell proliferation and/or cell differentiation. TANGO-139 is useful for treating neoplasia, TANGO-130 is useful for treating cancer, are useful to treat pancreatic discase, and tumours, and injury or trauma to the brain TANGO-125, 110, 175 molecules treat heart discase, e.g., ischaemic cheart disease, cardiovascular discases (e.g., acute and chronic glomerulonephritis), TANGO-135 molecules are useful to treat chieving profers, hyperplasia of the endometrium. TANGO-110 is useful to treat uterine disorders, hyperplasia of the endometrium. TANGO-110 is useful for treat uterine and thumours. TANGO-139, 125, 110, 175 or WDNM-2 are useful for treating proliferation disorders, under a single disorders, such as inflammatory diseases Crohn's cheared proliferation disorders, inflammatory diseases Crohn's cheared proliferation disorders, inflammatory diseases and tumours discase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WDNM-2 activity also include apoptotic disorders, rheumatoid arthritis, systemic lupus erythematosus, insulin-dependent diabetes mellitus, immune-related disorders, e.g., immunodeficiency disorders, viral disorders, c., cancers and inflammatory disorders and apoptotic disorders. The nucleic acids of the invention are used in gene therapy. The present sequence is a PCR primer used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel TANGO polypeptides and nucleic acid molecules useful as modulating agents in regulating cellular processes and for diagnosing and treating heart, liver, lung, kidney, inflammatory and cellular proliferative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mccarthy SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 65; 138pp; English.
                                                                                                                                                  98US-00065363.
98US-00065661.
98US-00102705.
98US-00124538.
99US-00238531.
                                                                                                      21-FEB-2001; 2001US-00790264
                                                                                                                                                                                                                                                                                                                 99US-00363630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goodearl ADJ,
                                                                                                                                                                                                                                                                                                                                                                   (HOLT/) HOLTZMAN D A.
(GOOD/) GOODEARL.A D J.
(MCCA/) MCCARTHY S A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-303420/34.
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Katz E, Pabalan J, Aguilar D;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                           The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genemic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 1 A; 6 C; 10 G; 3 T; 0 U; 0 Other;
Claim 15; SEQ ID NO 2463; 872pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1093 GCCCAGCTTCGCGGCCAGCA 1112
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681 GGCACAGCCAGTGAGGGGCT 700

Local Similarity 85.0 tes 17; Conservative

Query Match Matches

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Gaps

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0.9%; Score 15.2; DB 1; Length 20; 85.0%; Pred. No. 6.5e+02; vative 0; Mismatches 3; Indels

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20 GCCGAGCTCCGCGCCCAGCA

ABZ89486 standard; DNA; 20 BP

ABZ89486;

17-OCT-2003 (first entry)

Human oligonucleotide sequence

Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Homo sapiens.

WO200285308-A2.

31-OCT-2002

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC.

ä Pabalan J, Aguilar Katz E, Li Y, Sandrasagra A, K. Tang L, Shahabuddin S; Nyce JW, L Miller S,

WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

Disclosure; SEQ ID NO 4728; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding regalon, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dystunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiathmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antisense gene therapy. The composition is useful for treating or preventing sensitivity to adenosine, reducing levels of or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ung unflammation, lung allergies, or a respiratory disease or condition, or the sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 20 BP; 15 A; 4 C; 0 G; 1 T; 0 U; 0 Other;

Gaps ö 0.9%; Score 15.2; DB 1; Length 20; 15.0%; Pred. No. 6.5e+02; ve 0; Mismatches 3; Indels 82.04; Query Match Best Local Similarity 85.0° Matches 17; Conservative

1 TACAACAACAAAAAAA 20

RESULT 991 ABZ9037

BP ABZ90374 standard; DNA; 20

ABZ90374;

(first entry) 17-OCT-2003 Juman oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction; antinflammatory; antiallergic; antianflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Homo sapiens.

WO200285308-A2.

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

Aguilar Li Y, Sandrasagra A, Katz E, Pabalan J, Tang L, Shahabuddin S; (EPIG-) EPIGENESIS PHARM INC. Nyce JW, | Miller S,

ä

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or WPI; 2003-229219/22.

Disclosure; SEQ ID NO 5616; 872pp; English.

ubiquinone.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation coodon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2.10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an entile flammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiathment, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ung surfactant in a subject's tissue, or treating bronchoconstriction, lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published\_pct\_sequences 

Sequence 20 BP; 17 A; 3 C; 0 G; 0 T; 0 U; 0 Other;

Gaps ö 0.9%; Score 15.2; DB 1; Length 20; 85.0%; Pred. No. 6.5e+02; tive 0; Mismatches 3; Indels Capery Match 0.97
Sest Local Similarity 85.07
Matches 17; Conservative

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1736 AAAAAAAAAAAAAAAAAAAA 1755

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1733 TACAAAAAAAAAAAAAA 1752

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## 1 AAAACAAAACAAAAAAAA 20

Human oligonucleotide sequence. ABZ89084 standard; DNA; 20 (first entry) 17-OCT-2003 ABZ89084; RESULT 992 ABZ8908 

BP.

Human, antisense; lung dysfunction, nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Homo sapiens.

WO200285308-A2

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P

(EPIG-) EPIGENESIS PHARM INC

Nyce JW,

Katz E, Pabalan J, Aguilar D; Li Y, Sandrasagra A, Ke Tang L, Shahabuddin S; Miller S,

WPI; 2003-229219/22

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone

Disclosure; SEQ ID NO 4326; 872pp; English

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the instance codon, coding regalon, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genee encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing bronchoconstriction, lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition.

Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO.

Sequence 20 BP; 16 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

0; Gaps 0.9%; Score 15.2; DB 1; Length 20; 15.0%; Pred. No. 6.5e+02; 3; Indels 0; Mismatches 82.08; 17; Conservative Best Local Similarity Query Match Matches

1 ACGAGAAGAAAAAAAA 20

g

ABZ85668/

ABZ85668 standard; DNA; 20 BP

ABZ85668;

(first entry) 17-0CT-2003

Human oligonucleotide sequence.

Human, antisense, lung dysfunction, nasal airway dysfunction, antinflammatory, antiallergic; antianflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Homo sapiens.

WO200285308-A2

31-OCT-2002

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P

(EPIG-) EPIGENESIS PHARM INC.

Pabalan J, Aguilar D; Katz E, Li Y, Sandrasagra A, K Tang L, Shahabuddin S; Miller S, Nyce JW,

WPI; 2003-229219/22

Pharmaceutical composition for treating ailments associated with impaired ö respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid ubiquinone.

Claim 15; SEQ ID NO 910; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' interon-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or masal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an artiinflammatory steroid in a subject, for reducing levels of adenosine receptor, producing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO ftp.wipo.int/pub/published\_pct\_sequences 

Sequence 20 BP; 0 A; 3 C; 0 G; 17 T; 0 U; 0 Other;

Gaps ö / Match 0.9%; Score 15.2; DB 1; Length 20; Local Similarity 85.0%; Pred. No. 6.5e+02; nes 17; Conservative 0; Mismatches 3; Indels Query Match Matches

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1736 AAAAAAAAAAAAAAAAA 1755

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1734 ACAAAAAAAAAAAAAAAA 1753

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20 AAAGAAAAAAAAAAAGAAGA 1

RESULT 994

ABZ85670 standard; DNA; 20

AB285670;

(first entry) 17-OCT-2003

Human oligonucleotide sequence,

antinflammatory steroid; ubiquinone; antinflammatory; antiallergic; antiantergressive; cytostatic; gene therapy; antiense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds. Human; antisense; lung dysfunction; nasal airway dysfunction;

Homo sapiens.

WO200285308-A2.

31-OCT-2002

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC.

Pabalan J, Aguilar D; Katz E, Tang L, Shahabuddin S; Sandrasagra A, Li Y, Miller S, Nyce JW,

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or WPI; 2003-229219/22.

Claim 15; SEQ ID NO 912; 872pp; English.

ubiquinone

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the intitation coodon, coding regains, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiathmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an entistic manner or steroid in a subject, for reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung allergies, or a respiratory disease or condition. Note: The sequence date for this patent is not represented in the printed appears in the printed and prophylation in the printed prophylation in the printed and prophylation in the printed and prophylation in the printed and prophylation in the printed prophylation in the printed and prophylation in the printed prop at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 20 BP; 1 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

Gaps ö 0.9%; Score 15.2; DB 1; Length 20; 85.0%; Pred. No. 6.5e+02; ative 0; Mismatches 3; Indels Best Local Similarity 85.0 Matches 17; Conservative Query Match

20 AAAAATAGAAAAAAAGAAAA 1

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ABZ89131 RESULT

BP. ABZ89131 standard; DNA; 20

ABZ89131;

(first entry) 17-OCT-2003

Human oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiinflammatic; hypotensive; functionsuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine seceptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

Homo sapiens.

WO200285308-A2

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P. (EPIG-) EPIGENESIS PHARM INC. â Pabalan J, Aguilar Katz E, Li Y, Sandrasagra A, Ke Tang L, Shahabuddin S; Nyce JW, Miller S,

WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

Disclosure; SEQ ID NO 4373; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5 or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2.10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antialpergic, antiacehmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition may have a presenting a respiratory, lung or mailignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO antinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject setissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. at ftp.wipo.int/pub/published\_pct\_sequences 

Sequence 20 BP; 0 A; 8 C; 1 G; 11 T; 0 U; 0 Other;

Gaps ö 0.9%; Score 15.2; DB 1; Length 20; 85.0%; Pred. No. 6.5e+02; iive 0; Mismatches 3; Indels Best Local Similarity 85.0 Matches 17; Conservative "Query Match

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23 AGGGGGAAGAGAAAAA 42

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1736 AAAAAAAAAAAAAAAA 1755

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Human; antisense; lung dysfunction; nasal airway dysfunction; antinflammatory steroid; ubiquinone; antinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li Y, Sandrasagra A, Ka
Tang L, Shahabuddin S;
AGGCGGAAAGAGGAAAGAA 1
                                                                                                                                                                                                                                                                                                                                                             Human oligonucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-APR-2002; 2002WO-US013135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-APR-2001; 2001US-0286137P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EPIG-) EPIGENESIS PHARM INC
                                                                                                                                                            ABZ88781 standard; DNA; 20
                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200285308-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                17-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Miller S,
                                                                                                                                                                                                                            ABZ88781;
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                                                                                                                          ABZ88781/C
IID ABZ8781/C
XX ABZ81
XX AB
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Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid WPI; 2003-229219/22. ubiquinone

Pabalan J, Aguilar D;

Katz E,

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Disclosure; SEQ ID NO 4023; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the intitation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an natiniflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallargic, antiathmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing sensitivity to adenosine, reducing sensitivity to adenosine, reducing sensitivity to adenosine, reducing sensitivity to adenosine, reducing bronchodilation, increasing bronchoconstriction, lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 20 BP; 0 A; 0 C; 4 G; 16 T; 0 U; 0 Other;

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Score 15.2; DB 1; Length 20;
Pred. No. 6.5e+02;
0; Mismatches 3; Indels
                                                                                     1735 CAAAAAAAAAAAAAAAAA 1754
  Query Match 0.9%;
Best Local Similarity 85.0%;
                                             17; Conservative
                                         Matches
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Gaps

; 0

20 CAAAAAACAAAACAAAACAA 1

ВР

ABZ89925 standard; DNA; 20

RESULT 997 ABZ89925 ABZ89925;

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Human, antisense, lung dysfunction, nasal airway dysfunction; antinflammatory; antiallergic; antinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
                                                                                                                                                                                                                Pabalan J, Aguilar D;
                                                                                                                                                                                                                Katz E,
                                                                                                                                                                                                                       Shahabuddin S;
                                                                                                                                                                                                                Sandrasagra A,
                                        Human oligonucleotide sequence
                                                                                                                                                                23-APR-2002; 2002WO-US013135.
                                                                                                                                                                               24-APR-2001; 2001US-0286137P.
                                                                                                                                                                                               (EPIG-) EPIGENESIS PHARM INC.
                       (first entry)
                                                                                                                                                                                                               Li Y, Sar
Tang L,
                                                                                                                                                                                                                                       WPI; 2003-229219/22
                                                                                                                               WO200285308-A2
                                                                                                                Homo sapiens.
                        17-OCT-2003
                                                                                                                                                                                                                       Miller S,
                                                                                                                                                                                                                Nyce JW,
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Pharmaceutical composition for treating ailments associated with impaired 占 respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid

Disclosure; SEQ ID NO 5167; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' interon-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or masal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallargic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition may have a use in antisense gene therapy. The composition may have a use in antisense yet repropriatory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an artifinflammatory steroid in a subject, for reducing levels of or reducing sensitivity to adenosine, reducing levels of dependinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 20 BP; 1 A; 9 C; 5 G; 5 T; 0 U; 0 Other;

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Gaps
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Query Match 0.9%; Score 15.2; DB 1; Length 20; Best Local Similarity 85.0%; Pred. No. 6.5e+02; Matches 17; Conservative 0; Mismatches 3; Indels
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20 CAGAGGGAGCCTGGGCCAAG

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The present sequence is that of antisense oligonucleotide ISIS #114628. This chimeric phosphorothloate oligonucleotide, having 2'-MOE wings and a deoxy gap, is trageted to the 5' untranslated region of human Toll-like receptor 4 mRNA. It exhibits 32% inhibition of human Toll-like receptor 4 and THP-1 cells. It is useful for inhibiting the expression of Toll-like receptor 4 in cells or tissues. The oligonucleotide is particularly useful for treating or preventing a disease or condition associated with Toll-like receptor 4, e.g. an inflammatory disorder or a condition involving an immune response, particularly Thl or Th2 responses
                                                                                                                 Human; Toll-like receptor 4; receptor; antiinflammatory; immunomodulator;
phosphorothioate; antisense; 88.
                                                                                                                                                                                                                             "Mod_base= OTHER
/note= "OTHER = phosphorothioate nucleotides, the oligonucleotide comprises a central gap region of 10 2'-deoxymucleotides flanked on both sites by 5-nucleotides wings composed of 2'-methoxyethyl nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antisense oligonucleotides for modulating Toll-like receptor 4.gene expression, particularly useful for preventing, delaying or treating e.g. inflammatory disorders, or conditions involving Th1 or Th2 immune
                                                                                    Human Toll-like receptor 4 antisense oligonucleotide ISIS #114628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 3 A; 4 C; 10 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                        Location/Qualifiers
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/mod_base= m5c
                                                                                                                                                                                                                                                                                                                                 mod_base= m5c
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/mod_base= m5c
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ACC83605 standard; DNA; 20
                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-468766/44.
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modified_base
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                                                       08-SEP-2003
                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Karras JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 responses.
                            ACC83605;
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Determining bcr-abl translocation rearrangements in a biological sample, useful for diagnosing chronic myeloid leukemia or acute lymphoblastic leukemia, comprises performing real time polymerase chain reaction on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method of determining bcr-abl translocation rearrangements (the Philadelphia chromosome) in a biological sample, which comprises reverse transcribing extracted RNA from the sample to CDNA and performing polymerase chan reaction (PCR) on the CDNA, Also included is a method of diagnosing chronic myeloid leukaemia (CML) or acute lymphoblastic leukaemia (ALL) by performing the assay cited above. The method is useful in assaying biological samples for bcr-abl translocation rearrangements and reporting the results of such assays useful in the diagnosis of CML and/or ALL. The present sequence represents the human bcr-abl gene rearrangement assay primer BCR-P2, P3F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                 Gape
                                                                                                                                                                                                                                                                                 CML; ALL;
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                                                                                                                                                                                                                                                                          Human, primer, PCR, ss; Philadelphia chromosome; bcr-abl; chronic myeloid leukaemia; acute lymphoblastic leukaemia; translocation rearrangement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                 Indels
                                                                                                                                                                                                                                                  Human bcr-abl gene rearrangement assay primer BCR-P2, P3F
   Pred. No. 6.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 15.2; DB 1;
Pred. No. 6.5e+02;
                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Page 6; 18pp; English.
                                                101 GGTGAAGGCCAGAGGCTCGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     922 GAGCTGGATAGGCTGACGAA 941
                                                                             gereaagecreagecree 20
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                                                                                                                                                          BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD49622 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                      22-DEC-2000; 2000US-00747165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.9%;
82.0%;
                                                                                                                                                        ABX95028 standard; DNA; 20
                                                                                                                                                                                                                    (first entry).
 Best Local Similarity 85.0
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TSEN/) TSENG R W.
(SAMO/) SAMOSZUK M K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-361830/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                           US2002192645-A1
                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-DEC-1999;
                                                                                                                                                                                                                    13-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                         19-DEC-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Iseng RW,
                                                                                                                                                                                     ABX95028;
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RESULT 1000
AAD49622
ID AAD49622
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AC AAD49622
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DB 1; Length 20;

0.9%; Score 15.2;

Query Match

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Human, erythropoietin, single nucleotide polymorphism, psoriasis; SNP; acquired immune deficiency syndrome; veneral disease; carcinoma; EPO; autoimmune disease; gastrointestinal disorder; cardiovascular disease; Kaposi s sarcoma; ulcerative colitis; central nervous system disease; renal insufficiency; inflammatory process; radiotherapy; chemotherapy; metabolic disease; Alzheimer's disease; Parkinson's disease; melanoma; schizophrenia; Crohn's disease; rheumatoid arthritis; cancer; obesity; tumour; depression; lymphoma; leukaemia; infection; pneumonia; asthma; genital wart; allergy; multiple myeloma; anaemia; therapy; AIDS; PCR;
                                                                      Human BPO gene fragment amplifying antisense PCR primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-DEC-2001; 2001US-0343163P.
04-JAN-2002; 2002US-0345440P.
21-FEB-2002; 2002US-0358598P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAR-2002; 2002WO-EP004331
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
24-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer; ss.
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erythropoietin gene with single nucleotide polymorphisms, for diagnosing, preventing and treating cancers, infections and autoimmune diseases. Novel polypeptide encoded by nucleotide sequence derived from human

Example 2; Page 74; 76pp; English.

derived from human erythopoletin gene (BPO) with single nucleotide gequences of the invention are useful for preventing or treating diseases such as cancers and tumours which include metalanomas, metalating diseases such as cancers and tumours which include metalanomas, metalating renal carcinomas, leukaemias such as follicular lymphomas cancers of the liver, neck, head and cutaneous T cell lymphoma, leukaemia, cancers of the liver, neck, head and kidneys, multiple myelomas, cancers of the liver, neck, head and kidneys, multiple myelomas, carcinoid tumours and tumours that appear following an immune deficiency comprising Kaposi's sarcoma in the case of following an immune deficiency comprising Kaposi's sarcoma in the case of following an immune deficiency comprising kaposi's sarcoma in the case of following an immune deficiency survail infections including chronic hepatitis B and C and human immunodeficiency virus (HIV)/acquired immune deficiency syndrome (AIDS) and infectious pneumonias; venereal diseases of deficiency syndrome (AIDS) and infectious pneumonias; venereal diseases of alseases and diseases and ulcerative colitis; cardiovascular diseases such as allergies, asthma, psoriasis, rheumaterid arthritis, multiple solerosis, cronn's diseases and ulcerative colitis; cardiovascular diseases such as well as anaemia resulting from chronic control infections, inflammatory processes, radiocherapies and chemotherapies; chears in control and control metabolic diseases such as more immune associated diseases such as metabolic diseases such as more immune associated diseases. obesity, central nervous system diseases including Alzheimer's disease, Parkinson's disease, schizophrenia and depression. gastrointestinal disorders and disorders connected with chemotherapy treatments. The present sequence is human BPO gene fragment amplifying PCR primer The invention relates to polypeptides encoded by nucleotide sequences

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                     Score 15.2; DB 1; Length 20;
Pred. No. 6.5e+02;
0; Mismatches 3; Indels
Sequence 20 BP; 3 A; 8 C; 1 G; 8 T; 0 U; 0 Other;
                      0.9%;
        Query Match
Best Local Similarity 85.00,
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AAD61440 standard; DNA; 20 BP.

RESULT 1002 AAD61440/c

AAD61440;

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The invention relates to a novel method for detecting a point mutation in a DNA strand. The novel method comprises hybridising a target DNA strand containing or suspected of containing a point mutation with a test nucleic acid strand duplex, contacting the duplex with an strand/test nucleic acid strand duplex, contacting the duplex with an nucleotide sequence are cleaved by Rwase H. The method is useful for detecting a point mutation in a DNA strand, where the point mutation to be detected is a single nucleotide polymorphism, preferably a polymorphism in a genome, e.g., a viral, bacterial, eukaryotic, mammalian or human genome. The method is useful to detect any nucleic acids from any species of organisms such as Acintobacter, Bacillus, Candida, Enterococcus, Haemophilus, Mycobacterium and Streptococcus, and viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting point mutation in DNA strand, by hybridizing target DNA strand having mutation with test DNA strand to form duplex, contacting the duplex with RNase H and determining the cleavage of test strand by RNase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This polynucleotide sequence represents a ribonucleotide relating to the mutation detecting method of the invention
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                                                                                                                                                                                                                                   Detecting; point mutation; hybridising; target DNA; duplex; RNase single nucleotide polymorphism; 88.
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                                                                                                                                                                                                   DNA mutation detection related ribonucleotide, SEQ ID No 18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 17 A; 0 C; 0 G; 3 T; 0 U; 0 Other;
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GATCATTCTCCCTTTCATCC 20
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                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2001; 2001US-00823634.
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                                                                                         AAL53968 standard; DNA; 20
                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dattagupta N,
                                                                                                                                                               18-FEB-2003
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                                                      RESULT 1001
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(first entry) 15-JAN-2004 Human TANGO cDNA related PCR primer #4.

Human; TANGO, kidney failure, hyperplasia; inflammatory disorder; cancer; angiogenesis; hematopoietic disorder; pancreatic disorder; hypertension; heart disorder; hepatic disorder; diabetes mellitus; placental disorder; cerebrovascular disease; Goodpasture's syndrome; cardiovascular disorder; foetal spleen associated disease; reproductive disorder; atherosclerosis; glomerular disease; intestinal disorder; proliferative disorder; tumour; ovulation disorder; testicular disorder; lung disorder; crohn's disease; prostate disorder; Mhipple's disease; haemophilia; anaemia; thalassaemia; gene therapy; tranquillizer; vulnerary; vasotropic; psoriasis; leukaemia; sathma; PCR; primer; ss.

Homo sapiens.

JS2003104447-A1

05-JUN-2003

11-OCT-2002; 2002US-00269353

23-APR-1998; 98US-00065661. 23-APR-1999; 99US-00298531. 21-FEB-2001; 2001US-00790264.

(MILL-) MILLENNIUM PHARM INC

Goodearl ADJ, Mccarthy SA; Holtzman DA,

WPI; 2003-787050/74.

New TANGO polypeptides useful as modulating agents in regulating cellular processes and for diagnosing, treating heart, liver, lung, kidney, inflammatory and cellular proliferative disorders.

Disclosure; Page 65; Opp; English.

The invention relates to an isolated polypeptide termed human T139 (TANGO - 139), T125, T110, murine T175, human T175 or murine MDNM-2. T139 is useful for treating kidny defects such as kidney failure or hyperplasia, useful for treating wound healing and cancer, T110 is useful for treating monopolate. T125 is useful for treating and cancer, T110 is useful for treating cancer, inflammatory disorders and nemacopolatic disorders. T125 and 110 are useful to treat pancreatic disorders such as pancreatitis, diabetes mellitus, and Zollinger-Ellison syntome, placental disorders such as placentitis or abortion and syntome, placental disorders such as placentitis or abortion and clisorders of the brain such as crebral edema, cerebrovagular disease and tumours and injury or trauma to the brain. T125, 110, 175 molecules treat heart disorders e.g., ischaemic heart disease, atherosoclerosis, chypertension, angina pectoris, pulmonary (lung) disorders such as treumatoid lung disease, bronchial asthma and Goodpasture's syndrome, disorders of skeletal muscale such as muscular dystrophy, motor neuron disorders e.g., amyotrophic lateral sclerosis, cardiovascular disorders such as theumatic heart disease or myocardial disease, hepatic disorders including jaundice, hepatic failure, Crigler-Naijar syndromes or anignant tumours. T139, 125, 110 and 175 molecules are useful to treat crenic glomerulonephritis) and reproductive disorders and sperm cell crenic glomerulonephritis) and reproductive disorders and sperm cell disorders. T175 is useful to treat uterine disorders and sperm cell caseociated diseases and disorders, hyperplasia of the endometrium, uterine cancer, bonne marrow, blood and haematopoietic sansociated diseases and disorders, e.g., acute myelulia, ansamia and thalassaemia. T-110 is useful to treat spleen e.g., the foetal spleen associated diseases and disorders such as sincetive connecoplastic cysts and tumours, intestinal disorders such as inflammatory diseases.

Connecoplastic cysts and tumours, intestinal disease, colo

Detecting the presence of a target nucleic acid molecule in templates by combining a detection probe, a first oligonucleotide, second oligonucleotide, a primer and templates suspected of containing the

(SYGN ) SYNGENTA PARTICIPATIONS AG

SHI L

(SHIL/)

13-MAR-2002; 2002US-0364230P

Example 2; SEQ ID NO 9; 42pp; English.

target nucleic acid molecule.

WPI; 2003-803888/75.

The invention comprises a method for detecting a target nucleic acid molecule in a plurality of templates, the method involves combining a detection probe, a first oligonucleotide, second oligonucleotide, a primer and a plurality of templates suspected of containing the target nucleic acid molecule. The method of the invention is useful for detecting the presence of a target nucleic acid molecule in a plurality of templates. The method is also useful for quantitating a particular nucleic acid molecule in a sample. The invention provides a rapid, reliable and cost-effective method for detecting a particular nucleic

represents a

DNA sequence

universal sequence that was used in an example of the invention.

present

acid molecule in a sample. The

Sequence 20 BP; 7 A; 0 C; 13 G; 0 T; 0 U; 0 Other;

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Gaps

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0.9%; Score 15.2; DB 1; Length 20; 15.0%; Pred. No. 6.5e+02; ve 0; Mismatches 3; Indels

85.0%;

17; Conservative

Matches

Query Match Best Local Similarity

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such as congenital anomalies and tumours. T139, 125, 110, 175 or WDNM-2 are useful for treating proliferative disorders, inflammatory disorders e.g., bacterial infection, psoriasis, e.g., ulcerative colitis, arthritis and allergic inflammatory disorders (e.g., asthma, psoriasis). The invention is useful in gene therapy. The present sequence is human TANGO CDNA related PCR primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid detection; nucleic acid quantitation; universal sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid detection method-related universal DNA sequence #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.9%; Score 15.2; DB 1; Length 20; Best Local Similarity 85.0%; Pred. No. 6.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 2 A; 9 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  681 GCCACAGCCAGTGAGGGCT 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 GCCACAGGCCATGAGGGGCT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADD71322 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003078587-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADD71322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1003
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AAQ79182-Q79186 contain one or more 9-methyl-acyclo-adenosines, acylic nucleoside analogues which inhibit nuclease degradation. The nuclease resistant oligonucleotides can themselves be used to inhibit gene expression as antiense agente, in nucleic acid sequencing and diagnostic assays. (Updated on 25-WAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enzymatic nucleic acid, ribozyme; trans cleavage; inhibition, gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; atherosclerosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
                                                                                                                                                                                                                                                                                                                                                                       New acyclic nucleoside analogues - used to prepare nuclease resistant oligo-nucleotide(s) used partic. for inhibiting gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human ICAM hammerhead ribozyme target sequence (nt. position 2910).
             Nuclease resistant oligonucleotide; inhibition of gene expression; 9-methyl-8-acyclo-adenosine; antisense agents; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.9%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 5.6e+02;
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                                                                                                                                           /note= "9-methyl-acyclo-adenosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
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Matches 15; Conservative 0; Mismatches
                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                  Example 10; Page 20; 37pp; English
                                                                                                                                                                                                                                                                                                                  Guinosso C;
                                                                                                                           /mod_base= OTHER
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AAT52136 standard; RNA; 15 BP.
                                                                                                                                                                                                                                                                                      (STER ) STERLING WINTHROP INC
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                                                                                                                 *tag= a
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                                                                                                                                                                                                                                                                                                                                          WPI; 1994-333078/41.
                                                                                    Key
modified_base
                                                                                                                                                                                                                               21-MAR-1994;
                                                                                                                                                                                                                                                           30-MAR-1993;
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                                                                                                                                                                        WO9422864-A1
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25-MAR-1997
                                                                                                                                                                                                  13-OCT-1994
                                                        Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New acyclic nucleoside analogues - used to prepare nuclease resistant oligo-nucleotide(s) used partic. for inhibiting gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                             Nuclease resistant oligonucleotide, inhibition of gene expression, 9-methyl-8-acyclo-adenosine, antisense agents, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 0.9%; Score 15; DB 1; Length 15; Local Similarity 100.0%; Pred. No. 5.6e+02; No. 5.5e+02; No. 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                              /*tag= a
/mod_base= OTHER
/note= "9-methyl-acyclo-adenosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nuclease resistant oligonucleotide.
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                                                                                                                                                                                                 Nuclease resistant oligonucleotide
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GGAAGAGGAAGAGGAGGCGA 881
                GGAGGAGGAGGAGGAGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guinosso
                                                                                                ВР
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                                                                                               AAQ79185 standard; DNA; 15
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                                                                                                                                                                        (first entry)
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Delecki DJ,
                                                                                                                                                         (revised)
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                                                                                                                                                                                                                                                                                                   Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                      WO9422864-A1
                                                                                                                                                                                                                                                                                                                                                                                                                 13-OCT-1994.
                                                                                                                                                      25-MAR-2003
21-JUN-1995
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21-JUN-1995
                                                                                                                                                                                                                                                                       Synthetic.
862
                                                                                                                            AAQ79185;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cook PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                     1004
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ID AAQ7
XX AAC AAQ7
XX 25-N
DT 21-C
XX XX
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Gaps

luman ICAM hammerhead ribozyme target sequence (nt. position 2911).

(revised)
(first entry)

25-MAR-2003 25-MAR-1997

AAT52138;

AAT52138 standard; RNA; 15 BP

us10008789-3.rng

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Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; atherosclerosis; myocardial infarction; stroke; reetenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial ischaemia; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                   15-AUG-1994;
16-AUG-1994;
17-AUG-1994;
19-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-SEP-1994;
08-SEP-1994;
23-SEP-1994;
23-SEP-1994;
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03-OCT-1994;
07-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-OCT-1994;
04-NOV-1994;
10-NOV-1994;
28-NOV-1994;
The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the uncleotide base position indicated in the DE line. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes cleave the ICAM-1 target sequences and thereby inhibit ICAM-1 expression, making them useful for reducing transplant sejection and alleviating symptoms in patients with rheumatoid arthritis, asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                            Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW; Grimm S, Karpelsky A, Kisich K, Matulic-Adamic J, Mcswiggen JA; Modak A, Pavco P, Baleleman L, Sullivan SM, Sweedler D, Thompson JD; Tracz D, Usman N, Wincott FE, Woolf T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ribozymes having modified bases and methods for producing them - for use in inhibiting disease related genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 175; 407pp; English.
                                                               94US-00201109.
94US-00228934.
94US-002224955.
94US-00228041.
94US-00228041.
94US-00291433.
94US-00291433.
94US-00291433.
94US-00291433.
94US-00291439.
94US-00291439.
94US-00391439.
94US-00301499.
94US-00314397.
                                             95WO-IB000156
                                                                                                                                                                                                                                                                                                                                                                                        (RIBO-) RIBOZYME PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1995-351090/45.
                                                                                                                                                                                                                                                       28-SEP-1994;
03-OCT-1994;
07-OCT-1994;
11-OCT-1994;
04-NOV-1994;
                                                                                                                                                             15-AUG-1994;
16-AUG-1994;
                                             23-FEB-1995;
                                                                                                                            15-APR-1994;
18-MAY-1994;
                                                                                                                                                                                    17-AUG-1994;
                                                                                                                                                                                                                         08-SEP-1994;
                       31-AUG-1995
                                                                                                                                                    06-JUL-1994
                                                                                                                                                                                                           02-SEP-1994
                                                                                                                                                                                                                                              23-SEP-1994
                                                                                                                                                                                                                                   23-SEP-1994
                                                                                                                                                                                                                                                                                                                   10-NOV-1994
                                                                                                                                                                                                                                                                                                                                 28-NOV-1994
                                                                               29-MAR-1
04-APR-1
                                                                                                                15-APR-
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94US-00291433. 94US-00292620. 94US-00293520. 94US-00300000.

94US-00311486. 94US-00311749. 94US-00314397.

94US-00316771 94US-00319492

94US-00321993. 94US-00334847. 94US-00337608.

94US-00345516

16-DEC-1994 23-DEC-1994

94US-00228041. 94US-00245736. 94US-00271280.

94US-00291932

94US-00218934. 94US-00222795. 94US-00224483. 94US-00227958.

15-APR-1994

95WO-IB000156

33-FEB-1995; 31-AUG-1995

Homo sapiens W09523225-A2

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Chowrira B, Direnzo A, Draper KG, Dudycz LW;
isky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
N, Wincott PS, Woolf T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the nucleotide base position indicated in the DE line. Regions of the mRNA
                                                                                                                                                                                                                                                                                                                                                        methods for producing them - for use
                                                                                                                                                                                                                                                                                                                                                     Ribozymes having modified bases and in inhibiting disease related genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 175; 407pp; English.
95US-00380734
                                                            (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                        Grimm S, Karpeisky A,
Modak A, Pavco P, Beig
Tracz D, Usman N, Wind
                                                                                                                                                                                                                                                                                           WPI; 1995-351090/45
                                                                                                                                占,
30-JAN-1995
                                                                                                                                Stinchcomb
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Gaps ö

9%; Score 15; DB 1; Length 15; 0.0%; Pred. No. 5.6e+02; 0; Mismatches 0; Indels

100.0%; Pr.

Best Local Similarity 100. Matches 15; Conservative

1736 AAAAAAAAAAAA 1750

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15 AAAAAAAAAAAAA 1

RESULT 1007 AAT52138/c

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Gaps

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0

Score 15; DB 1; L. Pred. No. 5.6e+02; D; Mismatches 0;

Length 15; Indels

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that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes cleave the ICAM-1 target sequences and thereby inhibit ICAM-1 expression, making them useful for reducing transplant rejection and alleviating symptoms in patients with rheumatoid arthritis, asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide containing phosphoramidate linkages.
                                                                                                                                                                                                           Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
                                                                                                                                                                                                                                                     0.5.,
100.0%; Pre-
                                                                                                                                                                                                                                                                                                                                 1736 AAAAAAAAAAAAA 1750
                                                                                                                                                                                                                                                   0.9%;
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(first entry)
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1es 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-JUN-1996;
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                                                                                                                                                                                                                                                   Query Match
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BP

A new method is provided for the synthesis of oligonucleotides having N3'->P5' phosphoramidate linkages. The method comprises (a) attaching a 3'-protected amino nucleoside to a solid support; (b) deprotecting the 3'-amino; (c) reacting with a 3'-protected aminouncleoside-5'-phosphoramidite monomer to form an internucleoside N3'->P5' phosphoramidite link; (d) oxidising this link to phosphoramidate; and optionally repeating steps (b)-(d) until the required oligonucleotide is completed. This method provides better yields with lower reagent consumption than known processes, and can be operated on a large scale. Synthesis of N3' to P5' phosphoramidate oligo:nucleotide - by reacting immobilised 3'-amino nucleotide with new amino:nucleoside 5'-phosphoramidite then oxidation, useful as research, diagnostic and /\*tag= a /note= "these residues have N3′->P5′ phosphoramidate linkages" Nelson JS; SN, phosphoramidate linkage; solid phase synthesis; ss. Mccurdy Gryaznov SM, Location/Qualifiers Disclosure; Page 28; 60pp; English. (LYNX-) LYNX THERAPEUTICS INC. 96WO-US010418 96US-00603566 Fearon KL, WPI; 1997-435080/40. therapeutic Schultz RG, 

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The obtained oligos, containing phosphoramidate linkages, have favourable binding properties, nuclease resistance and solubility, and are useful as research, diagnostic and therapeutic agents. The present sequence is an example of an oligonucleotide in which N3'->P5' phosphoramidate linkages have been introduced by the new method. (Updated on 25-WAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phosphoramidite link; (d) oxidising this link to phosphoramidate; and optionally repeating steps (b)-(d) until the required oligonucleotide is completed. This method provides better yields with lower reagent consumption than known processes, and can be operated on a large scale. The obtained oligos, containing phosphoramidate linkages, have favourable binding properties, nuclease resistence and solubility, and are useful as research, diagnostic and therapeutic agents. The present sequence is an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A new method is provided for the synthesis of oligonucleotides having N3' ->PS' phosphoramidate linkages. The method comprises (a) attaching a 3'-protected amino nucleoside to a solid support; (b) deprotecting the 3'-amino; (c) reacting with a 3'-protected aminouncleoside-5'-phosphoramidite monomer to form an internucleoside N3'->PS'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthesis of N3' to P5' phosphoramidate oligo:nucleotide - by reacting immobilised 3'-amino nucleotide with new amino:nucleoside 5'-phosphoramidite then oxidation, useful as research, diagnostic and therapeutic agents.
                                                                                                                                                                                            Gaps
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note= "these residues have N3'->P5' phosphoramidate
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                                                                                                                                                          Length 15;
                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide containing phosphoramidate linkages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphoramidate linkage; solid phase synthesis; ss.
                                                                                                                      Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                        Score 15; DB 1; Le
Pred. No. 5.6e+02;
                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 28; 60pp; English.
                                                                                                                                                        Match 0.9%; So.
Local Similarity 100.0%; P:
es 15; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                   AAV01603 standard; DNA; 15
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(first entry)
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*tag=
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                                                                                        correct PR field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                    AAV01603;
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                                                                                                                                                          Query Match
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Pred. No.

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New release tag compounds for detecting target molecule(s) - comprising a reactive group, a release group and a releasable non-volatile mass label detectable by mass spectrometry.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genotyping, clone and gene mapping, and gene expression analysis. The RTCs permit the ready detection of releasable mass labels by mass spectroscopy. The releasable mass labels permit the multiplexing of tens, hundreds and perhaps even thousands of different mass labels that can be used to uniquely identify each desired target
example of an oligonucleotide in which N3'->P5' phosphoramidate linkages have been introduced by the new method. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oligonucleotide; peptide; conjugate; release tag compound; mass spectrometry; detection; identification; diagnosis; primer; ss.
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                                                                                                                                                                                                                                                    Length 15;
                                                                                                                                                                                                                                                                                                                   0; Indels
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                                                                                                                                                                         Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic peptide-labeled oligonucleotide primer.
                                                                                                                                                                                                                                        0.9%; Score 15; DB 1; Le
100.0%; Pred. No. 5.6e+02;
tive 0; Mismatches 0;
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ID AAV07431 standard; DNA; 15 BP.

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AAV07431;
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AAV07431;
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AAV07431;
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Synthetic peptide-labeled oligom
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Oligonucleotide; peptide; conjug.
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Oligonucleotide; peptide; conjug.
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Synthetic.
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Best Local Similarity 100."
Matches 15; Conservative
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0.9%; Score 15; DB 1; Length 15;

Query Match

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This sequence represents an oligonucleotide receptor molecule covalently bound to a polyacrylamide gel via a linking group. The invention relates to selective separation of electrically charged target molecules in an analytical mixture. It comprises capillary affinity gel electrophoresis using a capillary tube which is at least partly filled with a polymer. C gel. Receptors for target molecules are covalently bound to the polymer. C gel. Receptors for target molecules are covalently bound to the polymer. C an electric field of at least 50 volte/C m is applied. The capillary tube is charged with the analytical mixture. In a first separation stage, the target molecules in the mixture are bound to the receptors and the c second stage, the elution conditions are changed, optionally in stages, conditions are changed, optionally in stages, conditions and of the target molecules for the receptor is contact the affinity of the target molecules for the receptor is climinated and the target molecules are eluted and detected, optionally whilst splitting open. The process is useful for selective separation and/or determination of charged organic compounds, such as oligonucleotides, peptides or carbohydrates. It may be used, e.g. for isolation of specific proteins and DNA molecules, purification of specific proteins and DNA molecules, purification of specific proteins and DNA molecules, purification of papering or antibodies, analysis of antisense compounds or screening for enzyme inhibitors. The process especially in the case of complex mixtures. It has high sensitivity, even with small amounts of samples. The derivatised polymers may be synthesised specifically using candard methods
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/note= "Thymine at 5' end attached to a polyacrylamide
gel via a linking group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Separation of electrically charged target molecules - by capillary affinity gel electrophoresis using polymer-gel to which receptors for target molecules are bound.
                        Gaps
                                                                                                                                                                                                                                                                                                                                                      Capillary afinity gel electrophoresis; separation; polymer-gel;
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                      Indels
                        0; Mismatches
                                                                                                                                                                                                                                                                                                                 Oligonucleotide linked to polyacrylamide.
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                                                             1736 AAAAAAAAAAAA 1750
                                                                                                                                                                                                 AAT86675 standard; DNA; 15 BP
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                      15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                            polyacrylamide; ss.
Best Local Similarity
Matches 15; Conserv
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modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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Gaps

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Indels

100.0%; Pred. No. 5.6e+02; ive 0; Mismatches 0;

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Best Local Similarity 100. Matches 15; Conservative

Query Match

0.9%; Score 15; DB 1; Length 15;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  process using capillary affinity gel electrophoresis. The invention relates to selective separation of electrically charged target molecules in an analytical mixture. It comprises capillary affinity gel electrophoresis using a capillary tube which is at least partly filled with a polymer gel. Receptors for target molecules are covalently bound to the polymer. An electric field of at least 50 volts/m is applied. The capillary tube is charged with the analytical mixture. In a first capillary tube is charged with the analytical mixture are bound to the receptors and the remaining components are eluted, optionally whilst splitting open. In a second stage, the elution conditions are changed, optionally in stages, so that the affinity of the target molecules for the receptor is eliminated and the target molecules are eluted and detected, optionally whilst splitting open. The process is useful for selective separation and/or determination of charged organic compounds, such as oligonuclectides, peptides or carbohydrates. It may be used, e.g. for isolation of specific proteins and DNA molecules, purification of antibodies, analysis of antisense compounds or screening for enzyme thibitors. The processes, especially in the case of complex biological analytical mixtures. It has high sensitivity, even with small amounts of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             analytical mixtures. It has high sensitivity, even with small amounts of samples. The derivatised polymers may be synthesised specifically using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Separation of electrically charged target molecules - by capillary affinity gel electrophoresis using polymer-gel to which receptors for target molecules are bound.
                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide separated by capillary affinity gel electrophoresis.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Capillary afinity gel electrophoresis; separation; polymer-gel;
                                       Query Match 0.9%; Score 15; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 5.6e+02; Matches 15; Conservative 0; Mismatches 0; Indels
Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                          AAT86605 standard; DNA; 15 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NOVS ) NOVARTIS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                            polyacrylamide; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents an example of an oligonucleotide containing novel 3'-amino-5'-phosphoramidite nucleoside of the invention. The sequence is generated synthetically by using an amine-exchange reaction of phosphoramidites in which a deprotected 3'-amino group of an oligonucleotide chain is exchanged for the amino portion of a 5'-phosphoramidite with a protected 3' amino group. The resulting phosphoramidite internucleotide linkage is oxidised to form a stable protected phosphoramidate linkage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New 3'-protected-amino-nucleoside-5'-phosphoramidite monomers - used in the synthesis of oligo-nucleotide(s).
                                                                                                                                                                                                                                                                                                      /*tag= a
/note= "contains internucleotide N3-P5 phosphoramidate
internucleotide linkages"
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                                                                                                                                                                                                                 Oligonucleotide; phosphoramidate; phosphoramidite; nucleoside; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schultz RG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mccurdy SN, Hirschbein BL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                      N3-P5 phosphoramidate oligonucleotide #3.
                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 10; Col 33; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THERAPEUTICS INC.
                                                                                                 AAX00787 standard; DNA; 15 BP.
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96US-00663918.
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                          15 AAAAAAAAAAAA 1
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                                                                                                                                                         (first entry)
1736 AAAAAAAAAAAA
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                                                                                                                                                                                                                                                                                          .15
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                                                                                                                                                                                                                                                                                     misc_difference
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14-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                             US5859233-A.
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                                                                                                                                                                                                                                             Synthetic
                                                                                                                             AAX00787;
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In present sequence claims are presented raisers and enzymatic nucleic acid, especially a hammerhead riboxyme, which cleaves the Hepatitis C virus (HCV) RNA sequence in the 3' non-core region. The HV sequence was screened for optimal riboxyme target sites using a computer folding algorithm and regions of the mRNA which did not form secondary folding structures and contained potential riboxyme cleavage sites were identified. Riboxymes were synthesised to target these sites and their activities optimised by either varying the length of the binding arms or by modification to prevent degradation by nucleases. The riboxymes of the invention inhibit gene expression and/or viral replication, and are used to treat diseases associated with Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and hepatocellular carcinoma. The riboxymes may be used in combination with interferon to treat HCV infection, other infectious diseases, autoimmune diseases, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage; cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer; autoimmune disease; 88.
                                                                                                                                                                                                                                                                                                          Novel ribozymes for the treatment of diseases and conditions related to hepatitis C infection.
                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents the preferred target sequence of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Substrate for HH ribozyme HCV.3-118 which cleaves HCV at nt. 9418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.9%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 5.6e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
                                                                                                                                                                                                                                       Pavco PA,
                                                                                                                                                                                                                                     Blatt L, Mcswiggen JA, Roberts E,
                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 49; 123pp; English
                                                                                                     98US-0083217P.
98US-0100842P.
99US-00257608.
99US-00274553.
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WO9955847-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         409955847-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-APR-1999;
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18-SEP-1998;
                                                                      26-APR-1999;
                                                                                                                          18-SEP-1998;
25-FEB-1999;
                                                                                                                                                                23-MAR-1999;
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                                  04-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents an example of an oligonucleotide containing novel 3. amino-5. phosphoramidite nucleoside of the invention. The sequence is generated synthetically by using an amine-exchange reaction of phosphoramidites in which a deprotected 3. amino group of an oligonucleotide chain is exchanged for the amino portion of a 5. phosphoramidite with a protected 3 amino group. The resulting phosphoramidite internucleotide linkage is oxidised to form a stable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŗ
                                                                                                                                                                                                                    /*tag= a
/note= "contains internucleotide N3-P5 phosphoramidate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New 3'-protected-amino-nucleoside-5'-phosphoramidite monomers - used the synthesis of oligo-nucleotide(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                       Oligonucleotide; phosphoramidate; phosphoramidite; nucleoside; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schultz RG
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100.0%; Pred. No. 5.6e+02;
Ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
                                                                    N3-P5 phosphoramidate oligonucleotide #4.
                                                                                                                                                                                                                                                        internucleotide linkages'
                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 10; Col 33; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protected phosphoramidate linkage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LYNX-) LYNX THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                    96US-00771789.
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96US-00663918.
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                                  13-APR-1999 (first entry)
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Les 15; Conservative
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                                                                                                                                                                                             misc_difference
                                                                                                                                                                                                                                                                                                                                                                    20-DEC-1996;
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14-JUN-1996;
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                                                                                                                                             Synthetic
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enzymatic nucleic acid, respectably a hammerhood ribozyme, which cleaves the Hepatitis C virus (HCV) RNA sequence at the base position given in the descriptor line. The HCV sequence was screened for optimal ribozyme target sites using a computer folding algorithm and regions of the mRNA which did not form secondary folding structures and contained potential ribozyme cleavage sites were identified. Ribozymes were synthesised to target these sites and their activities optimised by either varying the length of the binding arms or by modification to prevent degradation by viral replication, and are used to treat diseases associated with Hepatics C virus (HCV) infection, e.g. cirrhosis, liver failure and hepatocellular carcinoma. The ribozymes may be used in combination with
                                                                                                                                                                                                                                                                                                                                                                                                                          interferon to treat HCV infection, other infectious diseases, autoimmune diseases, and cancer
                                                                                                                                         Novel ribozymes for the treatment of diseases and conditions related to hepatitis C infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New DNA encoding endo-beta-mannanase from coffee, used e.g. in pharmaceutical, cosmetic or food compositions to hydrolyze polymannans.
                                                                                                                                                                                                                       The present sequence represents the preferred target sequence of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolysis; polysaccharide; mannan; coffee; endo-beta-mannanase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR primer used to amplify DNA encoding an endo-beta-mannanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.9%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 5.6e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
                                                                              Pavco PA,
                                                                             Roberts E,
                                                                                                                                                                                       Claim 1; Page 102; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA46502 standard; cDNA; 15 BP
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99US-00257608.
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                                             (RIBO-) RIBOZYME PHARM INC.
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                                                                             Blatt L, Mcswiggen JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-399535/34.
                                                                                                          WPI; 2000-062023/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coffea arabica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200028046-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR primer; ss
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25-FEB-1999;
23-MAR-1999;
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                                 PCR primers AAA46501-02 were used to amplify DNA encoding an endo-betamennase enzyme, which is involved in the hydrolysis of polysaccharides that consist of molecules of mannan, either simple or branched, linked together by beta (1-4) bonds. The mannanase polynucleotide sequence is used for in vivo modification of the coffee endo-beta-mannanase gene. It is also used to produce transgenic plant cells (especially coffee cells) which have modified properties of mannan polysaccharide, and thus altered flavour or structure. The enzyme is used for modification, degradation or synthesis of mannan polysaccharides in vitro, particularly to treat coffee beans to increase the percentage of dry matter extraction, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present primer was used to reverse transcribe human RNA, from which a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA sequence encoding a protein with heparanase catalytic activity was amplified. The heparanase (hpa) polynucleotide is useful in gene therapy, particularly, the polynucleotide is useful in modulating the bioavailability of heparin-binding growth factors, cellular responses to heparin-binding growth factors (e.g. bFGF) and cytokines (e.g. heparin-binding proteins), cellular responses to interleukin (IL)-8), cell interaction with plasma lipoproteins, cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides encoding a polypeptide having heparanase activity, useful in wound healing and in gene therapy, particularly in treating tumor, inflammation, autoimmunity, neurodegenerative diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, heparanase; gene therapy; tumour; inflammation; autoimmunity; heparin-binding growth factor; cytokine; neurodegenerative plaque; wound healing; infection; burn; angiogenesis; restenosis; atherosclerosis; inflammation; neurodegenerative disease; gerstmann-Straussler Syndrome; Creutzfeldt-Jakob disease; primer; ss.
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                                                                                                                                                                                                                                                                                                                            Length 15;
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                                                                                                                                                                                                                                                                                                                       0.9%; Score 15; DB 1; Le
100.0%; Pred. No. 5.6e+02;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer used to reverse transcribe human RNA.
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Disclosure; Page 32; 41pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA75048 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 AAAAAAAAAAAAA 1
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                                                                                                                                                                                                                                                                                                                                                                    Conservative
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nes 15; Conserva
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                                                                                                                                                                                                                                                                                                                         Query Match
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susceptibility to certain viral and some bacterial and protozoa infections, or disintegration of neurodegenerative plaques. The polynucleocide is also useful in wound healing (e.g. thermal, chemical or radiation burns), and in the treatment of angiogenesis, restenosis, atherosclerosis, inflammation, neurodegenerative diseases (Geretmann-Straussler Syndrome or Creutzfeldt-Jakob disease), and some viral,
                                                                                                                                                                        bacterial or protozoa infections
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Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

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0.9%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 5.6e+02; tive 0; Mismatches 0; Indels
                                                                   1736 AAAAAAAAAAAAA 1750
                                 15, Conservative
 Query Match
Best Local Similarity
                                 Matches
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15 AAAAAAAAAAAA 1 셤

AAA07792 standard; DNA; 15 AAA07792;

Nucleic acid sequence of ODN-e. 23-JUN-2000 (first entry)

Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation; psoriasis; duplex; ss.

Synthetic.

WO200011013-A1.

02-MAR-2000.

99WO-US019029 20-AUG-1999;

98US-0097712P 22-AUG-1998;

(UYNE-) UNIV NEBRASKA

WPI; 2000-246530/21.

non-toxic Modified nucleomonomers, used in physiologically stable, non-toxicoligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics.

Disclosure; Page 20; 42pp; English.

their pharmaceutically acceptable sales. The nucleomonomers are used as monomores in oligomers, which are used in pharmaceutical compositions to monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in calls such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, antisense technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, funging and viruses, oncogenes, growth hormones, serum proteins, adhesion molecules, receptor molecules, cytokines, oncogenes, growth factors and molecules, receptor molecules, cytokines, oncogenes, growth factors and infections associated with pathological conditions cancer, viral infections and bacterial infections (see AAA07786 for details of other uses for which the oligomers are suitable for). Oligomers comprising the nucleomonomers exhibit increased duplex DNA stability when hybridizing to target nucleic acid sequences, are physiologically stable, non-toxic and able to penetrate into cells while maintaining stringent base pair invention provides modified nucleomonomers of specified formula and 

The invention provides modificate inclearmonionmers of the invention provides and provides, oncogenes, growth hormones and enzymes, to target genes or and viruses, oncogenes, growth hormones and enzymes, to target genes or molecules, receptor molecules, receptor molecules, receptor molecules, receptor molecules, provines, oncogenes, growth factors and infections associated with pathological conditions such as inflammatory conditions, cardiovascular disorders, immune reactions, cancer, viral infections and bacterial infections (see AAAO,786 for details of other infections and bacterial infections (see AAAO,786 for details of other or proceed and processed duples DNA stability when hybridizing to be arget into each sequences, are physiologically stable, non-toxic and carge into cales while maintaining stringent base pair fidelity for target DNA sequences. The oligomers described by the form single- or double-stranded target nucleic acid binding activity to form

The invention provides modified nucleomonomers of specified formula and

Disclosure; Page 20; 42pp; English.

Modified nucleomonomers, used in physiologically stable, non-toxic oligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics.

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fidelity for target DNA sequences. The oligomers demonstrate significant single-or double-stranded target nucleic acid binding activity to form duplexes, triplexes or other forms of stable association. Sequences AAA07788-803 represent oligonucleotides forming a third strand along with
                                                                                                                                                                                                                                                       Nucleomonomer; cancer; gene regulation; antigense technology; leukemia; viral infection; inflammatory response; cellular proliferation; psoriasis; duplex; ss.
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                                                                         Score 15; DB 1; Length 15;
Pred. No. 5.6e+02;
                                                                                           0; Indels
                                                       Seguence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;
                                                                               100.0%; Pred. No.
                                                                                                                                                                                                                                     Nucleic acid sequence of ODN-g.
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                                                                          0.9%;
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                                      the duplex sequences
                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                             WO200011013-A1
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                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                AAA07794;
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                                                                                           Matches
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duplexes, triplexes or other forms of stable association. Sequences AAA07788-803 represent oligonucleotides forming a third strand along with

Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;

the duplex sequences

883333

Gaps ö Length 15; 0; Indels DB 1; Le 5.6e+02; Query Match 0.9%; Score 15; DB Best Local Similarity 100.0%; Pred. No. 5.6 Matches 15; Conservative 0; Mismatches

1736 AAAAAAAAAAAAA 1750

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15 AAAAAAAAAAAA 1

AAA07828 standard; DNA; 15 23-JUN-2000 (first entry) AAA07828;

BP.

Nucleic acid sequence of a strand of triplex oligomer 15.

Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation; psoriasis; duplex; triplex; ss.

Synthetic.

WO200011013-A1.

02-MAR-2000

99WO-US019029 0-AUG-1999; 98US-0097712P 22-AUG-1998;

(UYNE-) UNIV NEBRASKA

WPI; 2000-246530/21.

Modified nucleomonomers, used in physiologically stable, non-toxic oligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics.

Disclosure; Page 30; 42pp; English

their pharmaceutically acceptable salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutically acceptable salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, antisense technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, funging and viruses, oncogenes, growth hormones, serum proteins, adhesion and viruses, oncogenes, growth hormones, serum proteins, adhesion molecules, receptor molecules, cytokines, oncogenes, growth factors and interleukins associated with pathological conditions such as inflammatory conditions, cardiovascular disorders, immune reactions, cancer, viral interteukins and bacterial infections (see AAAO7786 for details of other uses for which the oligomers are suitable for). Oligomers comprising to target nucleic acid sequences, are physiologically stable, non-toxic and able to penetrate into cells while maintaining stringent base pair fidelity for target DNA sequences. The oligomers demonstrate significant singles. Triplexes or other forms of table association. Sequences and uplasses, triplexes or other forms of stable association. Sequences invention provides modified nucleomonomers of specified formula and 

Gaps ö 0.9%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 5.6e+02; tive 0; Mismatches 0; Indels Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other; 15, Conservative Query Match Best Local Similarity Matches X S

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1736 AAAAAAAAAAAAA 1750 15 AAAAAAAAAAAA 1 g

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790/c AAA07790 standard; DNA; 15 BP.

AAA07790;

(first entry) 23-JUN-2000 Nucleic acid sequence of ODN-c.

Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation; psoriasis; duplex; ss.

Synthetic.

WO200011013-A1

02-MAR-2000.

99WO-US019029 20-AUG-1999; 98US-0097712P. 22-AUG-1998;

(UYNE-) UNIV NEBRASKA

Gold B;

WPI; 2000-246530/21.

Modified nucleomonomers, used in physiologically stable, non-toxic oligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics.

Disclosure; Page 20; 42pp; English.

The invention provides modified nucleomonomers of specified formula and their pharmaceutically acceptable salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, antisense ceromology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, fungi and viruses, oncogenes, growth hormones and enzymes, to target genes or encoded RNAs that encode enzymes, hormones, serum proteins, adhesion molecules, receptor molecules, cytokines, oncogenes, growth factors and interleukins associated with pathological conditions such as inflammatory conditions, cardiovascular disorders, immune reactions, cancer, viral infections and bacterial infections (sound bacterial infections (sound bacterial) the conditions included to be apply to target nucleic acid sequences, are physiologically stable, non-toxic and able to penetrate into cells while maintaining stringent base pair and allower or double stranded target nucleic acid sequences. The oligomers demonstrate significant and sequences in the oligomers demonstrate significant and sequences. The oligomers demonstrate significant and sequences. inplexes, triplexes or other forms of stable association. Sequences AAA07788-803 represent oligonucleotides forming a third strand along with the duplex sequences AAA07790/C
XX AAA07790/C
XX AAA07790/C
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5.6e+02; hes 0;

Mismatches Pred. No.

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100.08;

Best Local Similarity 100.

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Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation;
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        Length 15;
                       0; Indels
       Score 15; DB 1; Le
Pred. No. 5.6e+02;
                         Mismatches
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0.9%; Sco...
100.0%; Pred
                                                                                                                                                 Nucleic acid sequence of ODN-b
                                                                                               AAA07789 standard; DNA; 15 BP
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                                                        15 AAAAAAAAAAAA 1
                                                                                                                                23-JUN-2000 (first entry)
     Query Match
Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                  Synthetic.
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The invention provides modified nucleomonomers of specified formula and their pharmaceutically acceptable salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, antisense technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, funging and viruses, oncogenes, growth hormones and enzymes, to target genes or encoded RNAs that encode enzymes, hormones, serum proteins, adhesion molecules, receptor molecules, cytokines, oncogenes, growth factors and intections as associated with pathological conditions such as inflammatory conditions, cardiovascular disorders immune reactions, cancer, viral infections and bacterial infections (see AAAO7786 for details of other uses for which the oligomers are suitable for). Oligomers comprising the turled number acid sequences, are physiologically stable, non-toxic and carget nucleic acid sequences, are physiologically stable, non-toxic and carget into cells while maintaining stringent base pair. fidelity for target DNA sequences. The oligomers demonstrate significant single- or double-stranded target nucleic acid binding activity to form duplexes, triplexes or other forms of stable association. Sequences AAA0,7788-803 represent oligonucleotides forming a third strand along with the duplex sequences

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0.9%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 5.6e+02; tive 0; Mismatches 0; Indels
Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;
                                                                                             15; Conservative
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DB 1; Length 15;

0.9%; Score 15;

Query Match

Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;

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The invention provides modified nucleomonomers of specified formula and their pharmaceutically acceptable salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virallycinfected cells. They are used in oligomers for gene regulation, antisense technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, funging and viruses, oncogenes, growth hormones and enzymes, to target genes or encoded RNAs that encode enzymes, hormones, serum proteins, adhesion molecules, receptor molecules, cytokines, oncogenes, growth factors and interleukins associated with pathological conditions such as inflammatory conditions, cardiovascular disorders, immune reactions, cancer, viral infections and bacterial infections (see AAA07786 for details of other uses for which the oligomers are mittable for). Oligomers comprising the nucleonomers exhibit increased duplex DNA steablify when hybridizing to duplexes, triplexes or other forms of stable association. Sequences AAA07788-803 represent oligonucleotides forming a third strand along with target nucleic acid sequences, are physiologically stable, non-toxic and able to penetrate into cells while maintaining stringent base pair fidelity for target DNA sequences. The oligomers demonstrate significant single- or double-stranded target nucleic acid binding activity to form Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation; Modified nucleomonomers, used in physiologically stable, non-toxic oligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics. Disclosure, Page 20, 42pp, English Nucleic acid sequence of ODN-h. 1736 AAAAAAAAAAAAA 1750 AAA07795 standard; DNA; 15 BP 99WO-US019029. (first entry) 15 AAAAAAAAAAAAAA psoriasis; duplex; ss. (UYNE-) UNIV NEBRASKA WPI; 2000-246530/21. WO200011013-A1. 20-AUG-1999; 22-AUG-1998; 23-JUN-2000 AAA07795; Gold B; AAA07795/ ٤,

15 AAAAAAAAAAAAA

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The invention provides modified nucleomonomers of specified formula and their pharmaceutically acceptable salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fundal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, antisense technology, dagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, fungicand viruses, oncogenes, growth hormones and enzymes, to target genes or encoded RNAs that encode enzymes, hormones, serum proteins, adhesion molecules, receptor molecules, containing pathogenic such as inflammatory inferieukins associated with pathological conditions such as inflammatory conditions, cardiovascular disorders, immune reactions, cancer, viral infections and bacterial infections (see AAAO7786 for details of other uncleomonomers exhibit increased duplex DNA stability when hybridizing to nucleomonomers exhibit increased duplex DNA stability when hybridizing to ancepted and an antiable for). Oligomers comprising the cuses for which the oligomers are suitable for). Oligomers base pair fidelity for target DNA sequences. The oligomers demonstrate significant and sequences are suitable acid demonstrate significant and control or acute and acute into cells while maintaining stringent base pair and control or con
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AAA07788-803 represent oligonucleotides forming a third strand along with
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1736 AAAAAAAAAAAAA 1750
                                                                                                                                                                                AAA07797 standard; DNA; 15 BP
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The invention provides modified nucleomonomers of specified formula and their pharmaceutically acceptable salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, antisense technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, funging technology, diagnostic applications to detect target sequences in concoded RNAs that encode enzymes, hormones, serum proteins, adhesion molecules, prowth hormones and enzymes, to target genes or encoded RNAs that encode enzymes, hormones, serum proteins, adhesion molecules, receptor molecules, cytokines, oncogenes, growth factors and interleukins associated with pathological conditions such as inflammatory conditions, cardiovascular disorders; immune reactions, cancer, viral infections and bacterial infections (see AAA07786 for details of other uses for which the oligomers are suitable for). Oligomers comprising to target nucleic acid sequences, are physiologically stable, non-toxic and able to penetrate into cells while maintaining stringent base pair carriangle. The argued DNA sequences. The oligomers demonstrate significant single- or double-stranded target nucleic acid binding activity to form duplexes, triplexes or other forms of stable association. Sequences
                                                                                                                                                                                                    Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation; psoriasis; duplex; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Page 20, 42pp; English.
                                                                                                                                                                 Nucleic acid sequence of ODN-1.
                                      AAA07799 standard; DNA; 15 BP
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es 15; Conserva
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RESULT 1026
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0.9%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 5.6e+02; tive 0; Mismatches 0; Indels

Best Local Similarity 100.0 Matches 15; Conservative

Query Match

us10008789-3.rng

AAA07825 standard; DNA; 15 BP

1028

AAA07825/

(first entry)

23-JUN-2000

AAA07825;

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their pharmaceutically acceptable matternations to be promised as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, antisense technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, fungiand viruses, oncogenes, growth hormones and enzymes, to target genes or molecules, receptor molecules, hormones, serum proteins, adhesion molecules, receptor molecules, cytokines, oncogenes, growth factors and interleukins associated with pathological conditions such as inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conditions, cardiovascular disorders, immune reactions, cancer, viral infections and bacterial infections (see AAA07786 for details of other uses for which the oligomers are suitable for). Oligomers comprising the nucleomonomers exhibit increased duplex DNA stability when hybridizing to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 et nucleic acid sequences, are physiologically stable, non-toxic and to penetrate into cells while maintaining stringent base pair lity for target DNA sequences. The oligomers demonstrate significant
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                                                                                                                                                                                                  Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention provides modified nucleomonomers of specified formula and
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AAA07788-803 represent oligonucleotides
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                                                                                                                                                            Nucleic acid sequence of ODN-0.
                                        ВР
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                                        AAA07802 standard; DNA; 15
                                                                                                                  23-JUN-2000 (first entry)
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                                                                                                                                                                                                                                                                                     Synthetic.
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RESULT 1027
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The invention provides modified nucleomonomers of specified formula and their pharmaceutically acceptable salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, antisense technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, funging and viruses, oncogenes, growth hormones and enzymes, to target genes or encoded RNAs that encode enzymes, hormones, serum proteins, adhesion molecules, receptor molecules, cytchines, oncogenes, gandhesion conditions, cardiovascular disorders, immune reactions, cancer, viral infections and bacterial infections (see AAAA07786 for details of other uncelecomonomers exhibit increased duplex NNA stability when hybridizing to nucleomonomers exhibit increased duplex NNA stability when hybridizing to
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                                                                                                                                                  Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation; psoriasis; duplex; triplex; ss.
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100.0%; Pred. No. 5.68+02;
tive 0; Mismatches 0; Indels
                                                                                                                Nucleic acid sequence of a strand of triplex oligomer 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;
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Best Local Similarity
Local 15; Conservative
Then 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYNE-) UNIV NEBRASKA.
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                                                                                                                                                                                                                                                                                 VO200011013-A1.
                                                                                                                                                                                                                                                                                                                                                                20-AUG-1999;
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                                                                                                                                                                                                                                                                                                                        12-MAR-2000
                                                                                                                                                                                                                                           Synthetic.
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ID AAA078
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Gaps

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1736 AAAAAAAAAAAAA 1750

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Conservative

Best Local Similarity Matches 15; Conserva

Query Match

15 AAAAAAAAAAAAA 1

Length 15; 0; Indels

stable association. Sequences es forming a third strand along with

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AAA07831;
      Gold B;
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                                               Gaps
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0
                      Score 15; DB 1; Length 15;
Pred. No. 5.6e+02;
0; Mismatches 0; Indels
Seguence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;
                     0.9%; Pre
                                               Conservative
                                 Local Similarity
                      Query Match
                                              Matches
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1736 AAAAAAAAAAAA 1750

Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation; psoriasis; duplex; triplex; ss. Nucleic acid sequence of a strand of triplex oligomer 16 Disclosure; Page 30; 42pp; English. 99WO-US019029 98US-0097712P 23-JUN-2000 (first entry) (UYNE-) UNIV NEBRASKA WPI; 2000-246530/21 WO200011013-A1. 22-AUG-1998; 20-AUG-1999; 02-MAR-2000. Synthetic.

Modified nucleomonomers, used in physiologically stable, non-toxicoligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics.

Disclosure; Page 20; 42pp; English

The invention provides modified nucleomonomers of specified formula and their pharmaceutically acceptable salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, antisense technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, funging an viruses, oncogenes, growth hormones and enzymes, to target genes or encoded RNAs that encode enzymes, hormones, serum proteins, adhesion molecules, receptor molecules, octokines, oncogenes, growth factors and intectleukins associated with pathological conditions such as inflammatory conditions and bacterial infections (see AAA07786 for details of other uses for which the oligomers are suitable for). Oligomers comprising the target nuclear acid sequences, are physiologically stable, non-toxic and target nuclear acid sequences, are physiologically stable, non-toxic and target into cells while maintaining stringent base pair files the pathology. fidelity for target DNA sequences. The oligomers demonstrate significant single- or double-stranded target nucleic acid binding activity to form duplexes, triplexes or other forms of stable association. Sequences AAA07820-834 represent sequences forming triplex oligomers

15 AAAAAAAAAAAAA 1 RESULT 1030

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AAA07803/c ID AAA07803 standard; DNA; 15 XX XX AC AAA07803; XX

Nucleomonomer; cancer; gene regulation; antieense technology; leukemia; viral infection; inflammatory response; cellular proliferation; psoriasis; duplex; ss. Modified nucleomonomers, used in physiologically stable, non-toxic oligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics. Nucleic acid sequence of ODN-p. 99WO-US019029. 98US-0097712P. (first entry) UYNE-) UNIV NEBRASKA WPI; 2000-246530/21. WO200011013-A1. 23-JUN-2000 20-AUG-1999; 22-AUG-1998; 02-MAR-2000 Synthetic. Gold B; 

their pharmaceutically acceptable salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutically acceptable salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in calls such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, antisense technology, diagnostic applications to detect target sequences in and viruses, oncogenes, growth hormones and enzymes, to target genes or encoded RNAs that encode enzymes, hormones, serum proteins, adhesion molecules, receptor molecules, cytokines, oncogenes, growth factors and interleukins associated with pathological conditions such as inflammatory conditions, cardiovascular disorders, immune reactions, cancer, viral infections and bacterial infections (see AAAO/7786 for details of other uses for which the oligomers are sulitable for). Oligomers comprising the nucleomonomers exhibit increased duplex DNA stability when hybridizing to duplexes, triplexes or other forms of stable association. Sequences AAA07788-803 represent oligonucleotides forming a third strand along with target nucleic acid sequences, are physiologically stable, non-toxic and able to penetrate into cells while maintaining stringent base pair fidelity for target DNA sequences. The oligomers demonstrate significant single- or double-stranded target nucleic acid binding activity to form invention provides modified nucleomonomers of the duplex sequences

Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

Gaps ö 0.9%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 5.6e+02; tive 0; Mismatches 0; Indels 15; Conservative Local Similarity Query Match Matches

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1736 AAAAAAAAAAAAA 1750

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AAA07834 standard; DNA; 15 BP. AAA07834; AAA07834/c SAXAX

RESULT 1031

(first entry) 23-JUN-2000

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The invention provides modified nucleomonomers of specified formula and their pharmaceutically acceptable salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally. Infected cells. They are used in oligomers for gene regulation, antisense in clected cells. They are used in oligomers for gene regulation, antisense technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, fungi and viruses, oncogenes, growth hormones and enzymes, to target genes or encoded RNAs that encode enzymes, hormones, serum proteins, adhesion molecules, receptor molecules, cytokines, oncogenes, growth factors and interleukins associated with pathological conditions such as inflammatory conditions, cardiovascular disorders, immune reactions, cancer, viral infections and bacterial infections (see AAA07786 for details of other uncleomonomers exhibit increased duplex DNA stability when hybridizing to nucleomonomers exhibit increased duplex DNA stability when hybridizing to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fidelity for target DNA sequences. The oligomers demonstrate significant single- or double-stranded target nucleic acid binding activity to form duplexes, triplexes or other forms of stable association. Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             target nucleic acid sequences, are physiologically stable, non-toxic and able to penetrate into cells while maintaining stringent base pair
                                             Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation; psoriasis; duplex; triplex; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified nucleomonomers, used in physiologically stable, non-toxic oligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics.
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AAA07820-834 represent sequences forming triplex oligomers
Nucleic acid sequence of a strand of triplex oligomer 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Page 30; 42pp; English
                                                                                                                                                                                                                                                                                                                                          98US-0097712P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-246530/21.
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                                                                                                                                                                                                                                                                                          20-AUG-1999;
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                                                                                                                                                                                                                                            02-MAR-2000
                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gold B;
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Gaps ö 0.9%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 5.6e+02; 0; Indels Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other; 100.0%; Pred. ...ive 0; Mismatches Ouery Match Best Local Similarity 100.0 Matches 15. Conservative

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1736 AAAAAAAAAAAAA 1750

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AAA07796 standard; DNA; 15 BP 23-JUN-2000 (first entry) AAA07796; RESULT 1032 

Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; Nucleic acid sequence of ODN-i.

The invention provides modified nucleomonomers of specified formula and their pharmaceutically acceptable salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, antisense technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, funging on viruses, oncogenes, growth hormones and enzymes, to target genes or encoded RNAs that encode enzymes, hormones, serum proteins, adhesion molecules, receptor molecules, crockines, oncogenes, growth factors and interleukins associated with pathological conditions such as inflammatory conditions, cancer, viral infections and bacterial infections (see AAA07786 for details of other uses for which the oligomers are suitable for). Oligomers comprising to target nucleic acid sequences, are physiologically stable, non-toxic and able to penetrate into cells while maintaining stringent base pair fidelity for target DNA sequences. The oligomers demonstrate significant single-kep, triplexes or other forms of stable association. Sequences duplexes, triplexes or other forms of stable association. Sequences Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation; psoriasis; duplex; ss. Gaps Modified nucleomonomers, used in physiologically stable, non-toxic oligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics. viral infection; inflammatory response; cellular proliferation; ö Query Match

0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels Seguence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 Other; Disclosure; Page 20; 42pp; English. Nucleic acid sequence of ODN-m. 1736 AAAAAAAAAAAAA 1750 AAA07800 standard; DNA; 15 BP 99WO-US019029 98US-0097712P 15 AAAAAAAAAAAA 1 (first entry) psoriasis; duplex; ss (UYNE-) UNIV NEBRASKA the duplex sequences WPI; 2000-246530/21. 40200011013-A1 22-AUG-1998; 20-AUG-1999; 23-JUN-2000 02-MAR-2000 Synthetic. AAA07800; Gold B; RESULT 1033 AAA078 \$\$\$\$\$\$\$\$\$\$\$\$\$\$ 윤

WO200011013-A1.

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Modified nucleomonomers, used in physiologically stable, non-toxic oligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics.
                                                                                                                          Disclosure; Page 20; 42pp; English.
                                       99WO-US019029.
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                                                               (UYNE-) UNIV NEBRASKA
                                                                                       WPI; 2000-246530/21.
                 WO200011013-A1.
                                        20-AUG-1999;
                                                    22-AUG-1998;
                             02-MAR-2000
     Synthetic.
                                                                                                                                                                                                                                                     single-
                                                                           Gold B;
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Gaps ö 0.9%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 5.6e+02; live 0; Mismatches 0; Indels Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other; 1736 AAAAAAAAAAAAA 1750 15; Conservative Local Similarity Query Match Matches ò

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Gaps

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AAA07793; RESULT 1034
AAA07793/c
XX
AC AAA07793
XX
XX
XX
DE Nucleic
XX
XW Nucleom
XW Nucleom
XW Sontheti 요

Nucleic acid sequence of ODN-f.

23-JUN-2000 (first entry)

Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation;

psoriasis; duplex; ss.

WO200011013-A1

Synthetic

Nucleic acid sequence of ODN-k.

Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation; psoriasis; duplex; ss.

Synthetic

The invention provides modified nucleomonomers of specified formula and their pharmaceutically acceptable salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, antisense technology, diagnostic applications to detect target sequences in the biological samples such as those containing pathogenic bacteria, funging and viruses, oncogenes, growth hormones and enzymes, to target genes or encoded RNAs that encode enzymes, hormones, acrum proteins, adhesion molecules, receptor molecules, cancer, viral interleukins associated with pathological conditions such as inflammatory conditions, cardiovascular disorders, immune reactions, cancer, viral conditions, cardiovascular disorders, immune reactions, cancer, viral unfections and bacterial infections (see AAAOT786 for details of other uses for which the oligomers are suitable for). Oligomers comprising to nucleomonemers exhibit increased duples, but stability when proprieting and companied the consumers are suitable for). Oligomers comprising to nucleomonemers exhibit increased duples, when the validations when the consumers are suitable for a pathility when providing to nucleomonemers. duplexes, triplexes or other forms of stable association. Sequences AAA07788-803 represent oligonucleotides forming a third strand along with target nucleic acid sequences, are physiologically stable, non-toxic and able to penetrate into cells while maintaining stringent base pair y for target DNA sequences. The oligomers demonstrate significant or double-stranded target nucleic acid binding activity to form Eidelity for target DNA sequences. duplex sequences

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BP. AAA07793 standard; DNA; 15 15 AAAAAAAAAAAAA

their pharmaceutically acceptable salts. The nucleomonomers are used and check their pharmaceutically acceptable salts. The nucleomonomers are used an monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, antisense centonology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, fungi and viruses, oncogenes, growth hormones and enzymes, to target genes or encoded RNAs that encode enzymes, hormones, serum proteins, adhesion molecules, receptor molecules, cythines, oncogenes, growth factors and interleukins associated with pathological conditions such as inflammatory conditions, cardiovascular disorders, immune reactions, cancer, viral infections and bacterial infections (see AAAO7786 for details of other uses for which the oligomers are suitable for). Oligomers comprising to target nucleic acid sequences, are physiologically stable, non-toxic and able to penetrate into cells while maintaining stringent base pair fidelity for target DNA sequences. The oligomers demonstrate significant single-kes, triplexes or other forms of stable association. Sequences and AAAO7788-803 represent oligomucleotides forming a third strand along with The invention provides modified nucleomonomers of specified formula and non-toxic Modified nucleomonomers, used in physiologically stable, non-toxioligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics. Score 15; DB 1; Length 15; Pred. No. 5.6e+02; 0; Mismatches 0; Indels Seguence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other; Disclosure; Page 20; 42pp; English. AAA07798 standard; DNA; 15 BP. 0.9%; 1736 AAAAAAAAAAAA 1750 99WO-US019029. 98US-0097712P. 23-JUN-2000 (first entry) Query Match 0.9 Best Local Similarity 100. Matches 15, Conservative 15 AAAAAAAAAAAAAA (UYNE-) UNIV NEBRASKA the duplex sequences WPI; 2000-246530/21 20-AUG-1999; 22-AUG-1998; 02-MAR-2000. AAA07798; Gold B; RESULT 1035 AAA07798/c ò 셤  us10008789-3.rng

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the invention provides montrial interendential or specified to indicate and characterizatly acceptable aslts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in calls such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, antisense technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, fungicand viruses, oncogenes, growth hormones and enzymes, to target genes or encoded RNAs that encoded enzymes, hormones, serum proteins, adhesion molecules, receptor molecules, cytokines, oncogenes, growth factors and interleukins associated with pathological conditions such as inflammatory conditions, cardiovascular disorders, immune reactions, cancer, viral infections and bacterial infections (see AAAO/796 for details of other uses for which the oligomers are suitable for). Oligomers comprising to target nucleic acid sequences, are physiologically stable, non-toxic and able to penetrate into cells while maintaining stringent base pair fidelity for target DNA sequences. The oligomers demonstrate significant single-xes, triplexes or other forms of stable association. Sequences of the forms of stable association. Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                             invention provides modified nucleomonomers of specified formula and
                                                                                                                                                                                                                                                                                                 Modified nucleomonomers, used in physiologically stable, non-toxic oligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics.
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                                                                                                                                                                                                                                                                                                                                                                                               Disclósure; Page 20; 42pp; English.
                                                                 99WO-US019029
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                                                                                                                                                           (UYNE-) UNIV NEBRASKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the duplex sequences
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                                                                 20-AUG-1999;
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                     02-MAR-2000.
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The invention provides modified nucleomonomers of specified formula and their pharmaceutically acceptable salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally-colls amples such as those containing pathogenic bacteria, funging technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, funging and viruses, oncogenes, growth hormones and enzymes, to target genes or encoded RNAs that encode enzymes, hormones, serum proteins, adhesion molecules, receptor molecules, conceptions and pathological conditions such as inflammatory conditions, cancer, viral infections and bacterial infections (see AAA07786 for details of other uses for which the oligomers are suitable for). Oligomers comprising the uncleic acid sequences, are physiologically stable, non-toxic and able to penetrate into cells while maintaining stringer base pair fidelity for target DNA sequences. The oligomers demonstrate significant single- or double-stranded target nucleic acid binding activity to form the angles of the collipomers forms of stable association. Sequences and allong with the collipomers or other forms of stable association.

Modified nucleomonomers, used in physiologically stable, non-toxic oligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics.

98US-0097712P.

(UYNE-) UNIV NEBRASKA

WPI; 2000-246530/21.

3old B;

99WO-US019029.

20-AUG-1999; 22-AUG-1998; Disclosure; Page 20; 42pp; English.

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Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation;
                          Gaps
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O.9%; Score 15; DB 1; Length 15; Local Similarity 100.0%; Pred. No. 5.6e+02; les 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                              Nucleic acid sequence of ODN-d.
                                                   1736 AAAAAAAAAAAAA 1750
                                                                                                                                      AAA07791 standard; DNA; 15 BP
                                                                        15 AAAAAAAAAAAA 1
                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                               psoriasis; duplex; ss
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                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                              AAA07791;
  Query Match
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                                                                                                                                      BXBXBXBXBXBXBXBXBXBXBXBXB
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99WO-US019029.

20-AUG-1999;

Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation; psoriasis; duplex; ss.

WO200011013-A1

Synthetic.

02-MAR-2000

Nucleic acid sequence of ODN-a.

23-JUN-2000 (first entry)

AAA07788;

788/c AAA07788 standard; DNA; 15 BP

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Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

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Gaps

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0; Indels

0.9%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 5.6e+02;

100.0%; Prec. ...

15; Conservative

Local Similarity

Query Match Matches 1736 AAAAAAAAAAAAA 1750

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AAAAAAAAAAAAA

the duplex sequences

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The invention provides modified nucleomonomers of specified formula and their pharmaceutically acceptable salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virally-infected cells. They are used in oligomers for gene regulation, antisense technology, diagnostic applications to detect target sequences in the cechnology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, funging anythuses, oncogenes, growth hormones and enzymes, to target genes or encoded RNAs that encode enzymes, hormones, serum proteins, adhesion molecules, receptor molecules, cytokines, oncogenes, growth factors and molecules, raceptor molecules, cytokines, oncogenes, growth factors and conditions, cardiovascular disorders, immune reactions, cancer, viral infections and bacterial infections (seee AAA07786 for details of other uses for which the oligomers are suitable for). Oligomers comprising to target nucleic acid sequences are physiologically stable, non-toxic and able to penetrate into cells while maintaining stringent base pair fidelity for target by a sequences. The oligomers demonstrate singlicant single- or double-stranded target nucleic acid binding activity to form the dunlar seament oligonucleotides forming a third strand along with the dunlar seament oligonucleotides forming a third strand along with
                                                                                                                                                                       Modified nucleomonomers, used in physiologically stable, non-toxic oligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics.
                                                                                                                                                                                                                                                      Disclosure; Page 20; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid sequence of ODN-n.
                    98US-0097712P
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                                                        (UYNE-) UNIV NEBRASKA.
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                                                                                                                                   WPI; 2000-246530/21.
                    22-AUG-1998;
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ö Gaps ö 0.9%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 5.6e+02; tive 0; Mismatches 0; Indels Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 Other; Query Match Best Local Similarity 100. Matches 15; Conservative

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Nucleomonomer; cancer; gene regulation; antisense technology; leukemia; viral infection; inflammatory response; cellular proliferation;

psoriasis; duplex; ss.

Synthetic.

WO200011013-A1.

02-MAR-2000.

99WO-US019029 20-AUG-1999;

98US-0097712P. 22-AUG-1998;

(UYNE-) UNIV NEBRASKA

The invention provides modified nucleomonomers of specified formula and their pharmaceutically acceptable salts. The nucleomonomers are used as monomers in oligomers, which are used in pharmaceutical compositions to inhibit expression of nucleic acid molecules including DNA and RNA in cells such as bacterial, fungal, yeast, mammalian, cancer and virallycificated cells. They are used in oligomers for gene regulation, antisense technology, diagnostic applications to detect target sequences in biological samples such as those containing pathogenic bacteria, funging and viruses, oncogenes, growth hormones and enzymes, to target genes or encoded RNAs that encode enzymes, hormones, serum proteins, adhesion concecules, receptor molecules, cytokines, oncogenes, growth factors and interleukins associated with pathological conditions such as inflammatory conditions, carcial vascular disorders, immune reactions, cancer, viral infections and bacterial infections (see AAA07786 for details of other uses for which the oligomers are suitable for). Oligomers comprising to target nucleic acid sequences, are physiologically stable, non-toxic and able to penetrate into cells while maintaining stringent base pair conditions target DNA sequences. The oligomers demonstrate significant single or deuble-stranded target nucleic acid binding activity to form duplaces, triplexes or other forms of stable association. Sequences

Gaps ö 0.9%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 5.6e+02; 0; Indels 15, Conservative Local Similarity Query Match Matches

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Oligonucleotide #2 containing 3'-C-amino-5'(S)-C,3'-N-ethanothymidine.

Conformationally-locked oligonucleotide; antisense inhibitor; bicyclic sugar nucleoside analogue; gene probe; ds.

/mod\_base= OTHER /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine" '\*tag= a modified base

/\*tag= b /mod\_base= OTHER /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"

Modified nucleomonomers, used in physiologically stable, non-toxic oligomers used to inhibit expression of nucleic acids and in gene regulation, antisense technology and diagnostics. Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 Other; 100.0%; Prec. ... Location/Qualifiers Disclosure; Page 20; 42pp; English. 1736 AAAAAAAAAAAAA 1750 AAA62350 standard; DNA; 15 BP 15 AAAAAAAAAAAAA 1 06-NOV-2000 (first entry) the duplex sequences WPI; 2000-246530/21 Key modified\_base Synthetic. AAA62350; Gold B; RESULT 1039 AAA62350/ ò d 

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The present sequence is an oligonucleotide containing 3'-C-amino-5'(R)-C'3'-N'-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in the sequence were incorporated by phosphoramidite chemistry using a DNA synthesiser. Bicyclic sugar nucleosides are conformationally restricted 3',5'-bridged nucleosides which can be used as building blocks for oligonucleotides on legonucleotides can be produced that have certain, desired, geometrical shapes and entropy advantages. They may have superior hybridisation to DNA and RNA, and excellent biological as antisense inhibitors of gene expression or as gene probes, and may therefore be used in antisense therapeutics or gene-specific diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New conformationally restricted 3',5'-bridged nucleosides and oligonucleotides useful as antisense therapeutics or as gene-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide #4 containing 3'-C-amino-5'(R)-C,3'-N-ethanothymidine.
/mod_base= OTHER
/note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
                                                                                              note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
                                                                                                                                                                                                                                                /note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
                                                                                                                                                                     'note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conformationally-locked oligonucleotide, antisense inhibitor;
bicyclic sugar nucleoside analogue, gene probe; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.9%; Score 15; DB 1; Length 15;
100.0%; Pred. No. 5.6e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 20; Col 15; 10pp; English.
                                                                                                                                     /*tag= f
/mod_base= OTHER
                                                                                                                                                                                                             /*tag= g
/mod_base= OTHER
                                                                              OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1736 AAAAAAAAAAAAA 1750
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                                                          /*tag= e
/mod base=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ICNC ) ICN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-451496/39.
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les 15; Conserv
                              modified base
                                                                                                                                                                                             modified base
                                                                                                                modified base
                                                                                                                                                                                                                                                                                                                                                                       11-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                           11-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnostics.
                                                                                                                                                                                                                                                                                          US6083482-A
                                                                                                                                                                                                                                                                                                                                04-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA62348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA62348/c
  8
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                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is an oligonuclectide containing 3'-C-amino-5'(S)-C'3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in the sequence were incorporated by phosphoramidite chemistry using a DNA synthesiser. Bicyclic sugar nucleosides are conformationally restricted 3',5'-bridged nucleosides which can be used as building blocks for oligonucleotides. Oligonucleotides can be produced that have certain, desired, geometrical shapes and entropy advantages. They may have superior hybridisation to DNA and RNA, and excellent biological as antisense inhibitors of gene expression or as gene probes, and may therefore be used in antisense therapeutics or gene-specific diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide #3 containing 3'-C-amino-5'(R)-C,3'-N-ethanothymidine.
                                                                                                                                                                                                                                                                    New conformationally restricted 3',5'-bridged nucleosides and oligonucleotides useful as antisense therapeutics or as gene-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mod_base= OTHER
'note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *tag= b
mod_base= OTHER
'note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mod_base= OTHER
/note= "3'-C-amino-5'(R)-C,3'-N-ethanothymidine"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conformationally-locked oligonucleotide; antisense inhibitor;
bicyclic sugar nucleoside analogue; gene probe; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.9%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 5.6e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                Example 20; Col 16; 10pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA62347 standard; DNA; 15 BP
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                                                                          99US-00309742
                                                                                                                99US-00309742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-NOV-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                       (ICNC ) ICN PHARM INC
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modified_base
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                                                                                                                  11-MAY-1999;
                                                                            11-MAY-1999;
                                                                                                                                                                                                                                                                                                              diagnostics.
US6083482-A
                                  04-JUL-2000
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Mon Aug 16 16:46:36 2004

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/mod_base= OTHER
/note= "Optionally thymidine has EDTA covalently attached
at C-5"
                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is an oligonucleotide containing 3'-C-amino-5'(R)-C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in the sequence were incorporated by phosphoramidite chemistry using a DNA synthesiser. Bicyclic sugar nucleosides are conformationally restricted 3',5'-bridged nucleosides which can be used as building blocks for oligonucleotides. Oligonucleotides can be produced that have certain, desired, geometrical shapes and entropy advantages. They may have superior hybridisation to DNA and RNA, and excellent biological stability. The conformationally-modified oligonucleotides may be useful as ancisense inhibitors of gene expression or as gene probes, and may therefore be used in antisense therapeutics or gene-specific diagnostics
                                                                                                                                                                                                                                                                                                                                                 New conformationally restricted 3',5'-bridged nucleosides and oligonucleotides useful as antisense therapeutics or as gene-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                   /*tag= b
/mod_base= OTHER
/note= "3'-C-amino-5'(R)-C,3'-3'-N-ethanothymidine"
                                                        /note= "3'-C-amino-5'(R)-C,3'-3'-N-ethanothymidine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hybridisation probe; DNA cleavage; double-helix; oncogene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.9%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 5.6e+02; vative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                            Example 20; Col 15; 10pp; English.
                           /*tag= a
/mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligo dT15 EDTA labelled probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1736 AAAAAAAAAAAA 1750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP
                                                                                                                                                                                                     99US-00309742
                                                                                                                                                                                                                                  99US-00309742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 AAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH20308 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15; Conservative
                                                                                                                                                                                                                                                             (ICNC ) ICN PHARM INC
                                                                                                                                                                                                                                                                                                                       WPI; 2000-451496/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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modified_base
 Key
modified base
                                                                     modified base
                                                                                                                                                                                                     11-MAY-1999;
                                                                                                                                                                                                                                  11-MAY-1999;
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                                                                                                                                             US6083482-A
                                                                                                                                                                        04-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                diagnostics.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH20308;
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                                                                                                                                                                                                                                                                                           Wang G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1042
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           /mod_base= OTHER
/note= "Optionally thymidine has EDTA covalently attached
at C-5"
                                                                                         /*tag= c
/mod base= OTHER
/note= "Optionally thymidine has EDTA covalently attached
at C-5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to hybridisation probes which target a specific sequence within a large double-helical nucleic acid. The probe is complementary to the target sequence and contains at least one nucleotide with an attached molecule that is able to cleave double-helical DNA e.g. EDTA-Fe(II) (ethylenediamineterracetic acid-iron complex). The probes where the attached molecule is a label or compound that alters gene expression, are used for specific detection and/or cleavage of doublehelical DNA, e.g. for disgnosis, for treatment of disease (particularly caused by viruses, genetic defects or oncogenes), for chromosomal analysis, and for the isolation and mapping of genes. The present
                                                                                                                                                                                                                                                                                                                                                                                                                   New hybridization probe for specific triplex formation with large double helices, useful e.g. for site-specific diagnostic cleavage, contains attached functional residue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore; hybridisation; detection; fluorescence; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence represents probe of the invention used in an example illustrating how the probe binds to and cleaves double stranded DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.9%; Score 15; DB 1; Length 15; 00.0%; Pred. No. 5.6e+02; ve. 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide portion of ODN-MGB-LF conjugate.
                                                                                                                                                                                                                                                                                                                             (FLEH-) FLEHR HOHBACH TEST ALBRITTON & HERBERT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.75,
100.0%; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Fig 3B; 20pp; English.
                                                                                                                                                                                                                                                            87US-00115922.
90US-00614205.
93US-00152250.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1736 AAAAAAAAAAAAA 1750
                                                                                                                                                                                                                                 98US-00128732.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence represents probe of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF30882/c
ID AAF30882 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 AAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.9
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                            Dervan PB, Moser HE;
                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-342909/36.
                                                                                                                                                                       US2001002314-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200131063-A1
modified base
                                                                            modified base
                                                                                                                                                                                                                               04-AUG-1998;
                                                                                                                                                                                                                                                                30-OCT-1987;
                                                                                                                                                                                                                                                                              16-NOV-1990;
12-NOV-1993;
                                                                                                                                                                                                    31-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF30882;
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DE10051726-A1.
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ID AAF4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of the oligonucleotide (ODN) component of an ODN-MGB (minor groove binder)-LF (latent fluorophore) conjugate of the invention. WGBB bind in a non-intercalating manner to the minor groove of non-single-stranded DNA, RNA or their hybrids, while a LF binds similarly but in an intercalating manner, or lies in the minor groove, or is cutented in some other way to the DNA molecule by MGB, such that it becomes fluorescent (or its fluorescent properties change detectably).

The conjugates are used as hybridisation probes and amplification primers for fluorescent detection of specifically hybridising sequences, for analysis or diagnosis, especially (real-time) PCR, for single-nucleotide mismatch discrimination, target or signal amplification, array-based assays and sequencing, including detection of double-stranded DNA by criples formation. Many different targets can be detected a single reaction vessel. The present ODN-MGB-LF conjugate was used to demonstrate hybridisation-triggered fluorescence. Upon hybridisation to the complementary target sequence there was an increase in fluorescence yield, measured as the ratio of the fluorescence emitted by the hybrid between the ODN-MGB-LF conjugate sequence of the fluorescence emitted by unhybridised (i.e. single-stranded) ODN-MGB-LF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                      Conjugate of oligonucleotide, minor groove binder and latent fluorophore, useful for detecting specific nucleic acids, e.g. for single-nucleotide mismatch discrimination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-linked vinyl acetate copolymer carrier material, AIDS treatment, phosphorothioate; solid phase synthesis; modified oligonucleotide; clinical diagnostic; cancer treatment; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide b) for solid phase synthesis of oligonucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mod_base= OTHER
/note= "Phosphorothioate deoxynucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.9%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 5.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Pred. ...
                                                                                                                                         Vermeulen NMJ;
                                                                                                                                                                                                                                                                     Disclosure, Page 58; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВР
                                                                                                          (EPOC-') EPOCH BIOSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1736 AAAAAAAAAAAAA 1750
                                              26-OCT-2000; 2000WO-US029786.
                                                                          99US-00428236
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                         Afonina IA,
                                                                                                                                                                       WPI; 2001-328656/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
modified_base
                                                                          26-OCT-1999;
              03-MAY-2001
                                                                                                                                         Dempcy RO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
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hydrolysed cross-linked vinyl acetere copolymer carrier material loaded with nucleotide derivative(s). The product is an intermediate for the large (gram) scale solid phase synthesis of modified obligonucleotides useful e.g. as clinical diagnostics and therapeutics, e.g. for the treatment of AIDS and cancers. The presence of the partially hydrolysed copolymer facilitates the synthesis of larger amounts of oligonucleotides compared with the use of Merckogel (RTM, macroporous polyvinyl acetate) described in Nucleic Acid Res Sympos. Ser. 31, p. 153, 1994.

Cligonucleotides are obtained in very good quality and high yields, Also, the nucleosides do not display the reduced activity seen in some prior art procedures, less carrier material, reagents and solvent are required. Further, the carrier material is biodegradable and thus does not present disposal problems. It also swells uniformly in a range of solvents, which obviates expansion or contraction during use or solvent exchange.

AAH20510-AAH20513 represent oligonucleotides containing modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Intermediate for oligonucleotide synthesis comprises partially hydrolysed cross-linked vinyl acetate copolymer loaded with nucleotide derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel chemical product comprising a partially
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                Seliger H, Sobkowski M, Hinz M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Page 5; 8pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF49041 standard; DNA; 15 BP.
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                                                                                                                                                                  99DE-01052376.
                                                                                   18-OCT-2000; 2000DE-01051726
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                                                                                                                                                                                                                                                 MERE ) MERCK PATENT GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IGF-I oligonucleotide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-336414/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40200078341-A1
                                                                                                                                                              30-OCT-1999;
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10-MAY-2001.
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99US-0140345P.

antisense agents

New DNA-peptide nucleic acid chimeras, useful e.g. as antisense for treating e.g. cancer, also as diagnostic probes and primers.

(AVET ) AVENTIS PHARMA DEUT GMBH

Uhlmann E, Breipohl G; WPI; 2001-591267/67.

95EP-00103332

08-MAR-1995; 14-MAR-1994;

08-MAR-1995; 2001EP-00104012.

04-JUL-2001.

Example 26; Page 40; 54pp; German.

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Wraight CJ, Werther GA, Edmondson SR;
           (MURD-) MURDOCH CHILDRENS RES INST.
21-JUN-2000; 2000WO-AU000693
      21-JUN-1999;
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The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF4151 and AAF45153-64516). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperpoliferation of the inside of blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                        Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inibits or reduces growth factor mediated cell proliferation and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                Example 8; Page 60; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vessels or any other hyperplasia
WPI; 2001-041421/05.
                                                                                                                                                                                                                                            inflammation.
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1735 CAAAAAAAAAAA 1749
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15 CAAAAAAAAAAAA 1

PNA-forming oligonucleotide #7. AAH49243 standard; DNA; 15 26-NOV-2001 (first entry) AAH49243; RESULT 1046 AAH49243/C
ID AAH4924
AC AAH4924
XX AAH4924
XX AAH4924
XX BND-E0
X

Polyamide-oligonucleotide derivative; anticancer; antiproliferative; antiviral; hepatotropic; vasotropic; antisense inhibition; ribozyme; integrin; cell-cell adhesion; cancer; restenosis; stability; PNA; peptide nucleic acid; ss

Synthetic

Location/Qualifiers

/\*tag= b /mod\_base= OTHER /note= "t-hex" /mod\_base= OTHER /note= "t-but" \*tag≕ a Key modified\_base modified\_base

EP1113021-A2

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This invention describes novel polyamide-oligomuclectide derivatives (I) and their physiologically acceptable salts of formula F((DNA)-Li)_g(PNA-Li) s(PNA)_Li) s(PNA)_Li). T(DNA-Li) s(PNA)_Li) a(PNA)_Li) and vasotropic activity and can be used for the inhibition of gene conservation by anticancer, antiproliferative, antiviral, hepatictisense, the intipoliferative and vasotropic activity and can be used for trapleholy activity and can be used for trapleholy and particular actions, for trapleholy and activity and antisense reagents. They are also useful in the increased affinity for complementary strands and better stability in the increased affinity for complementary strands and better stability in the increased affinity for complementary strands and better stability in the active than either DNA or PNA oligomers, when used as probes, (I) and advantages, i.e. have improved cellular uptake, do not aggregate in amplificant responses to base-pair mismatches in the DNA and PNA and PNA segments, allowing better discrimination between pathogenic conditions such as the transition from pathogenic and non-pathogenic conditions such as the transition from pathogenic and non-pathogenic conditions such as the transition from pathogenic and no elections such as the transition from pathogenic conditions such as the transition and pathogenic and no elections suc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 may be incorporated into a gene. AAH49208-AAH49264 represent oligonucleotides used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.9%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 5.6e+02; tive 0; Mismatches 0; Indels
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may be incorporated into a gene. AAH49208-AAH49264 repre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15; Conservative
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ABL40743/c
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(first entry)

03-JUL-2002

ABL40743;

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Gaps

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purification

and purifi

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This invention relates to oligonucleotide analogues comprising a protein nucleic acid molecule (PNA) monomer. They are used in the detection and connucled and confidence and molecules and as probes, primers, linkers, adapters and antisense agents on solid supports. Modifications enhance that use as capture and detection probes e.g. by the incorporation of their use as capture and detection probes e.g. by the incorporation of itorin, digoxigenen, radioisotopes, fluorescent labels such as illuminated are reporter molecules such as alkaline phosphatase. They are also used for enhancing or inhibiting the activity of an enzyme or callular activity. The compounds are stable to nucleases and proteases, backbone of PNAs is resistant to both nucleases and proteases. PNAs bind nucleic acid molecules with greater affinity than DNA or RNA concentration. The compounds are relatively simple to synthesize and are used in a wide variety of applications. This sequence represents a DNA oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mutation detection method tag peptide coding sequence SEQ ID NO: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mutation detection; primer; mutant; tag; tumour suppressor gene; protein production; cancer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.9%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 5.6e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                           separation
dimers and
                                                                      Efimov V, Fernandez J, Archdeacon D, Archdeacon J;
Chakhmakhcheau O, Buryakova A, Choob M, Hondorp K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
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                                                                                                                                                                                         Oligonucleotides analogs useful in detection, of nucleic acid molecules, comprise monomers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /partial
/note= "no start or stop"
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/product= "tag peptide"
                                                                                                                                                                                                                                                               Example 20; Page 123; 197pp; English,
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Best Local Similarity 100.0
Matches 15; Conservative
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                         (ACTI-) ACTIVE MOTIF.
                                                                                                                                            WPI; 2002-041177/05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated avian and reptile nucleic acid, encoding a polypeptide with heparanase catalytic activity. The signal peptide of the nucleic acid can be used to express membrane-associated or secreted proteins in heterologus expression systems. The encoded polypeptides can be used to prevent tumour angiogenesis, metastasis and hinasion, and to intervene with pathologise associated with impaired heparin-binding growth factors, cellular responses to heparin-binding growth factors, cellular responses to heparin-binding growth factors and cytokines, cell interaction with plasma lipoproteins, cellular ususceptibility to viral, protezoa and bacterial infections or disintegration of neurodegenerative plaques. The present sequence represents a chicken heparanase (hpa) cDNA cloning oligo dI(15) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid encoding avian and reptile heparanase polypeptide is useful to treat various heparin-related disorders and the signal peptide is useful in production of membrane-targeted or secreted recombinant
                                             Heparanase; catalytic; cytostatic; antiviral; antibacterial; enzyme; anti-protozoan; neuroprotective; heparin; hpa; chicken; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Chicken heparanase (hpa) cDNA cloning oligo dT(15) primer.
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                                                                                                                                                                                                                                                                                                                                                              (INSI-) INSIGHT STRATEGY & MARKETING LTD
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ABA97403 standard; DNA; 15 BP.
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30-NOV-2000; 2000US-0250334P.
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1es 15, Conservative
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                                                                                                                                                                  US2002034810-A1
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                                                                                                                   Gallus gallus
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proteins

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ABA97403/c

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Query Match Best Loca Matches

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Gaps

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P-PSDB; AA019056.

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(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
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                                                                                                                                                                                                                                                                                                             16-FEB-2001; 2001DE-01007317
                                                                                                                                                             1 AAAAAAAAAAAAA 15
                                                                                                                                                                                       AAL49455 standard; DNA; 15
                                                                                                                                                                                                         (first entry)
                                                                                                                                              15; Conservative
                                                                                                                                                                                                                                                                     /partial
Mueller 0;
                                                                                                                                                                                                                                                                                                                                Mueller 0;
                                                                                                                   used in the invention
        WPI; 2002-674959/72.
P-PSDB; AAO19054.
                                                                                                                                                                                                                                                                                                                                         WPI; 2002-674959/72.
                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                  WO200266675-A2
                                                                                                                                                                                                         14-NOV-2002
                                                                                                                                                                                                                                                                                            29-AUG-2002
Kahmann S,
                                                                                                                                                                                                                                                                                                                                Kahmann S,
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                                                                                                                                     Query Match
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                                                                                                                                                                             Matches
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The present invention relates to a method of detecting mutations in a nucleic acid by amplifying the nucleic acid to produce a double-stranded amplicon, in vitro transcription and translation of this amplicon, and detection of the transcription and translation of this amplicon, and detection of the translated protein. The primers used for amplification are designed to produce an amplicon that is translatable and allows of ifferentiation between translation products of wild-type and mutated nucleic acids. The method is used to detect mutations in tumour suppressor genes, for (early) diagnosis, monitoring and characterisation of tumours (especially of bladder and intestines) and in the germ line (using nucleic acids from embryos or blood cells). A new multi-tag vector is used to detect or verify the reading frame of a nucleic acid cloned in the and to determine the suitability of detectable peptides for analysis and/or purification of a recombinant protein, expressed from a sequence cloned in the invention Detecting mutations in nucleic acid, useful for diagnosis and characterization of tumors, by amplification, in vitro transcription and translation, then protein detection. Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other; Claim 11; Fig 5; 62pp; German Query Match
Best Local Similarity 100.
Matches 15, Conservative AAD29506/ ò g ö The present invention relates to a method of detecting mutations in a nucleic acid by amplifying the nucleic acid to produce a double-stranded amplicon, in vitro transcription and translation of this amplicon, and detection of the translated protein. The primers used for amplification are designed to produce an amplicon that is translatable and allows differentiation between translation that is translatable and mutated nucleic acids. The method is used to detect mutations in tumour suppressor genes, for (early) diagnosis, monitoring and characterisation of tumours (especially of bladder and intestines) and in the germ line (using nucleic acids from embryos or blood cells). A new multi-tag vector is used to detect or verify the reading frame of a nucleic acid cloned in it, and to determine the suitability of detectable peptides for analysis and/or purification of a recombinant protein, expressed from a sequence cond in the vector. The present sequence encodes a tag peptide and was Detecting mutations in nucleic acid, useful for diagnosis and characterization of tumors, by amplification, in vitro transcription and translation, then protein detection. Gaps Mutation detection method tag peptide coding sequence SEQ ID NO: 3. Mutation detection, primer; mutant, tag, tumour suppressor gene, protein production, cancer, ds. ; Length 15; 0; Indels Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other; Score 15; DB 1; Le Pred. No. 5.6e+02; 100.0%; Pred. /note= "no start or stop" /\*tag= a /product= "tag peptide" Location/Qualifiers Claim 11; Fig 5; 62pp; German 1736 AAAAAAAAAAAAA 1750

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                                                                                                                                                                                                                                                                                 Pre-adipose cell line; white adipocyte; food ingredient; obesity; lipid; diabetes; cardiovascular disease; reverse transcription; RT-PCR primer;
                                                                                                                                                                                                                                                     Primer used for the expression of adipocytes in human preadipose cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human pre-adipose cell line capable of differentiating to adipose cells, useful in developing drug, food ingredients, and supplements against obesity, diabetes and cardiovascular diseases.
                              Gaps
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0.9%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 5.6e+02; tive 0; Mismatches 0; Indels
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                                                            1736 AAAAAAAAAAAA 1750
                                                                                                                                                                AAD29506 standard; DNA; 15 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                   13-JUL-2001; 2001WO-EP008165
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                                                                                       1 AAAAAAAAAAAAA 15
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                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                             Unidentified.
                                                                                                                                                                                                                           17-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Darimont C,
                                                                                                                                                                                                                                                                                                                                                                                                        24-JAN-2002.
                                                                                                                                                                                             AAD29506;
                                                                                                                                    RESULT 1051
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substituted phenyl compound. The derivatised oligoribonucleotides are used, to decrease the expression of oncogenes and thereby decrease the expression of cancer cells which rely upon oncogene expression for their phenotypic and pathological properties. The oligoribonucleotides are also used for increasing the effectiveness of antisense oligonucleotide transpetted to a gene associated with a disease or a condition in an animal. To alter gene transcription and/or translation for any gene segment responsible for expression, to inhibit viral reverse transcriptase, to inhibit the expression of leukaemia virus, hepatitis virus, oncogenes and human immunodeficiency virus. The present sequence is retroviral reverse transcriptase inhibitor DNP-poly [A] RNA fragment which is used in the treatment of moloney murine leukaemia virus (MuLV) and mammals. (Updated on 07-AUG-2003 to correct OS field.) (Updated on 29-AUG-2003 to standardise OS field)

Seguence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

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cellular properties of normal white adipose cells. The human pre-adipose cell lines are useful for the identification of substances controlling the regulation of lipid uptake and release by human white adipocytes, and substances controlling the differentiation of preadipocytes into mature adipocytes. They are useful for screening compounds capable to regulate the servetion of any metabolites or hormones from human white adipocytes. Sequences of the invention are useful for developing drugs, food ingredients and supplements against obesity, diabetes and cardiovascular diseases. The present DNA sequence is a reverse transcription (RT) -PCR primer which is used for the expression of adipocytes in differentiated immortalised human preadipose cells. This primer is used RNase inhibitor; anti-HIV; cytostatic; hepatotropic; antinflammatory; virucide; oncogene; cancer; transcription; translation; leukaemia virus; hepatitis virus; human immunodeficiency virus; retroviral; DNP-poly [A]; poly-2'-0-(2,4-dinitrophenyl)-poly [A]; viral reverse transcriptase; ss. Derivatized antisense oligoribonucleotide useful to inhibit e.g. viral reverse transcriptase comprises at the 2'-O position of the oligoribonucleotide, a hydrophobic carrier reagent containing a poly substituted phenyl compound. Gaps Retroviral reverse transcriptase inhibitor DNP-poly [A] RNA fragment . Query Match 0.9%; Score 15; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 5.6e+02; Matches 15; Conservative 0; Mismatches 0; Indels Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other; in the exemplification of the invention 93US-00022055. 94US-00200650. 96US-00604871. 1736 AAAAAAAAAAAAA 1750 98US-00167375 15 AAAAAAAAAAAAA 1 AAD22531 standard; RNA; 15 (first entry) unidentified retrovirus. Unidentified. (revised) (revised) WPI; 2002-009339/01. (WANG/) WANG J H. 06-OCT-1998; US6291438-B1 24-FEB-1993; 23-FEB-1994; 22-FEB-1996; 29-AUG-2003 07-AUG-2003 12-FEB-2002 18-SEP-2001 AAD22531; Wang JH; RESULT 1052 ઠે 요

ö The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Escherichia coll; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites; (iii) if transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and fourth recombination sites, or the second and third recombination sites New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of doublestranded RNA. Gaps Chimeric nucleic acid construct; recombinational cloning; silencing; recombination site; double stranded RNA; plant; ds. ö Acceptor vector pHELLSGATE 4 nucleotide sequence SEQ ID NO:23. 0.9%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 5.6e+02; tive 0; Mismatches 0; Indels (CSIR ) COMMONWEALTH SCI & IND RES ORG. Helliwell C; Claim 14; Page 74; 104pp; English. BP 1736 AAAAAAAAAAAA 1750 26-JAN-2001; 2001US-0264067P. 29-NOV-2001; 2001US-0333743P. 24-JAN-2002; 2002WO-AU000073 1 AAAAAAAAAAAA 15 ABQ82140 standard; DNA; 15 (first entry) Best Local Similarity 100. Matches 15; Conservative Waterhouse P, WPI; 2002-682669/73 WO200259294-A1 11-DEC-2002 01-AUG-2002. Synthetic. Vesley S, ABQ82140; Query Match RESULT 1053 ABQ82140 8 셤 

The invention relates to derivatised antisense oligoribonucleotides with enhanced membrane permeability and stability. The derivatised antisense oligoribonucleotide complementary to a sequence of nucleotides found in a virus or a cell is useful for inhibiting e.g., viral reverse transcriptase. Derivatised antisense oligoribonucleotide is conjugated at the 2'-O position with a hydrophobic carrier reagent containing a poly

Example 3; Col 24; 56pp; English.

sequence from the present invention 99US-00274553. ABX00240 standard; RNA; 15 (first entry) BLATT L. MCSWIGGEN J A. WPI; 2002-617759/66. Best Local Similarity ROBERTS B. PAVCO P A. MACE/) MACEJACK D Hepatitis C virus. US2002082225-A1 23-MAR-1999; 23-MAR-1999; 23-DEC-2002 27-JUN-2002. Query Match ABX00240; (MCSW/) (ROBE/) (PAVC/) BLAT/) Matches à

are capable of reacting with a same recombination site, and preferably are identical. The first and second recombination sites, or the third and fourth recombination sites, do not recombine with each other or with a same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic acids. The present sequence represents an acceptor vector nucleotide

Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Gaps ; 0 0.9%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 5.6e+02; 0; Indels 100.0%; Pred. No. ... 15; Conservative

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Hepatitis C virus substrate #22 for HCV hammerhead ribozyme #22.

Enzymatic nucleic acid, RNA cleavage, Hepatitis C virus infection, HCV ribozyme; HCV expression, HCV replication, cirrhosis, virucide, liver failure, hepatocellular carcinoma, HCV infection, drug therapy, type I interferon; interferon alpha; interferon beta; cytostatic; interferon gamma; consensus interferon; hepatotropic; antiinflammatory; substrate; hammerhead ribozyme; HH ribozyme; ss.

99US-00274553

Roberts B, Pavco PA, Macejack D; Blatt L, Mcswiggen JA, New ribozymes targeting RNA derived from hepatitis C virus inhibit viral replication and are useful to treat hepatitis C virus infections and cirrhosis, liver failure or hepatocellular carcinoma.

Claim 1; Page 21; 80pp; English.

The present invention relates to enzymatic nucleic acids which specifically cleave RNA derived from Hepatitis C virus (HCV). The enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin (HP) motif where the binding arms comprise sequences complementary to one of the substrate sequences defined in the specification. The HCV of the substrate sequences defined in the specification and/or replication of HCV. They can be used to treat cirrhosts, liver failure and/or hepatocellular carcinoma. The HCV ribozymes are also useful for treating The present invention relates to enzymatic nucleic acids which specifically cleave RNA derived from Hepatitis C virus (HCV). The enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin (HP) motif where the binding arms comprise sequences complementary to one of the subserate sequences defined in the specification. The HCV ribozymes are useful for modulating the expression and/or replication of

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HCV. They can be used to treat cirrhosis, liver failure and/or hepatocellular carcinoma. The HCV ribozymes are also useful for treating a condition associated with HCV infection in conjunction with one or more other drug therapies, particularly type I interferon, especially interferon alpha, beta or gamma or consensus interferon. The present sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note: Some of the sequence data for this patent did not form part of the printed specification. The complete sequence data for this patent was obtained in electronic format directly from the USPTO web site at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection; HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide; liver failure; hepatocellular carcinoma; HCV infection; drug therapy; type I interferon; interferon alpha; interferon beta; cytostatic; interferon gamma; consensus interferon; hepatotropic; antiinflammatory; substrate; hammerhead ribozyme; HH ribozyme; ss.
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New ribozymes targeting RNA derived from hepatitis C virus inhibit vireplication and are useful to treat hepatitis C virus infections and cirrhosis, liver failure or hepatocellular carcinoma.
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Pred. No. 5.6e+02;
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                                                                                                                                                                           Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
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100.0%; Pred. No. 5...
                                                                                                                                              seqdata.uspto.gov/psipsDIDEntry.html
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                                                                                                                                                                                                                                                                                                                                                                               ABX03406 standard; RNA; 15 BP.
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                                                                                                                                                                                                         Query Match 0.9
Best Local Similarity 100.
Matches 15; Conservative
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MCSWIGGEN J A.
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PAVCO P A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-617759/66.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                              ABX03406;
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(PAVC/) F
(MACE/) N
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a condition associated with HCV infection in conjunction with one or more other drug therapies, particularly type I interferon, especially interferon alpha, beta or gamma or consensus interferon. The present sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note: Some of the sequence data for this patent did not form part of the printed specification. The complete sequence data for this patent was obtained in electronic format directly from the USPTO web site at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mod_base= OTHER
/note= "biethyl 5-(((2-cyanoethoxy) (diisopropylamino)
phosphanyloxy)methyl)isophthalate, synthetic branching
amidite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Compound for binding macromolecule to substrate surface or conjugation targets, contains phosphorous containing reactive group, hydrazide protecting group and benzene ring, and has predefined formula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Windhab N;
                                                                                                                                                                                               Gaps
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                                                                                                                                                                 Length 15;
                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Hydrazide precursor phosphoramidite oligonucleotide 035.
                                                                                                                                    Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
                                                                                                                                                               Score 15; DB 1; Lt
Pred. No. 5.6e+02;
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'note= "phosphoramidite linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          er J, Schweitzer M,
Greef CH, Wang D;
                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              Macromolecule; hydrazide; immobilisation;
                                                                                                       segdata.uspto.gov/psipsDIDEntry.html
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/note= "3' Cy3 dye"
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                                                                                                                                                                                                                                                    15 AAAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                            ABLS7064 standard; DNA; 15
                                                                                                                                                            Query Match 0.9%
Best Local Similarity 100.0
Matches 15; Conservative
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modified_base
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Havens JR,
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amidite compound. The invention describes an improved process for immobilisation of macromolecules including DNA, RNA, peptide nucleic acids, pyranosyl-RNA and peptides, especially macromolecules containing multiple reactive sites, to a substrate surface or other conjugation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Compound for binding macromolecule to substrate surface or conjugation targets, contains phosphorous containing reactive group, hydrazide protecting group and benzene ring, and has predefined formula.
                                                                 target. It also describes the preparation of oligos containing one or more hydrazides, which can be used for conjugation to surface binding moieties, or for other conjugation reactions. The process is useful e. in nucleic acid hybridisation based assays, DNA chip technology and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Windhab N;
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phosphanyloxy)-N'-tritylhexanohydrazide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bruecher C,
                                                                                                                                                                                                     0.9%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 5.6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                     Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "phosphoramidite linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Macromolecule; hydrazide; immobilisation; ss.
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Onofrey TJ, Greef CH, Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrazide phosphoramidite oligonucleotide
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/mod_base= OTHER
                                                                                                                                                                                                                                                                          1736 AAAAAAAAAAAAA 1750
                                                                                                                                                                                                                                                                                                                                                                                              ABL57054 standard; DNA; 15 BP
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                                                                                                                                                                                                                                                                                                           AAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                          15; Conservative
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*tag=
                                                                                                                                       biosensor applications
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Havens JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                ABL57054;
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Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "1,3-Bis-(3',5'-bis(ethyloxycarbonyl) benzyloxy)-5-((2'-cyanoethyl)(diisopropylamino) phosphanyloxymethyl)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is of a hydrazine treated hydrazide precursor phosphoramidite 15-mer, designated oligo 039, which was produced in an example from the invention. The invention describes an improved process for immobilisation of macromolecules including DNA, RNA, peptide nucleic acids, pyranosyl-RNA and peptides, especially macromolecules containing multiple reactive sites, to a substrate surface or other conjugation target. It also describes the preparation of oligos containing one or
which can be used for conjugation to surface binding moieties, or for other conjugation reactions. The process is useful e.g. in nucleic acid hybridisation based assays, DNA chip technology and biosensor
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                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              targets, contains phosphorous containing reactive group, hydrazide
protecting group and benzene ring, and has predefined formula.
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                                                                                          0.9%; Score 15; DB 1; Length 15;
100.0%; Pred. No. 5.6e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                            Hydrazide precursor phosphoramidite oligonucleotide 039.
                                                                   Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
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/note= "phosphoramidite linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schweitzer M,
CH, Wang D;
                                                                                                                                                                                                                                                                                                                                                     Macromolecule, hydrazide, immobilisation; ss
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/mod_base= OTHER
/note= "3' Cy3 dy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mueller-Ibeler J,
Onofrey TJ, Greef
                                                                                                                                                                                                                                             BP.
                                                                                                                                                 1736 AAAAAAAAAAAAA 1750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-AUG-2001; 2001WO-US041663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-AUG-2000; 2000WO-US022205
                                                                                                                                                                                                                                            ABL57063 standard; DNA; 15
                                                                                                                                                                         15 AAAAAAAAAAAAA 1
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                                                                                                                      Conservative
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                                         applications
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Havens JR,
                                                                                                                                                                                                                                                                                                                                                                               Synthetic
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                      e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Compound for binding macromolecule to substrate surface or conjugation targets, contains phosphorous containing reactive group, hydrazide protecting group and benzene ring, and has predefined formula.
more hydrazides, which can be used for conjugation to surface binding moieties, or for other conjugation reactions. The process is useful e in nucleic acid hybridisation based assays, DNA chip technology and
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                                                                                                                                                              Gaps
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                                                                                                                         0.9%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 5.6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Amino-C6-modified and Cy3 labeled T15 oligonucleotide.
                                                                                          Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mod_base= OTHER
/note= "Amino-C6 modification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Raddatz S, Mueller-Ibeler J, Schweitzer M,
Havens JR, Onofrey TJ, Greef CH, Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Macromolecule; hydrazide; immobilisation; ss.
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/note= "3' Cy3 dye"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                        ABL57066 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                              15; Conservative
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Seguence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                     ABL57061;
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                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Compound for binding macromolecule to substrate surface or conjugation targets, contains phosphorous containing reactive group, hydrazide protecting group and benzene ring, and has predefined formula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Windhab N;
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mod_base= OTHER
/note= "4-((2-cyanoethyl)(diisopropylamino)
phosphanyloxymethyl)-benzoic acid methyl ester"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bruecher C,
                                           Length 15;
                                                                       0; Indels
                                                                                                                                                                                                                                                                                            Hydrazide precursor phosphoramidite oligonucleotide 033.
               Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
                                       Query Match 0.9%; Score 15; DB 1; Lv
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                              l. .15
/*tag= b
note= "phosphoramidite linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mueller-Ibeler J, Schweitzer M,
Onofrey TJ, Greef CH, Wang D;
                                                                                                                                                                                                                                                                                                                       Macromolecule; hydrazide; immobilisation; ss
                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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/mod_base= OTHER
/note= "3' Cy3 dy
                                                                                                  1736 AAAAAAAAAAAAA 1750
                                                                                                                                                                                                      ABL57059 standard; DNA; 15 BP
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                                                                                                                    (first entry)
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Havens JR,
                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                              12
                                                                                                                                                                                                                                  ABL57059;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Compound for binding macromolecule to substrate surface or conjugation targets, contains phosphorous containing reactive group, hydrazide protecting group and benzene ring, and has predefined formula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       target. It also describes the preparation of oligos containing one or more hydrazides, which can be used for conjugation to surface binding moleties, or for other conjugation reactions. The process is useful ein nucleic acid hybridisation based assays, DNA chip technology and biosensor applications
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                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                        /mod_base= OTHER
/note="1,1 = 181s-(3',5'-bis(ethyloxycarbonyl)
phenylcarbonylamido)-2-((2''-cyanoethyloxy)
(disopropyl)amino)-phosphanyloxy)-propane"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bruecher C,
     Score 15; DB 1; Length 15;
Pred. No. 5.6e+02;
                                   0; Indels
                                                                                                                                                                                                                                                 Hydrazide precursor phosphoramidite oligonucleotide O37.
                                                                                                                                                                                                                                                                                                                                                                               'note= "phosphoramidite linkage"
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CH, Wang D;
                                                                                                                                                                                                                                                                                Macromolecule; hydrazide; immobilisation; ss
                100.0%; Prec. ...
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/note= "3' Cy3 dye"
                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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/mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Raddatz S, Mueller-Ibeler J,
Havens JR, Onofrey TJ, Greef
                                                               1736 AAAAAAAAAAAAA 1750
                                                                                                                                                                 ABL57061 standard; DNA; 15 BP
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        0.9%;
                                                                                (first entry)
                                     15; Conservative
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Query Match
Best Local Similarity
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modified_base
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0.9%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 5.6e+02;

100.0%; Pred. ...

Local Similarity 100.

Best Loca Matches

Query Match

1736 AAAAAAAAAAAAA 1750

15 AAAAAAAAAAAAA

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The present sequence is of a trityl deprotected hydrazide phosphoramidite 15-mer, designated oligo 031, which was produced in an example from the invention. The invention describes an improved process for immobilisation of macromolecules including DNA, Proptide nucleic acids, pyranosyl-RNA and peptides, especially macromolecules containing multiple reactive sites, to a substrate surface or other conjugation target. It also describes the preparation of oligos containing one or more hydrazides, which can be used for conjugation to surface binding moieties, ot for other conjugation reactions. The process is useful e.g. in nucleic acid hydridisation based assays, DNA chip technology and biosensor
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Onofrey TJ, Greef CH, Wang D;
                                                                                                                            Gaps
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/note= "6-((2Cyanoethoxy)(diisopropylamino)
phosphanyloxy)-N'-tritylhexanohydrazide"
                                                               Length 15;
                                                      0.9%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 5.6e+02; rative 0; Mismatches 0; Indels
Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
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/*tag= b
/note= "phosphoramidite linkage"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Macromolecule; hydrazide; immobilisation; ss.
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/mod_base= OTHER
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                                                                                                                                                                                                                                                                                                                                                                                              ABL57056 standard; DNA; 15
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                                                      Query Match
Best Local Similarity
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                                                                                                                         15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Raddatz S,
Havens JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL57056;
                                                                                                                                                                                                                                                                                                                                           RESULT 1062
                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                               ABL57056/c
XX
XX
ABL57056/c
XX
ARL57056/c
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ARL57056/c
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ARL57
BE Hydr 22 - JI
XX
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BE Hydr 12 2 - JI
XX
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BE Hydr ARL57
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Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

applications

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The present sequence is of a hydrazine treated hydrazide precursor phosphoramidite 15-mer, designated oligo 034, which was produced in an example from the invention. The invention describes an improved process for immobilisation of macromolecules including DNA, RNA, peptide nucleic acids, pyranosyl-RNA and peptides, especially macromolecules containing multiple reactive sites, to a substrate surface or other conjugation target. It also describes the preparation of oligos containing one or more hydrazides, which can be used for conjugation to surface binding moieries, or for other conjugation reactions. The process is useful e.g. in nucleic acid hybridisation based assays, DNA chip technology and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Compound for binding macromolecule to substrate surface or conjugation targets, contains phosphorous containing reactive group, hydrazide protecting group and benzene ring, and has predefined formula.
                                                                                                                                                                                                                                                                       /*tag= a
/mod_base= OTHER
/note= "biethyl 5-((2-cyanoethoxy)(diisopropylamino)
phosphanyloxy)methyl)isophthalate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Windhab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bruecher C,
                                                                                                        Hydrazide precursor phosphoramidite oligonucleotide 034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                            /*tag= b
/note= "phosphoramidite linkage"
                                                                                                                                     Macromolecule; hydrazide; immobilisation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mueller-Ibeler J, Schweitzer M,
Onofrey TJ, Greef CH, Wang D;
                                                                                                                                                                                                                                                                                                                                                   /*tag= c
/mod_base= OTHER
/note= "3' Cy3 dye"
                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Page 43; 120pp; English
               ВЪ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-AUG-2001; 2001WO-US041663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-AUG-2000; 2000WO-US022205.
 060/c
ABL57060 standard; DNA; 15
                                                                        (first entry)
                                                                                                                                                                                                               . .15
*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-404476/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NANO-) NANOGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                               WO200214558-A2
                                                                                                                                                                                                              modified base
                                                                                                                                                                                                                                                          modified base
                                                                                                                                                                                                                                                                                                                                      modified base
                                                                        22-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                             21-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Raddatz S,
Havens JR,
                                                                                                                                                                   Synthetic
                                          ABLS7060
ABL57060/
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                           Gaps
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         Length 15;
                          0; Indels
       0.9%; Score 15; DB 1; Le
100.0%; Pred. No. 5.6e+02;
                          Mismatches
                100.0%; P.
                                            1736 AAAAAAAAAAAA 1750
                                                             15 AAAAAAAAAAAAA 1
                           Conservative
Query Match
Best Local Similarity
                                                                                         RESULT 1064
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Triple-helix formation; purine-rich target sequence; double-helix DNA gene expression; regulatory sequence; pathogenic double-stranded DNA; pathogenic bacteria; virule; replication; virulence; cancer; oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss. Triple helix forming associated oligonucleotide #26. ВЪ 93US-00168920. 92US-00946976 ABK98141 standard; DNA; 15 (first entry) 17-SEP-1992; JS6403302-B1 07-0CT-2002 11-JUN-2002 Synthetic. ABK98141; 

A triple-helix comprising a double helical nucleic acid (DHNA) and an oligonuclectide which binds in parallel and antiparallel orientation, respectively, for targetting sequences on alternate strands of DHNA to (CALY ) CALIFORNIA INST OF TECHNOLOGY Beal PA; WPI; 2002-536030/57. Dervan PB,

A triple-helix comprising a double helical nucleic acid (DHNA) and an oligonuclectide which binds in parallel and antiparallel orientation, respectively, for targetting sequences on alternate strands of DHNA to

Example 7; Fig 24A; 108pp; English.

gene expression.

control

WPI; 2002-536030/57.

Example 1; Fig 3B; 108pp; English.

control gene expression.

The present invention relates to methods and oligonuclectides for forming a triple-helix comprising a double helical nucleic acid comprising first and second substantially complementary strands, and an oligonuclectide bound to a purine-rich target sequence within the double helical nucleic acid, where the oligonuclectide bluds in a parallel and antiparallel corientation, respectively, to target sequences on alternate strands of the double helical nucleic acid. The method has therapeutic applications, where gene expression is controlled by selective triple-helix formation where gene expression regulatory sequences of a target gene. The oligonuclectides can be used to form triple-helices, and are useful to configuration to a pasence of specific sequences within genomic DNA for diagnostic and therapeutic purposes. The oligonuclectides can be selected to specific sequences required by pathogenic bacteria or viruses for replication or virulence, reducing their pathogenicity. Alternatively, the oligonuclectide can be chosen to target a unique sequence of the configuration or virulence, reducing their pathogenic has triple helix the genome of pathogen whose The configuration or virulence, reducing their pathogenic sequence of the configuration or virulence, reducing their pathogenic the virules the configuration or virulence, reducing their pathogen which is not found in the genome of pathogen is host. The oligonuclectides can be used in cancer treatment by way of triple-helix suppression of specific oncogenes including those of endogenous or viral origin. Such therapeutic oligonucleotides are capable of forming triple-helices with such sequences in cancerous cells containing the activated oncogene, so preferentially killing or repressing the cancer causing cell. The present sequence represents an oligonucleotide used in the methods of the present invention

Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

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                                                                                                                                                Triple-helix formation; purine-rich target sequence; double-helix DNA; gene expression; regulatory sequence; pathogenic double-stranded DNA; pathogenic bacteria; virus; replication; virulence; cancer; oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
                   Gaps
                   ö
    Length 15;
                   0; Indels
                                                                                                                                  Triple helix forming associated oligonucleotide #48.
     DB 1; Le
5.6e+02;
0.9%; Sco...
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                 (CALY ) CALIFORNIA INST OF TECHNOLOGY.
                                  1736 AAAAAAAAAAAAA 1750
                                                                                      ABK98184 standard; DNA; 15 BP
                                                                                                                                                                                                                                     93US-00168920
                                                                                                                                                                                                                                                   92US-00946976
                                                 15 AAAAAAAAAAAA 1
                                                                                                                    (first entry)
                    15; Conservative
     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                Beal PA;
                                                                                                                    07-OCT-2002
                                                                                                                                                                                                      JS6403302-B1
                                                                                                                                                                                                                                     16-DEC-1993;
                                                                                                                                                                                                                                                    17-SEP-1992;
                                                                                                                                                                                                                     11-JUN-2002
                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                Dervan PB,
                                                                                                     ABK98184;
                    Matches
                                                                                ABK98184
                                                                                              셤
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The present invention relates to methods and oligonucleotides for forming a triple-helix comprising a double helical nucleic acid comprising first and second substantially complementary strands, and an oligonucleotide bound to a purine-rich target sequence within the double helical nucleic acid, where the oligonucleotide binds in a parallel and antiparallel confentation, respectively, to target sequences on alternate strands of the double helical nucleic acid. The method has therapeutic applications, where gene expression is controlled by selective triple-helix formation within expression regulatory sequences of a target gene. The oligonucleotides can be used to form triple-helices, and are useful to detect the presence or absence of specific sequences within genomic DNA or adamostic and therapeutic purposes. The oligonucleotides can be selected to specifically bind to pathogenic double-stranded DNA including specific sequences required by pathogenic double-stranded DNA including specific sequences required by pathogenic double-stranded DNA including the oligonucleotide can be chosen to target a unique sequence of the pathogen which is not found in the genome of pathogen's host. The oligonucleotides can be used in cancer treatment by way of triple-helix colling and the pathogen which is not found in the genome of pathogen's host. The origin. Such therapeutic oligonucleotides are capable of forming triple-helices with such sequences in cancerous cells containing the activated oncogene, so preferentially killing or repressing the cancer causing cell. The present sequence represents an oligonucleotide used in the methods of the present invention suppression of specific oncogenes including those of endogenous or viral

genetic packages that display and/or express a diverse family of peptides, polypeptides or proteins. ABZ36912 to ABZ37510 and ABP55464 to ABP55499 represent sequences used in the exemplification of the present

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Gaps

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cch 0.9%; Score 15; DB 1; Length 15; al Similarity 100.0%; Pred. No. 5.6e+02; 15; Conservative 0; Mismatches 0; Indels

Best Local Similarity

Matches

1736 AAAAAAAAAAAA 1750

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Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

invention

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Cleaving single-stranded nucleic acid sequences at a desired location by contacting the nucleic acid with an single strand oligonucleotide complementary to a nucleic acid region where cleavage is desired.
                                  Gaps
                                  ;
0
                 Length 15;
                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                      Cohen EH, Nastri HG, Rookey KL, Hoet R;
Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
                0.9%; Score 15; DB 1; Lv
100.0%; Pred. No. 5.6e+02;
vative 0; Mismatches 0;
                                                                                                                                                                                   Library; cleavage; display; diverse family; ss.
                                                   1736 AAAAAAAAAAAAA 1750
                                                                                                               ВР
                                                                                                                                                                 Oligonuclectide SEQ ID NO:622
                                                                                                                                                                                                                                                      17-APR-2002; 2002WO-US012405.
                                                                                                                                                                                                                                                                       17-APR-2001; 2001US-00837306.
24-OCT-2001; 2001US-0000516.
25-OCT-2001; 2001US-00045674.
                                                                                                                                                                                                                                                                                                                                                    HOOG/) HOOGENBOOM H R J M.
                                                                   15 AAAAAAAAAAAA 1
                                                                                                              ABZ37501 standard; DNA; 15
                                 15; Conservative
                                                                                                                                                                                                                                                                                                        LADNER R C.
COHEN E H.
NASTRI H G.
ROOKEY K L.
                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-093015/08.
                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             Hoogenboom HRJM;
                                                                                                                                                                                                                    WO200283872-A2.
                                                                                                                                                                                                                                                                                                                                            HOET R
                                                                                                                                                18-FEB-2003
                                                                                                                                                                                                                                      24-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                      Ladner RC,
                                                                                                                                                                                                    Synthetic.
                                                                                                                               ABZ37501;
                 Query Match
                                                                                                                                                                                                                                                                                                                   (COHE/)
                                                                                                                                                                                                                                                                                                                                    (ROOK/)
(HOET/)
                                                                                                                                                                                                                                                                                                         LADN/)
                                                                                              RESULT 1066
                                Matches
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The present sequence is that of the 5' end of a cDNA clone was isolated a cDNA library e.g. a mosquito antenna library. A clone was isolated a cDNA library e.g. a mosquito antenna library. A clone was isolated to rapidly array and normalize a complex cDNA library obtained from a target species. Clones are arrayed into multilibrary obtained from a target species. Clones are arrayed into multilibrary obtained from a target species. Clones are ABV74137) with a complementary a poly-T run capable of binding cDNAs by their poly-A tail and a unique 3' sequence of liprace of liprace and complementary 5' end. The unique 3' key sequences are designed to give a complementary 5' end. The unique 3' key sequence can be bound by an comprehensive level of degeneracy since they are diverse and numerous complementary 5' end. The unique 3' key sequence can be bound by an individual, specific oligonucleotide in a single well. The cDNA library is heated to denature the clones into single stranded DNA, and an aliquot is added to every well. The anchored oligonucleotide serves as the 3' priming site. Denaturing and washing leave anchored cDNA in each well The library is now arrayed and normalised. The method was complement receptors, and active effectors involved in the capecially odourant receptors, and active effectors involved in the oligance clones encoding c-protein complex receptors, and scrive as clones encoding c-protein complex receptors, and active effectors involved in the oligance clones and vertebrates, e.g. odourant binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying nucleic acid encoding novel sex-linked-tissue-linked receptors, useful for isolating odorant binding proteins or pesticide alternatives, by analyzing sequences from a male- and female-specific nucleic acid library.
                                                                                                                                                                                                                                 G-protein coupled receptor; odourant; receptor; olfaction; array; microarray; anosmia; attractant; arometic; pesticide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Fig 5, 83pp; English.
                                              ABV74142 standard; DNA; 15 BP
                                                                                                                                                                                   5' End of cDNA library clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAR-2001; 2001US-0279168P.
31-JAN-2002; 2002US-0353392P.
                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2002; 2002WO-US009559.
                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Woods D, Dimitratos S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INSC-) INSCENT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-029930/02.
                                                                                                                                                                                                                                                                                                                                                   WO200277200-A2.
                                                                                                                                       23-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                               03-OCT-2002.
                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                       ABV74142;
RESULT 1067
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The present invention describes a method for cleaving single-stranded nucleic acid sequences at a desired location. Also described: (1) methods of driverse family of peptides, collectively displaying at least a member of a diverse family of peptides, polypeptides or proteins on the surface of a genetic package and collectively displaying at least a part of the diversity of the family, where the displaying at least a part of the diversity of the family, collectively displayed or expressed peptide, polypeptide or protein is encoded at least in part by a mucleic acid that has been cleaved at a desired location; (2) a method for preparing single-stranded nucleic genetic packages that display a member of a diverse family of peptides, polypeptides or proteins and that collectively display at least a portion of the family; (4) a vector comprising a DNA sequence encoding an antibody variable region linked to a version of PIII anchor which does not method for producing a population or a library of immunoglobulin genes; and (6) a library of immunoglobulins that comprise members having at least one variable domain in which at least one of CDR1 and CDR2 contain comprise in entity of sequences at a synthetic diversity and CDR3 diversity and cDR3 diversity and cDR3 diversity and contain subsequently used to produce libraries or

Disclosure; Page 481; 485pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of a poly-T oligonucleotide used in a method designed to rapidly array and normalize a complex cDNA library obtained from a target species. Clones are arrayed into multi-well plates. Each well contains 16 oligonucleotides with a 5' polylinker, a poly-T run capable of binding cDNAs by their poly-A tail and a unique 3' sequence, which allows an anchored oligonucleotide in each well to selectively hybridise only to those cDNA clones with a complementary 5' end. The unique 3' key sequences are designed to give a comprehensive level of degeneracy since they are diverse and numerous enough to ensure that
proteins, or other olfactory or neuronal proteins. The identified receptors and proteins are useful for identifying compounds that reduce a target animal's sensitivity to oddours, for manufacturing compounds or devices that mask oddurs, or trapping invertebrates with oddurants. Semiochemicals (e.g. arometics or pheromone mimetics) can be developed with desirable effects on specific species, for the development of pest monitoring systems or non-toxic, species-specific pesticide alternatives, for controlling insect feeding and breeding behaviour, detecting the presence of small air-borne molecules, etc
                                                                                                                                                                                                                                                                                                                                                                                         G-protein coupled receptor; odourant; receptor; olfaction; array; microarray; anosmia; attractant; arometic; pesticide; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying nucleic acid encoding novel sex-linked-tissue-linked receptors, useful for isolating odorant binding proteins or pesticide alternatives, by analyzing sequences from a male- and female-specific nucleic acid library.
                                                                                                                                                                             Gaps
                                                                                                                                                                             ö
                                                                                                                                                  0.9%; Score 15; DB 1; Length 15; 100.0%; Pred. No. 5.6e+02; tive 0; Mismatches 0; Indels
                                                                                                                            Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide used in cDNA library array.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "5' polylinker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 5; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mod_base= OTHER
                                                                                                                                                                                                                                                                                          BP
                                                                                                                                                                                                   1736 AAAAAAAAAAAAA 1750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002; 2002WO-US009559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-MAR-2001; 2001US-0279168P.
31-JAN-2002; 2002US-0353392P.
                                                                                                                                                                                                                            1 AAAAAAAAAAAAA 15
                                                                                                                                                                                                                                                                                        ABV74141 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag≔ a
                                                                                                                                                            Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dimitratos S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INSC-) INSCENT INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                 ABV74141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Woods D,
                                                                                                                                                    Query Match
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Matches
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cevery possible cDNA sequence can be bound by an individual, specific oligonucleotide in a single well. The cDNA library is heated to denature the clones into single stranded DNA, and an aliquot is added to every well. The anchored oligonucleotide serves as the 3' primar in PCR, and the common 5' region present in every CDNA clone serves as the 5' priming site. Denaturing and washing leave anchored cDNA in each well. The library is now arrayed and normalised. The method was used to identify and isolate clones encoding G-protein coupled receptors, especially candisolate clones encoding G-protein coupled receptors, especially colourant receptors, and active effectors involved in the olfactory pathway of invertebrates and vertebrates, e.g. odourant binding proteins, or other olfactory or neuronal proteins. The identified receptors and proteins are useful for identifying compounds that reduce a target proteins are useful for identifying compounds that reduce a target canimal's sensitivity to odours, for manufacturing compounds or devices that mask odours, or trapping invertebrates with odourants. Semiochemicals (e.g. arometics or pheromone mimetics) can be developed controlling insect feeding and breeding behaviour, detecting the monitoring systems or non-toxic, species-specific pesticide alternatives, correspondent of small air-borne molecules, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New oligonucleotide deprotection reagent useful for deprotecting oligonucleotide comprises an active methylene compound and an amine reagent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 0.9%; Score 15; DB 1; Length 15; Local Similarity 100.0%; Pred. No. 5.6e+02; Let 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
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/note= "phosphoramidite linkage"
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/note= "3' Q-CDPI3"
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Example 2; Page 25; 46pp; English
                                                            Query Match
Best Local Similarity 100.0
Warches 15; Conservative
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                                                                                                                                                                                               LOCA/) LOCASCIO M. LAND/) LANDRY D P.
                                                                                                                                                                  US2003013109-A1.
                                                                                                                                               misc binding
                                                                                                                                                                         16-JAN-2003.
                                                                                                                                      Synthetic.
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The invention discloses a hairpin sensor comprising a hairpin loop assembly including a complementary probe positioned between a first inverse repeat arm and a second inverse repeat arm, and a quenchable fluorescing agent joined, directly or indirectly, to the end of the complementary probe. Also claimed is a microarray comprising the hairpin sensor, where the end of the first inverse repeat arm opposite the complementary probe is bound, directly or indirectly, to a support, a kit for detecting a target nucleotide sequence in a sample comprising the hairpin sensor, and a support, and a hairpin sensor system, in which the complementary probe is support, and a hairpin sensor system, in which the particle is conductive or semi-conductive, including at least one of the particle is conductive or semi-conductive, including at least one of the particle is conductive or semi-conductive, including at least one of the particle is conductive probe, or first spacer comprises a composite the complementary probe, or first spacer composite the first inverse repeat arm, the functional group selected from amino, carboxyl, cincluding agent, where the ligand is selected from mercapto, hydroxyl, amino, nitrile and carboxyl, carboxylic acid, organic acid and amino acid. The second inverse repeat arm and the composite the ligand is selected from mercapto, hydroxyl, amino, nitrile and carboxyl, carboxylic acid, organic acid and amino acid. The contrible fluorescing agent which comprises a semiconductor nanocrystal or rhodamine B-labelled dye. Within the microarray the support is capable contrible active a charge. The two or more hairpin sensors include complementary probes that are the same or different and respective quenchable. hairpin sensors are arranged in a spatially-defined pattern. The sensor and system are useful for detecting a target nucleotide sequence in a sample. Further, the method involves identifying the target nucleotide sequence by the location of the complementary probe to which the target nucleotide sequence binds. The two or more hairpin sensors include complementary probes or quenchable fluorescing agents, that are different. The sequence presented is the hairpin oligonucleotide target sequence, #1, used in an example of the invention. Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other; 04-DEC-2003 (first entry) ADB68520; Query Match RESULT 1071 Matches ADB68520, 셤 XXXEXEXEXEXEXEXEXEXEX ò ö The present invention provides a method for deprotection of an oligonucleotide. This involves reacting a protected oligonucleotide, which is preferably covalently attached to a solid support through a linkage, with a deprotection reagent comprising an active methylene compound and an amine reagent. The process and reagent minimise sidereactions leading to certain impurities that contaminate synthetic oligonucleotides. The present sequence is a T15 phosphoramidite oligonucleotide having a quencher moiety (Q) and minor groove binder (CDPI3) at the 3' end, which was synthesised in an example of the invention. This protected oligonucleotide was treated either with 15% ethanolic ammonia or with 3% diethylmalonate (DEM) dissolved in 15% ethanolic ammonia for 2 hours at 55 degrees C. HPLC analysis showed that deprotection without DEM yielded a complex mixture of products containing analysis of the degired product. When DEM was used, 76.8% of the /bound\_moiety= "Hairpin oligonucleotide #1" /note= "Forms a doube-stranded region with the hairpin oligonucleotide shown in example 2" Hairpin sensor; hairpin loop; complementary probe; inverse repeat arm; quenchable fluorescing agent; microarray; semiconductor; nanocrystal; rhodamine B-labelled dye; detection; gold support; ss. Gaps Hairpin target sequence, #1, used in an example of the invention. ö Score 15; DB 1; Length 15; Pred. No. 5.6e+02; 0; Mismatches 0; Indels Seguence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other; Location/Qualifiers 0.9%; Scur 100.0%; Pre 0; } ВЪ. 1736 AAAAAAAAAAAA 1750 21-JUN-2002; 2002US-00176055. 21-JUN-2001; 2001US-0299460P. desired product was obtained ADA14836 standard; DNA; 15 15 AAAAAAAAAAAA 1 06-NOV-2003 (first entry) đ 1. .15 /\*tag=

ö Gaps ö hydroxyproline nucleic acid; HypNA, PNA, peptide nucleic acid; gene expression; respiration; secretion; signalling; ion-channel activity; cell mctility; developmental phenotype; tunour regression; single-base mismatch; ss; phosphono-peptide nucleic acid; pPNA. . Match 0.9%; Score 15; DB 1; Length 15; Local Similarity 100.0%; Pred. No. 5.6e+02; les 15; Conservative 0; Mismatches 0; Indels Single-base mismatch oligonucleotide SEQ ID 10 DNA |520/c | ADB68520 standard; DNA; 15 BP 1736 AAAAAAAAAAAA 1750 07-FEB-2003; 2003WO-US003904. 09-FEB-2002; 2002US-00072975. 1 AAAAAAAAAAAA 15 WO2003068798-A2. 21-AUG-2003. Synthetic.

Hairpin sensor useful for detecting a target nucleotide sequence in a sample, comprises a hairpin loop assembly including a complementary probe and a quenchable fluorescing agent.

Example 2; Page 11; 16pp; English

Ballinger CT, Locascio M, Landry DP;

WPI; 2003-596312/56.

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AAX18365
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                                                                                                                                       The invention relates to a novel method of inhibiting the expression of one or more genes or RNA transcripts by administering at least one oligonuclectide analogue that includes at least one hydroxyproline nucleic acid (HypNA) monometro a cell or organism or their extracts. In coligonuclectides of the invention may be used to monitor properties including gene expression, respiration, secretion, signalling, ion-channel activity, cell motility, developmental phenotype and tumour regression. Furthermore, they may be utilised to determine the effects of particular genes, as antisense or homologous recombination constructs e.g. for creating animal models of disease and finally, for increasing the activity of some enzymes, such as polymerases. The current sequence is etcivity of some enzymes, such as polymerases. The current sequence insention. This sequence may also comprise a peptide nucleic acid (PNA), a phosphono-PNA (PPNA) or a HypNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Annealing control primer to improve annealing specificity in nucleic acid amplification, has region complementary to target, arbitrary nucleotide sequence, regulator with universal base/non-discriminatory base analog.
                                                                    Method of inhibiting expression of genes or RNA transcripts, useful for therapy and determining effects of genes, by administering oligomers containing hydroxyproline nucleic acid.
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                      Choob M;
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                      Archdeachon J,
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Pred. No. 5.6e+02;
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                      Archdeacon D,
                                                                                                                     Example 20; Page 234; 240pp; English
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01-MAY-2002; 2002WO-KR000816.
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                      Efimov V, Fernandez J,
(ACTI-) ACTIVE MOTIF
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                                             WPI; 2003-689653/65
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inte present into present in autoextical an autoextical and printed for the present into present into present into present into present into present into present and a read and a read and a site on a template nucleic acid for hybridisation, as 5'-end portion having a pre-selected arbitrary nucleotide sequence, and a regulator portion having a pre-selected arbitrary nucleotide sequence, and a regulator portion having a pre-selected arbitrary nucleotide sequence, and a universal or non-confidence and angulation of the primer in association with a regulating an annealing portion of the primer in association with a negligible of regulating an annealing portion of the primer in association with an interest of angulativation of angulativation and angulativation of angulativation and angulativation and angulativation and angulativation and angulativation angulativation angulativation angulativation angulativation angulativation angulativation angulativation areaction using (I).

(I) is also useful for repidly amplifying a target confidence of the angulativation and angulativing a target of the angulativing a target of angulativing a target comprising a complementary to mRNAA, and amplifying 5'-end or 5'-end or 5'-end complementary to mRNAA, and amplifying 5'-enriched double-stranded cDNAB complementary to mRNAA, and amplifying 5'-enriched pequence simulation of for carget complementary to mRNAA, and amplifying appaining more than one pair of for carget and the paramagnetic sequence from the paramagnetic pequence simulation and paramagnetic peducation in the paramagnetic peducation in the paramagnetic peducation in the paramagnetic peducation in the paramagneti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primers in the same reaction, where the primers are derived from (1), for producing a DNA fingerprint of genomic DNA (gDNA), for producing a RNA fingerprint of an mRNA sample, identifying conserved homology segments in a multigene family from an mRNA sample, and for identifying conserved homology segments in a multigene family from gDNA. (1) is also useful for identifying a nucleotide variation in a target nucleic acid, and for mutagenesis in a target nucleic acid. The present sequence represents a primer which is used in the exemplification of the present invention.
                                                                                      The present invention describes an annealing control primer (ACP) (I) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptides having at least two new nucleotides - useful as primers in RT-PCR.
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100.0%; Pred. No. 5.6e+02;
iive 0; Mismatches 0; Indels
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Example 2; SEQ ID NO 54; 190pp; English.
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Disclosure; Page 10; 19pp; Japanese.

This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma) k-delta-N3'; where X = a labelled compound and/or nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, guanine or cytosine; N = adenine, guanine or thymine; amma = thymine; R = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene sednences

Sequence 16 BP; 0 A; 1 C; 1 G; 14 T; 0 U; 0 Other;

Gaps ô y Match 0.9%; Score 15; DB 1; Length 16; Local Similarity 100.0%; Pred. No. 5.9e+02; hes 15; Conservative 0; Mismatches 0; Indels Query Match Matches

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1735 CAAAAAAAAAAAA 1749 CAAAAAAAAAAA 1 15 ð ద

ВЪ AAX18366 standard; DNA; 16

AAX18366;

11-MAY-1999 (first entry)

RT-PCR primer of the invention SEQ ID 7.

RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

Synthetic

JP11032765-A

09-FEB-1999,

97JP-00208312

97JP-00208312 18-JUL-1997;

(TAKI ) TAKARA SHUZO CO

WPI; 1999-183822/16

Peptides having at least two new nucleotides - useful as primers in

Disclosure, Page 10; 19pp; Japanese.

This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)\*K-delta-N3'; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adennine, guanine or cytosine; N = adenine, guanine or thymine; A = netural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of repetition of gamma, in which thymine expressed by gamma is composed of 13 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene вестепсев RESULT 1074

AAX18366/C

XA AAX1836

XX AAX1836

XX AAX1836

XX RT-PCR

XX RT-PCR

XX NO 9-FE

XX NO 1103

XX NO 100

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Seguence 16 BP; 1 A; 0 C; 1 G; 14 T; 0 U; 0 Other;

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Gaps

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0.9%; Score 15; DB 1; Length 16; 100.0%; Pred. No. 5.9e+02; tive 0; Mismatches 0; Indels

1736 AAAAAAAAAAAA 1750

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Local Similarity 100. nes 15; Conservative

Best Loc Matches

Query Match

Sequence 16 BP; 15 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              molecular beacon comprising an oligonuclectide probe (see ABL57069) covalently attached at the 3' end to fluorescent dye and at the 5' end to a nanoparticle. In the native state, the probe forms a hairpin conformation with hybridised termini. The probinity of the fluorophore and quencher (gold nanoparticle) in the molecular beacon results in little or no detectable fluorescence. Upon hybridisation of the central complementary stretch of the probe to a target sequence, such as the present sequence, the hairpin undergoes a conformational change resulting in an increase in fluorescence, the extent of which is proportional to the amount of target sequence present. Single mismatches can be detected. The invention relates generally to the use of metal surface quenchers such as particles or fillms for high sensitivity applications in, for example, detection and diagnostic systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is that of a perfectly matched target sequence for a
                                                                                                                                                                                                                                                                                                             Molecular beacon; fluorophore; nanoparticle; nucleic acid detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sensitively detecting proximity changes in a system that utilizes an interacting fluorophore and quencher, for high sensitivity applications, involves utilizing a metal surface as quencher.
                                                                                                                                                                                                                                                                                                                                                                                                                          /bound_moiety= "Molecular beacon"
/note=""forms double-stranded region with bases 5-21 of
sequence in ABL57069"
                                   Gaps
                                   ö
0.9%; Score 15; DB 1; Length 16; 100.0%; Pred. No. 5.9e+02; Ve 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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 0.5%,
100.0%; Pre-
                                                                                                                                                                                                                                                                             Molecular beacon target sequence.
                                                                                                                                                                                BP.
                                                                 1735 CAAAAAAAAAAAA 1749
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2001US-0280350P.
                                                                                                                                                                               ABL57075 standard; DNA; 16
                                                                                     (first entry)
                                 15; Conservative
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*tag=
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                Best Local Similarity
Matches 15; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                          misc_binding
                                                                                                                                                                                                                                               22-JUL-2002
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                                                                                                                                                                                                                                                                                                                                           Synthetic
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 Query Match
                                                                                                                                             RESULT 1075
ABLS7075
ID ABLS7075
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us10008789-3.rng

RESULT 1076

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The invention relates to a novel method of inhibiting the expression of one or more genes or RNA transcripts by administering at least one oligonucleotide analogue that includes at least one hydroxyproline nucleic acid (HypNA) monomer to a cell or organism or their extracts oligonucleotides of the invention may be used to monitor properties including gene expression, respiration, secretion, signalling, ion-channel activity, cell motility, developmental phenotype and tumour regression. Furthermore, they may be utilised to determine the effects of particular genes, as antisense or homologous recombination constructs e.g. for creating animal models of disease and finally, for increasing the activity of some enzymes, such as polymerases. The current sequence is that of the PNA-HypNA hybridisation oligomer of the invention. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence may also comprise phosphono-PNA (pPNA) and serine nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Method of inhibiting expression of genes or RNA transcripts, useful f
therapy and determining effects of genes, by administering oligomers
containing hydroxyproline nucleic acid.
                                                                                                                                              /mod_base= OTHER /note= 0 (Phosphono PNA monomer with phenyl group attached to terminal phosphate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enzymatic nucleic acid, ribozyme, trans cleavage, inhibition, gene expression, downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RGV; bor-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat ICAM hammerhead ribozyme target sequence (nt. position 510)
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100.0%; Pred. No. 5.9e+02;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 17; Page 148; 240pp; English.
phosphono-peptide nucleic acid; pPNA
                                                                                    Location/Qualifiers
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                                                                                                                                  *tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-689653/65
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                                                                                       Key
modified_base
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                                      Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a method for detecting interactions between biological components using a nonlinear optical technique. The invention is used for screening candidate binding partner(s) for binding to test molecule. It can also be used to detect changes in orientation or conformation of the probe and/or target. The present sequence is a target oligonucleotide used in nonlinear optical technique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Screening candidate binding partner(s) for binding to test molecule by applying external force field to sample in homogeneous phase, illuminating sample with light beam(s) at fundamental frequencies, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hydroxyproline nucleic acid; HypNa; PNa; peptide nucleic acid; gene expression; respiration; secretion; signalling; ion-channel activity; cell motility; developmental phenotype; tumour regression; hybridisation; ss; serine nucleic acid; SerNa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                Parget oligonucleotide #2 used in nonlinear optical technique
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.9%; Score 15; DB 1; Le
100.0%; Pred. No. 5.9e+02;
                                                                                                                                                                                                                                                                                                            Nonlinear optical technique; screening; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PNA-HypNA hybridisation oligomer.
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Local Similarity 100.0%; P.
les 15; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             measuring physical properties.
                                                                                                                                AAD57845 standard; DNA; 16 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-OCT-2001; 2001US-0347821P.
06-FEB-2002; 2002US-0354668P.
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                      AAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SALA/) SALAFSKY J S
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                                                                                                                                                                                                                                                                                                                                                                                                 WO2003064991-A2
                                                                                                                                                                                                                                                                                                                                                     Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salafsky JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                          07-AUG-2003
                                                                                                                                                                         AAD57845;
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Best Loca Matches

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b DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
Karpelsky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
Usman N, Wincott RE, Woolf T;

Ribozymes having modified bases and methods for producing them - for use in inhibiting disease related genes.

Claim 2; Page 201; 407pp; English.

The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the nucleotide base position indicated in the DE line. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes cleave the ICAM-1 target sequences and thereby inhibit ICAM-1 expression, making them useful for reducing transplant rejection and alleviating symptoms in patients with rheumatoid arthritis, correct PI field.)

Seguence 17 BP; 2 A; 4 C; 7 G; 0 T; 4 U; 0 Other;

0.9%; Score 15; DB 1; Length 17; 100.0%; Pred. No. 6.1e+02; Best Local Similarity Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (VEGF). A patient (preferably human) having a growth factor (VEGF). A patient fims-like tyrosine kinase 1 (flt-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour anglogenesis, coular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient. AAX67275 to AAX75752 represent specific examples of nucleic acid molecules from the present invention
                                                                                                                                                                                                                                                                          Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
                                                                                                                                                                                                                                                                                       KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
tumour angiogenesis; psoriaais; rheumatoid arthritis; ocular disease;
fms-like tyrosine kinase 1; kinase insert domain containing receptor;
foetal liver kinase 1; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid molecule modulating VEGF receptor(s) gene expression or stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient.
 Gaps
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                                                                                                                                                                                                                                          Human flt1 VEGF receptor hammerhead ribozyme substrate #1094.
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100.0%; Pred. No. 6.1e+02;
ative 0; Mismatches 0; Indels
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 Mismatches
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AAX69802 standard; RNA; 17 BP.
                                                                                                                                             AAX69799 standard; RNA; 17 BP
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96US-00584040.
                                 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (RIBO-) RIBOZYME PHARM INC. (CHIR ) CHIRON CORP.
                                                                                                                                                                                                           (first entry)
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 15; Conservative
                                 CCCACGGAGCAGCAC
                                                             15 cccacedaecaecae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-1996;
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                                                                                                                                                                                                           28-JUL-1999
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AAX69802;

01-MAY-1997.

us10008789-3.rng

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The present invention describes enzymatic nucleic acid molecules (NAMS) which specifically cleave RNA derived from an epidermal growth factor receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090 represent specifically claimed target sequence from human EGF-R. AAV98044 to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and hairpin ribozymes respectively for human EGF-R. The NAMS are useful for cleaving EGF-R RNA in the treatment of a condition associated with EGFR expression lavels e.g. to inhibit cell profiferation in the prevention or treatment of cancers. The NAMS can also be used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of EGF-R RNA in a cell
                                                                                                                                                                                                                                                                                                                                                        Enzymatic nucleic acids - which cleave RNA derived from an epidermal growth factor receptor, useful for inhibiting cell proliferation and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leukocyte; IgA nephropathy; diagnosis; treatment; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.9%; Score 15; DB 1; Length 17; Best Local Similarity 86.7%; Pred. No. 6.1e+02;
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agase T, Sawada S, Takei M;
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(KAZU-) KAZUSA DNA RES INST FOUND.
                                                                                                                                                                                                                                                                          Mcswiggen JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Page 68; 109pp; English
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97US-00985162
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                                                                                                                                                                                                                                                                        Akhtar S, Fell P,
                                                                                                                                                                                                                                                                                                                  WPI; 1998-437449/37
                                                                                                                                                                                                                                                                                                                                                                                                      treating cancers
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                 WO9833893-A2
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04-DEC-1997;
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                                                           06-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (VEGF). A patient (preferably human) having a condition associated with the level of the fms-like tyrosine kinase 1 (fll-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the nucleic and molecule or the expression vector to the patient. AAX67575 to AAX75752 represent specific examples of nucleic acid molecules from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient.
                                                                                                                       Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence; hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation; cancer; genetic drift; detection; mutation; ss.
                                                                                                                                         KDR; hammerhead ribozyme; hairpin ribozyme; cleavage; tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease; fms-like tyrosine kinase 1; kinase insert domain containing receptor;
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                                                                               Human flt1 VEGF receptor hammerhead ribozyme substrate #1097
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100.0%; Pred. No. 6.1e+02;
lve 0; Mismatches 0; Indels
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100.0%; Pre
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                                     28-JUL-1999 (first entry)
                                                                                                                                                                                                            foetal liver kinase 1; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-259017/23.
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les 15; Conserv
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Gaps

Nishi T;

17-MAR-1999

AAV97255

RESULT 1081

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Query Match

Best Loca Matches

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DNA and encoded protein which activates eosinophil cells - for treatment of cancer, parasite infection, autoimmune disease and allergic inflammation.
                             Protein from leukocytes and DNA encoding it - useful as reagents for diagnosing and treating IgA nephropathy.
                                                                                                                                                                                                                                                                                                                                                                 Bosinophil cell activator; treatment; diagnosis; malignant tumour; parasitic infection; allergic inflammation; eosinophilic pneumonia; rapid onset eosinophilia; autoimmune disease; gene therapy; primer;
                                                                                                                                              Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                               Human eosinophil cell activator HVC002 primer #1
                                                                                                                                                                                                                                                                                  AAV49503 standard; cDNA to mRNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 64; 92pp; Japanese.
                                                             Example 2; Page 33; 41pp; Japanese.
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Nishi T;
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          WPI; 1998-333259/29
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                                                                                                                                                                                                                                                                                                                                                 Pollenosis-associated protein, high pollen-specific immunoglobulin B, IgE, diagnose, cedar pollenosis, treatment, human, PCR primer, ss.
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                                       Gaps
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                                                                                                                                                                                                                                                                                                                 PCR primer GT15A used in pollenosis associated gene identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene highly expressed in patients with high cedar pollen-specific levels, useful for diagnosing pollenosis, and screening candidate compounds for pollenosis treatment.
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0.9%; Score 15; DB 1; Length 17;
100.0%; Pred. No. 6.1e+02;
1ve 0; Mismatches 0; Indels
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100.0%; Pred. No. 6.1e+02;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kashiwabara T,
Lu N, Ogawa K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         compounds for pollenosis treatment
   0.5.,
100.0%; Pic
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                    1 Similarity 100.
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, Imai Y,
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Best Local Similarity
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   Query Match
Best Local S
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                                                                                                                                    PCR primers AAV37933-39 are used in the course of the invention. The specification descibes a novel protein isolated from leukocytes of patients with IgA nephropathy. Oligonuclectides based on the DNA sequence encoding this protein are useful as reagents for diagnosing and treating IgA nephropathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV49503-V49507 are primers used in the isolation of a human eosinophil cell activator. This protein and antibodies generated from the protein can be used for treatment and diagnosis of malignant tumours, parasitic infections, allergic inflammation, eosinophilic pneumonia, rapid onset eosinophilia, and autoimmune diseases. DNA can be used for diagnosis, and the antisense DNA in gene therapy of these disorders. The protein can be used for screening of potential agonists or antagonists of its activity
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Length 17; Indels

0.9%; Score 15; DB 1; Le 100.0%; Pred. No. 6.1e+02; 1ve 0; Mismatches 0;

100.0%; P

Conservative

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Koike

Shinkai A,

Kuga T,

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97WO-JP004470 96JP-00325762

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                                                                                                                                                                                                                                    Gunji S;
                                                                                                                                                                                                                                                                                                 Gene highly expressed in patients with high cedar pollen-specific IgE levels, useful for diagnosing pollenosis, and screening candidate compounds for pollenosis treatment.
                        Pollenosis-associated protein; high pollen-specific immunoglobulin B; IgE, diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
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PCR primer GT15C used in pollenosis associated gene identification.
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                                                                                                                                                                                                                                   Oshida T, Obayashi M,
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                                                                                                                                                                                                                                    Kashiwabara T,
Lu N, Ogawa K;
                                                                                                                                                                                                                                                                                                                                                                Example 6; Page 38; 44pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAAAAAAAAAAA 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.9
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                          RES INC
                                                                                                                                                                                                                                   Sugita Y,
, Imai Y,
                                                                                                                                                                                                                                                                            WPI; 2000-317712/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IgA nephropathy-as
human; primer; ss
                                                                                              WO200020575-A1.
                                                                                                                                                                                                          (GENO-) GENOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAY-1999;
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                                                                                                                                                     06-OCT-1999;
                                                                                                                                                                               06-OCT-1998;
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                                                                                                                                                                                                                                                   Obayashi I,
                                                                                                                        13-APR-2000
                                                                    Synthetic
                                                                                                                                                                                                                                    Nagasu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16
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                                                                                                                                                                 This invention describes novel DNA sequences preferentially expressed in IgA nephropathy patients, and DNA sequences stringently hybridizing to them. Independent claims cover diagnostic reagents for IgA nephropathy incorporating the antisense sequences; the treatment of IgA nephropathy using the antisense sequences; the treatment of IgA nephropathy using the antisense sequences for mRNA inhibition, proteins associated with IgA nephropathy, containing sequences encoded by the DNA sequences; antibodies recognizing these proteins by coulture of host cells transformed with DNA encoding them; diagnostic reagents for IgA nephropathy containing the antibodies; and compositions for the treatment of IgA nephropathy which contain the antibodies. The products of the invention can be used for the diagnosis and treatment of IgA nephropathy. This sequence represents a primer used in the isolation and identification of the human IgA nephropathy-associated proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel DNA sequences preferentially expressed in IgA nephropathy patients, and DNA sequences stringently hybridizing to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kuga T;
 Kuga T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gA nephropathy-associated protein; diagnosis; treatment; antisense;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA sequences preferentially expressed in IgA nephropathy patients,
proteins encoded by them, and antibodies to those proteins.
                                                                                   patients,
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kei M, Shibata K, Furuya A;
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                                                                                     DNA sequences preferentially expressed in IgA nephropathy proteins encoded by them, and antibodies to those proteins
Nishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.9%; Score 15; DB 1; Length 17;
100.0%; Pred. No. 6.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
 Nakagawa S,
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human IgA nephropathy-associated cDNA primer #61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Pred. No. v..
 Ishiwata T, Sakurada M, Kawabata A, Nak
Sawada S, Takei M, Shibata K, Furuya A;
                                                                                                                                                                                                                                                                                                                                                                                               described in the method of the invention
                                                                                                                                       Claim 3; Page 170; 180pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 169; 180pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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Sawada S, Takei M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4PI; 2000-097328/08
                                                   WPI; 2000-097328/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9963085-A1
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Stimulus-regulated nucleic acid; sequence profile; nucleic acid level; differentially expressed nucleic acid; disease state; cancer; autoimmune disease; infectious disease; aging; developmental disorder; proliferative disorder; neurological disorder; toxicity, primer; treatment resistance; differential expression; drug discovery; growth factor; epidermal growth factor; radiation; stress; pathogen; ss.

Anchored oligo(dT) primer AT15A used for modified differential display.

(first entry)

13-MAR-2000

AAZ36739

AAZ36739 standard; DNA; 17 BP

AAZ36739

15 AAAAAAAAAAAA 1

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This invention describes a novel method for analysis of an RNA sample which comprises amplifying cDNA with first and second differently labeled primers and analysis of the amplified labeled cDNA. The method is useful for analyzing differential gene expression, for identifying and/or characterizing pharmacological activities or for identifying target amplies. The use of different primer combinations allow more cDNAs to be amplified. The method also provides a more detailed analysis than prior art methods. This sequence represents a primer used to illustrate the
                                     incorporating the antiennes sequences; the treatment of 19A nephropathy using the antiennes sequences for mRNA inhibition; proteins associated with 19A nephropathy, containing sequences encoded by the DNA sequences; antibodies recognizing these proteins; the production of the proteins by culture of host cells transformed with DNA encoding them; diagnostic reagents for 19A nephropathy containing the antibodies; and compositions for the treatment of 19A nephropathy which contain the antibodies. The products of the invention can be used for the diagnosis and treatment of 19A nephropathy. This sequence reppresents a primer used in the isolation and identification of the human 19A nephropathy-associated proteins described in the method of the invention
them. Independent claims cover diagnostic reagents for 1gA nephropathy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.9%; Score 15; DB 1; Length 17;
100.0%; Pred. No. 6.1e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amplification; detection; gene expression; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HMRI ) HOECHST MARION ROUSSEL DEUT GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 10; 10pp; German.
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AAZ89372 standard; DNA; 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
es 15; Conservative
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    8 \times 9 
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display, in the method of the invention. The specification describes a method for measuring the level of two or more nucleic acid molecules in a method for measuring the level of two or more nucleic acid molecules in a target. The method comprises contacting a probe with an arbitrarily or statistically sampled target and detecting the amount of specific binding of the target to the probe. The methods can be used to identify disease of the target to the probe. The methods can be used to dentify disease states, such as cancer, autoimmune disease, infectious disease, aging, differentially expressed nucleic acid molecules associated with disease states, such as cancer, autoimmune disease, infectious disease, aging, developmental disorder, proliferative disorder or neurological disorder. Alternatively the methods can be used to assess the efficacy or toxicity of or a resistance to a treatment. Also the methods can be used to determine differential expression of nucleic acid molecules in response to a stimulus, e.g. a chemical, drug or growth factor (especially epidernal growth factor), radiation, stress or a pathogen. The methods can also be used to determine co-regulated genes that can be potential
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Pred. No. 6.1e+02;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Page 91; 187pp; English
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100.0%; Pre-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    targets for drug discovery
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nes 15; Conservative
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expression of low abundance reduced complexity target nucleic

Measuring expre acid molecules.

Trenkle T;

Mcclelland M, Welsh J, WPI; 2000-086388/07

(KIMM-) KIMMEL CANCER CENT SIDNEY

04-FEB-1999;

98US-0083331P. 98US-0098070P.

27-APR-1998;

99WO-US009119

27-APR-1999;

04-NOV-1999

W09955913-A2:

Synthetic

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Gaps

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Gaps

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0.9%; Score 15; DB 1; Length 17; 100.0%; Pred. No. 6.1e+02; ve 0; Mismatches 0; Indels

100.08; PA

Query Match 0.9 Best Local Similarity 100. Matches 15; Conservative

Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;

art methods. This sequer method of the invention

1736 AAAAAAAAAAAA 1750

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nucleic acids that interact, and optionally cleave, target sequences,
                                                     Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1946.
                                                                             hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide; gene expression modification; cancer; phosphorothioate; endonuclease; anticancer; breast cancer; endometrium cancer; ss.
                                                                      receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
                                                                                                                                                                                                                                     Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Reynolds M, Zwick M, Jarvis T, Woolf T, Haeberli P;
Matulic-Adamic J;
                                                                                                                                                                                                                                                                                                                     Claim 77; Page 79; 148pp; English
                                                                                                                                                                        99WO-US008547.
                                                                                                                                                                                         98US-0082404P.
                                                                                                                                                                                                                    (RIBO-) RIBOZYME PHARM INC.
AAA25448 standard; DNA; 17
                                    (first entry)
                                                                                                                                                                                                                                                                                                      used to treat cancer
                                                                                                                                                                                                                                                                          WPI; 2000-013248/01.
                                                                                                                                                                        19-APR-1999;
                                                                                                                   Homo sapiens
                                                                                                                                    WO9954459-A2
                                                                                                                                                                                          20-APR-1998;
                                                                                                                                                                                                   23-JUN-1998;
                                    19-JUL-2000
                                                                                                                                                      28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention
                  AAA25448
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Bellon L;

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with a target sequence and contain at least one phosphoroidilthicated link, having endonuclease activity. (A), and more generally any catalytic nucleic acid (A') that modulates expression of the oestrogen receptor gene, are used to treat cancer (particularly of breast or endometrium), in vivo or by transforming cells ex vivo and implanting treated cells, or for other conditions associated with levels of oestrogen receptor. Because of the high selectivity for targeted RNA, (A) can also be used to correlate inhibition of gene expression with alterations in phenotype, particularly for identification of therapeutic targets, and as research reagents (for RNA, in the same way that restriction endonucleases are used with DNA). The combination of modifications in (A) improves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            resistance to nucleases, binding affinity and/or activity. AAA23503 to AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and AAA24748 to AAA22992 represent their corresponding target sequences. AAA25993 to AAA26105 represent coestrogen receptor hairpin ribozyme sequences, and AAA26107 to AAA26118 represent their corresponding target sequences. AAA26219 to AAA26218 represent their corresponding target sequences. AAA26219 to AAA26217 represent other ribozyme sequences and antisense oligonucleotides used in the exemplification of the present
present invention describes nucleic acids (A) that interact stably
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                                                                                Gaps
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                                  0.9%; Score 15; DB 1; Length 17; 100.0%; Pred. No. 6.1e+02; ative 0; Mismatches 0; Indels
Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
                                                         Best Local Similarity 100.
Matches 15; Conservative
                                         Query Match
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AAC64202 standard; DNA; 17 BP RESULT 1091 AAC64202/ ID AAC6

PCR anchor primer, SEQ ID NO:4, used in human gene 373 isolation.

(first entry)

21-FEB-2001

AAC64203;

BXHXHXB

Bb

AAC64203 standard; DNA; 17

RESULT 1092 AAC64203/c

16 AAAAAAAAAAAA 2

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with high cedar pollen-specific IgE (immunoglobulin B) levels of individuals with high cedar pollen-specific IgE (immunoglobulin B) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen using the differential display method. The invention also relates also relates to the protein encoded by pollinosis gene 373; expression constructs and cost cells comprising pollinosis-associated gene 373 nucleic acids; pollinosis-associated gene 373 nucleic acids; pollinosis-associated gene 373 nucleic acids; pollinosis-associated gene 373 primers and probes; antibodies against the protein encoded by the gene; methods of detection of pollinosis-associated gene 373 nucleic acids; and a method of disgnosis of allergic diseases via the detection of pollinosis-associated gene 373 nucleic acids; and a method of disgnosis of allergic acids. The invention additionally encompasses methods of screening drug candidates for the treatment of allergic disease by measuring the expression of pollinosis-associated gene 373 in pollen antigen-stimulated T-cells in the presence of a test compound relative to a control.

Creals in the presence of a test compound relative to a control.

Creals in the presence of a test compound relative to a control.

Creals in the presence of a test compound relative to a control.

Creals in the presence sequence represents a PCR primer used in the cauch diseases. The present sequence represents a PCR primer used in the control of human pollinosis-associated gene 373 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pollinosis-associated gene 373 undergoing significantly low expression in subjects with high cedar pollen-specific immunoglobulin-E levels, useful in diagnosis of allergic diseases and screening drug candidates.
                                                                                                                          Human, pollinosis-associated gene 373; IgE; immunoglobulin E; cedar pollen allergy; T-cell; reduced expression; detection; diagnosis; drug screening; allergic disease; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the invention relates to the human pollinosis-associated gene 373 which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gunji
                                                                                    PCR anchor primer, SEQ ID NO:3, used in human gene 373 isolation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kashiwabara T, Oshida T, Obayashi M,
Yoshida N, Ogawa K, Matsui K;
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100.0%; Pred. No. 6.1e+02;
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                                                                                                                                                                                                                                                                                                                                                              26-APR-2000; 2000WO-JP002730.
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                                21-FEB-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENO-) GENOX RES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sugita Y,
, Imai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-687339/67
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                                                                                                                                                                                                                                                                     WO200065046-A1
                                                                                                                                                                                                                                                                                                                                                                                                           27-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nagasu T., S
Obayashi I,
                                                                                                                                                                                                                                                                                                                    02-NOV-2000.
                                                                                                                                                                                                                          Synthetic.
AAC64202;
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us10008789-3.rng

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Pollinosia-associated gene 373 undergoing significantly low expression in subjects with high cedar pollen-specific immunoglobulin-E levels, useful in diagnosis of allergic diseases and screening drug candidates.
        Human; pollinosis-associated gene 373; IgE; immunoglobulin E;
cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
drug screening; allergic disease; PCR primer; ss.
                                                                                                                                                                                                                               Example 6; Page 70; 80pp; Japanese.
                                                                                              26-APR-2000; 2000WO-JP002730.
                                                                                                                                 (GENO-) GENOX RES INC.
                                                                                                                                                   Sugita Y,
, Imai Y,
                                                                                                                                                                            WPI; 2000-687339/67.
                                                            WO200065046-A1
                                                                                                                27-APR-1999;
                                                                            02-NOV-2000.
                                                                                                                                                           Obayashi I,
                                           Synthetic.
                                                                                                                                                    Nagasu T,
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The invention relates to the human pollinosis-associated gene 373 which exhibits significantly reduced expression in the T-cells of individuals with high cedar pollen-specific IgE (immunoglobulin B) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen using the differential display method. The invention also relates also relates to the protein encoded by pollinosis gene 373; expression constructs and host cells comprising pollinosis-associated gene 373 nucleic acids; collinosis-associated gene 373 nucleic acids; pollinosis-associated gene 373 nucleic acids; protein encoded by the gene; methods of detection of pollinosis-considered gene 373 nucleic acids; associated gene 373 nucleic acids; associated gene 373 nucleic acids; and a method of dispnosis of allergic dispasses via the detection of pollinosis-associated gene 373 nucleic acids; acids. The invention additionally encompasses methods of screening drug acids. The invention additionally encompasses methods of screening drug candidates for the treatment of allergic diseases by measuring the expression of pollinosis-associated gene 373 in pollen antigen-stimulated T-cells in the presence of a test compound relative to a control.

Tollinosis-associated gene 373 is useful in the diagnosis of allergic diseases and in the screening of drug candidates for the treatment of such diseases. The present sequence represents a PCR primer used in the isolation of human pollinosis-associated gene 373 cDNA
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Gaps
                                  ö
0.9%; Score 15; DB 1; Length 17; 100.0%; Pred. No. 6.1e+02; tive 0; Mismatches 0; Indels
                                  15; Conservative
                                Matches
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1736 AAAAAAAAAAAAA 1750 셤

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AAC64181 standard; DNA; 17 BP AAC64181; MARKE KEYEK BY A KAN 
PCR anchor primer, SEQ ID NO:2, used in human gene 419 isolation

(first entry)

21-FEB-2001

Human; pollinosis-associated gene 419; FAF-1 homologue; Fas-associated factor-1; IgE; immunoglobulin B; cedar pollen allergy; T-cell; reduced expression; detection; diagnosis; drug screening; allergic disease; PCR primer; ss.

Synthetic. 

WO200065045-A1.

02-NOV-2000

26-APR-2000; 2000WO-JP002729.

99JP-00120490, 27-APR-1999;

(GENO-) GENOX RES INC

Gunji Obayashi M, Kashiwabara T, Oshida T, Obay Yoshida N, Ogawa K, Matsui K; Sugita Y, , Imai Y, Obayashi I, Nagasu T,

WPI; 2000-687338/67.

Gunji S;

T, Oshida T, Obayashi M, Ogawa K, Matsui K;

Kashiwabara Yoshida N,

99JP-00120489

Pollinosis-associated gene 419 undergoing significantly low expression in subjects with high cedar pollen-specific IgE levels, useful in diagnosis of allergic diseases and screening drug candidates.

Example 6; Page 49; 77pp; Japanese.

The invention relates to the human pollinosis-associated gene 419 which exhibits reduced expression in the T-cells of individuals with high cedar pollen specific IgB (immunoglobulin B) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen using the differential display method. Pollinosis-associated gene 419 has homology with the gene encoding human Pas-associated factor-1 [PRF-1]. The invention also callers to the protein encoded by pollinosis gene 419; expression relates to the protein encoded by pollinosis gene 419; expression calls; pollinosis-associated gene 419 primers and probes; antibodies against the protein encoded by the gene; method of detection of pollinosis-associated gene 419 nucleic acids; and a method of disquests of allergic diseases via the detection of pollinosis-associated gene 419 nucleic acids. The invention additionally encompasses of somethods of soreening drug candidates for the treatment of allergic methods of soreening drug candidates for the treatment of allergic completed gene 419 in the pollinosis-associated gene 419 in the diseases and in the screening of authorioral pollinosis-associated gene 419 in the diagnosis of allergic diseases and in the screening of drug candidates for the treatment of allergic diseases. The presente requence represents a PCR primer used in the isolation of human pollinosis-associated gene 419 cDNA

Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Gaps ö 0.9%; Score 15; DB 1; Length 17; 100.0%; Pred. No. 6.1e+02; tive 0; Mismatches 0; Indels 15; Conservative Query Match Best Local Matches

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1736 AAAAAAAAAAAA 1750 

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AAC64182 standard; DNA; 17 BP. RESULT 1094 AAC64182/

AAC64182;

(first entry) 21-FEB-2001

PCR anchor primer, SEQ ID NO:3, used in human gene 419 isolation. 

Human, pollinosis-associated gene 419; FAF-1 homologue; Fas-associated factor-1; IgE; immunoglobulin E; cedar pollen allergy; T\_cell; reduced expression; detection; diagnosis; drug screening;

allergic disease; PCR primer; ss.

Synthetic

26-APR-2000; 2000WO-JP002733.

99JP-00120491.

27-APR-1999;

(GENO-) GENOX RES INC.

Gunji S;

Obayashi M,

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The invention relates to the human pollinosis-associated gene 419 which exhibits reduced expression in the T-cells of individuals with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen using the differential display method. Pollinosis-associated gene 419 has homology with the gene encoding human Fas-associated gene 419 has homology with the gene condition and protein encoded by pollinosis-associated gene 419 primers and probes; antibodies against the protein encoded by pollinosis-associated gene 419 primers and probes; antibodies against the protein encoded by the gene; methods of detection of pollinosis-associated gene 419 mucleic acids; and a method of diagnosis of allergic diseases via the detection of pollinosis-associated gene 419 nucleic acids. The invention additionally encompasses methods of screening drug candidates for the treatment of allergic disease by measuring the expression of pollinosis-associated gene 419 in the presence of a test compound callagnosis of allergic diseases. The presence of a test compound callagnosis of allergic diseases. The presence expresents a PCR primer used in the isolation of human pollinosis-associated gene 419 cDNA
                                                                                                                                                                                                                                                                                                                        Pollinosis-associated gene 419 undergoing significantly low expression in subjects with high cedar pollen-specific IgE levels, useful in diagnosis of allergic diseases and screening drug candidates.
                                                                                                                                                                                                                Kashiwabara T, Oshida T, Obay
Yoshida N, Ogawa K, Matsui K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                 Example 6; Page 49; 77pp; Japanese
                                                                                   26-APR-2000; 2000WO-JP002729
                                                                                                                            99JP-00120490
                                                                                                                                                                                                                Sugita Y,
                                                                                                                                                                       (GENO-) GENOX RES INC
                                                                                                                                                                                                                                                                                  WPI; 2000-687338/67.
WO200065045-A1.
                                                                                                                            27-APR-1999;
                                                                                                                                                                                                                                       Obayashi I,
                                        02-NOV-2000
                                                                                                                                                                                                                    Nagasu T,
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ö Gaps . 0 Query Match 0.9%; Score 15; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 6.1e+02; Matches 15; Conservative 0; Mismatches 0; Indels ઠે

1736 AAAAAAAAAAAAA 1750 16 ААААААААААААА

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AAC64171 standard; DNA; 17 BP AAC64171;

PCR anchor primer, SEQ ID NO:2, used in human gene 513 isolation

Human, pollinosis-associated gene 513; IgE; immunoglobulin E; cedar pollen allergy; T-cell; reduced expression; detection; diagnosis; drug screening; allergic disease; PCR primer; ss.

02-NOV-2000

Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S; Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;

(GENO-) GENOX RES INC.

21-FEB-2001 (first entry) WO200065049-A1 Synthetic 

The invention relates to the human pollinosis-associated gene 513 which exhibits significantly reduced expression in the T-cells of individuals with high cedar pollen-specific 198 (immunoslobulin B) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen using the differential display method. The invention also relates to methods of detection of pollinosis-associated gene 513 nucleic acids; and methods of screening drug candidates for the cannot of allergic disease via the detection of pollinosis-associated correspond to a lergic disease by measuring the expression of pollinosis-associated gene 513 nucleic associated gene 513 nucleic associated gene 513 in pollen antigen-stimulated T-cells in the presence of a test compound relative to a control. Pollinosis-associated gene 513 is useful in the diagnosis of allergic diseases and in the screening of arung candidates for the treatment of such diseases. The present sequence represents a PCR primer used in the isolation of human pollinosis-Pollinosis-associated gene 513 undergoing significantly low expression in subjects with high cedar pollen-specific IgE levels, useful in diagnosis of allergic diseases and screening drug candidates. Human; pollinosis-associated gene 513; IgE; immunoglobulin E; cedar pollen allergy; T-cell; reduced expression; detection; diagnosis; drug screening; allergic disease; PCR primer; ss. Obayashi M, Gunji S; Gaps PCR anchor primer, SEQ ID NO:3, used in human gene 513 isolation ö 0.9%; Score 15; DB 1; Length 17; 100.0%; Pred. No. 6.1e+02; tive 0; Mismatches 0; Indels Sugita Y, Kashiwabara T, Oshida T, Obay , Imai Y, Yoshida N, Ogawa K, Matsui K; Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other; Example 6; Page 38; 46pp; Japanese. 1736 AAAAAAAAAAAAA 1750 AAC64172 standard; DNA; 17 BP 26-APR-2000; 2000WO-JP002733. 99JP-00120491. AAAAAAAAAAAA 2 (first entry) 15; Conservative Local Similarity WPI; 2000-687342/67 40200065049-A1 27-APR-1999; Obayashi I, 21-FEB-2001 32-NOV-2000 Synthetic. Nagasu T, 16 AAC64172; Query Match RESULT 1096 Matches AAC64172/ 8 셤

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WPI; 2000-687342/67
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Pollinosis-associated gene 513 undergoing significantly low expression in subjects with high cedar pollen-specific IgE levels, useful in diagnosis of allergic diseases and screening drug candidates.

Example 6; Page 38; 46pp; Japanese.

The invention relates to the human pollinosis-associated gene 513 which exhibits significantly reduced expression in the T-cells of individuals with high cedar pollen-specific 1gg (immunoglobulin E) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen using the differential display method. The invention also relates to method of deaction of pollinosis-associated gene 513 nucleic acids, a method of diagnosis of allergic diseases via the detection of pollinosis-associated gene 513 nucleic acids, and methods of screening the expression of pollinosis-associated gene 513 in pollen antigen-stimulated T-cells in the presence of a test compound relative to a control. Pollinosis-associated gene 513 in pollen antigen-stimulated T-cells in the presence of a test compound relative to a control. Pollinosis-associated gene 513 its useful in the diagnosis of allergic diseases and in the screening of drug candidates for the treatment of such diseases. The present sequence represents a PCR primer used in the isolation of human pollinosisassociated gene 513 cDNA

Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Gaps ö 0.9%; Score 15; DB 1; Length 17; 100.0%; Pred. No. 6.1e+02; tive 0; Mismatches 0; Indels 15; Conservative Query Match Best Local Similarity Matches

1736 AAAAAAAAAAAA 1750

16 AAAAAAAAAAAA 2 ò 셤

AAC64161 standard; DNA; 17 RESULT 1097 AAC64161 

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AAC64161;

21-FEB-2001 (first entry)

PCR anchor primer, SEQ ID NO:2, used in human gene 581 isolation.

Human; pollinosis-associated gene 581; IgE; immunoglobulin E; cedar pollen allergy; T-cell; reduced expression; detection; diagnosis; drug screening; allergic disease; PCR primer; ss.

Synthetic

WO200065048-A1

02-NOV-2000.

26-APR-2000; 2000WO-JP002732.

99JP-00120492 27-APR-1999;

(GENO-) GENOX RES INC.

Gunji S; Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;

WPI; 2000-687341/67.

Pollenosis-associated gene 581 undergoing significantly low expression in subjects with high cedar pollen-specific IgE levels, useful in diagnosis of allergic diseases and screening drug candidates.

Example 6; Page 39; 69pp; Japanese

The invention relates to the human pollinosis-associated gene 581 which

with high cedar pollen-specific 1gE (immunoglobulin E) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen using the differential display method. The invention also relates also relates to the protein encoded by pollinosis-associated gene 581, to expression constructs and host cells comprising pollinosis-associated gene 581 to expression constructs and host cells comprising pollinosis-associated gene 581 muches and probes; antibodies against the protein encoded by the gene; methods of detection of pollinosis-associated gene 581 nucleic acids. The invention additionally encompasses methods of screening drug candidates for the treatment of allergic disease by measuring the expression of pollinosis-associated gene 581 in pollen candidates for the treatment of allergic disease by measuring the expression of pollinosis-associated gene 581 in pollen candidates for the presence of a test compound relative to a control.Pollinosis-associated gene 581 in the presence of a control enganosis of allergic diseases and in the screening of drug candidates for the treatment of such diseases. The present sequence represents a PCR primer used in the isolation of human pollinosis-associated gene 581 cDNA exhibits significantly reduced expression in the T-cells of individuals

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Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Gaps ő 0.9%; Score 15; DB 1; Length 17; 100.0%; Pred. No. 6.1e+02; tive 0; Mismatches 0; Indel8 15; Conservative Local Similarity Query Match Matches

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1736 AAAAAAAAAAAA 1750 16 AAAAAAAAAAAAAA

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RESULT 1098 AAC64162/

AAC64162 standard; DNA; 17 BP

AAC64162;

(first entry) 21-FEB-2001

PCR anchor primer, SEQ ID NO:3, used in human gene 581 isolation.

Human; pollinosis-associated gene 581; IgE; immunoglobulin E; cedar pollen allergy; T-cell; reduced expression; detection; diagnosis; drug screening; allergic disease; PCR primer; ss.

Synthetic.

WO200065048-A1. 

02-NOV-2000.

26-APR-2000; 2000WO-JP002732.

99JP-00120492. 27-APR-1999;

(GENO-) GENOX RES INC.

Gunji S; Sugita Y, Kashiwabara T, Oshida T, Obayashi M, , Imai Y, Yoshida N, Ogawa K, Matsui K; Obayashi I, Nagasu T,

WPI; 2000-687341/67.

Pollenosis-associated gene 581 undergoing significantly low expression in subjects with high cedar pollen-specific IgE levels, useful in diagnosis of allergic diseases and screening drug candidates.

Example 6; Page 40; 69pp; Japanese.

The invention relates to the human pollinosis-associated gene 581 which exhibits significantly reduced expression in the T-cells of individuals with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen using the differential display method. The invention also relates also relates to the protein encoded by pollinosis-associated gene 581; to expression

constructs and host cells comprising pollinosis-associated gene 581 nucleic acids; pollinosis-associated gene 581 primers and probes; antibodies against the protein encoded by the gene; methods of detection of pollinosis-associated gene 581 nucleic acids; and a method of diagnosis of allergic diseases via the detection of pollinosis-associated gene 581 nucleic acids. The invention additionally encompasses methods of screening drug candidates for the treatment of allergic disease by measuring the expression of pollinosis-associated gene 581 in pollen antigen-stimulated T-cells in the presence of a test compound relative to a control.Pollinosis-associated gene 581 is useful in the diagnosis of allergic diseases and in the greening of drug candidates for the treatment of such diseases. The present sequence represents a PCR primer used in the isolation of human pollinosis-associated gene 581 cDNA The invention relates to the human pollinosis-associated gene 627 which exhibits significantly reduced expression in the T-cells of individuals with high cedar pollen specific IgE (immunoglobulin E) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen using the differential display method. The invention also relates to methods of detection of pollinosis-associated gene 627 nucleic acids; a method of diagnosis of allergic diseases via the detection of pollinosis-associated gene 627 nucleic acids; and a method of screening drug candidates for the treatment of allergic disease by measuring the expression of pollinosis-associated associated gene 627 in pollen antigen-stimulated T-cells in the presence of a test compound relative to a control. Pollinosis-associated gene 627 Pollinosis-associated gene 627 undergoing significantly low expression in subjects with high cedar pollen-specific IgE levels, useful in diagnosis of allergic diseases and screening drug candidates. Human, pollinosis-associated gene 627; IgE; immunoglobulin E; cedar pollen allergy; T-cell; reduced expression; detection; diagnosis; drug screening; allergic disease; PCR primer; ss. Gaps Gunji PCR anchor primer, SEQ ID NO:2, used in human gene 627 isolation. ö Obayashi M, 0.9%; Score 15; DB 1; Length 17; 100.0%; Pred. No. 6.1e+02; vative 0; Mismatches 0; Indels Sugita Y, Kashiwabara T, Oshida T, Obay , Imai Y, Yoshida N, Ogawa K, Matsui K; Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other; Example 6; Page 41; 51pp; Japanese. 213/c AAC64213 standard; DNA; 17 BP 1736 AAAAAAAAAAAAA 1750 26-APR-2000; 2000WO-JP002735 27-APR-1999; 99JP-00120493 16 AAAAAAAAAAAA 2 21-FEB-2001 (first entry) Matches 15; Conservative (GENO-) GENOX RES INC WPI; 2000-687344/67. Query Match Best Local Similarity 40200065051-A1. Nagasu T, Si Obayashi I, 02-NOV-2000 Synthetic. AAC64213; \$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$ 셤 ઠે

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The invention relates to the human pollinosis-associated gene 627 which exhibits significantly reduced expression in the T-cells of individuals with high cedar pollen-specific 19E (immunoglobulin B) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen using the differential display method. The invention also relates to methods of detection of pollinosis-associated gene 627 nucleic acids; and method of screening drug candidates for the diagnosis of allergic diseases via the detection of pollinosis-associated control and method of screening drug candidates for the associated gene 627 in pollen antigen-stimulated T-cells in the presence of a test compound relative to a control. Pollinosis-associated gene 627 in pollen antigen-stimulated T-cells in the presence of a test compound relative to a control. Pollinosis-associated gene 627 is useful in the diagnosis of allergic diseases and in the screening of drug candidates for the treatment of such diseases. The present sequence represents a PCR primer used in the isolation of human pollinosisö Pollinosis-associated gene 627 undergoing significantly low expression in subjects with high cedar pollen-specific IgE levels, useful in diagnosis of allergic diseases and screening drug candidates. is useful in the diagnosis of allergic diseases and in the screening of drug candidates for the treatment of such diseases. The present sequence represents a PCR primer used in the isolation of human pollinosis-associated gene 627 cDNA Human; pollinosis-associated gene 627; IgE; immunoglobulin E; cedar pollen allergy; T-cell; reduced expression; detection; diagnosis; drug screening; allergic disease; PCR primer; ss. ŝ Gaps Obayashi M, Gunji PCR anchor primer, SEQ ID NO:3, used in human gene 627 isolation. ö Length 17; 0; Indels Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obay Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K; Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other; Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other; O.9%; Score 15; DB 1; Le Local Similarity 100.0%; Pred. No. 6.1e+02; Les 15; Conservative 0; Mismatches 0; Example 6; Page 42; 51pp; Japanese. 1736 AAAAAAAAAAAAA 1750 AAC64214 standard; DNA; 17 BP 26-APR-2000; 2000WO-JP002735 99JP-00120493 16 AAAAAAAAAAAA 2 (first entry) (GENO-) GENOX RES INC WPI; 2000-687344/67. WO200065051-A1. 27-APR-1999; 21-FEB-2001 02-NOV-2000. Synthetic. AAC64214; Query Match RESULT 1100 Best Loca Matches AAC642 8888888 g 

0.9%; Score 15; DB 1; Length 17; 100.0%; Pred. No. 6.1e+02;

Best Local Similarity

Query Match

Human, pollinosis-associated gene 795; vimentin homologue; IgE; immunoglobulin E; cedar pollen allergy; T-cell; reduced expression; detection; diagnosis; drug screening; allergic disease; PCR primer; ss. Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E, PCR anchor primer, SEQ ID NO:3, used in human gene 795 isolation. Mismatches Page 45; Example 6; 73pp; Japanese. ö 1736 AAAAAAAAAAAAA 1750 AAC64231 standard; DNA; 17 BP. 26-APR-2000; 2000WO-JP002734. 99JP-00120494. 16 AAAAAAAAAAAA 2 21-FEB-2001 (first entry) 15; Conservative (GENO-) GENOX RES INC. (EISA ) EISAI CO LTD. WPI; 2000-687343/67. WO200065050-A1. 27-APR-1999; 02-NOV-2000. Synthetic. AAC64231; Tokoi A; RESULT 1101 AAC64231/c Matches 셤 ò

Pollinosie-associated gene 795 undergoing significantly low expression in subjects with high cedar pollen-specific IgE levels, useful in diagnosis of allergic diseases and screening drug candidates. The invention relates to the human pollinosis-associated gene 795 which

with high cedar pollen-specific IgE (immunoglobulin B) levels. The gene with high cedar pollen-specific IgE (immunoglobulin B) levels. The gene with high cedar pollen-specific IgE (immunoglobulin B) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen using the differential display method. Pollinosis-associated gene 795 has homology with the human vimentin gene. The invention also relates also relates to the protein encoded by pollinosis-associated gene 795; to expression constructs and host cells comprising pollinosis-associated gene 795 primers and probes; outleic acids; pollinosis-associated gene 795 primers and probes; on pollinosis-associated gene 795 primers and probes; of pollinosis-associated gene 795 primers and probes; of pollinosis-associated gene 795 primers and method of diagnosis of allergic diseases via the detection of pollinosis-associated gene 795 mucleic acids. The invention additionally encompasses methods of screening drug candidates for the treatment of allergic diseases by measuring the expression of pollinosis-associated gene 795 in pollen antigen-stimulated T-cells in the presence of a test compound relative to a control. Pollinosis-associated gene 795 in useful in the diagnosis of allergic diseases and in the screening of drug candidates for the creatment of such diseases. The present sequence represents a PCR primer  $_{
m cac}$  min or such diseases. The present sequence represents a PCR  $_{
m I}$  used in the isolation of human pollinosis-associated gene 795 cDNA

Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Gaps ; Query Match 0.9%; Score 15; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 6.1e+02; Matches 15; Conservative 0; Mismatches 0; Indels

1736 AAAAAAAAAAAAA 1750 16 AAAAAAAAAAAAAA ö g

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Gaps

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Indels

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AAC64230 standard; DNA; 17 BP

AAC64230;

21-FEB-2001 (first entry)

PCR anchor primer, SEQ ID NO:2, used in human gene 795 isolation.

88. Human, pollinosis-associated gene 795; vimentin homologue; 19B; immunoglobulin B; cedar pollen allergy; T-cell; reduced expression; detection; diagnosis; drug screening; allergic disease; PCR primer;

Synthetic.

WO200065050-A1

02-NOV-2000.

26-APR-2000; 2000WO-JP002734.

27-APR-1999; 99JP-00120494.

(GENO-) GENOX RES INC. (EISA) EISAI CO LTD.

Gunji Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji , Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E; Obayashi I, Nagasu T, Yokoi A;

WPI; 2000-687343/67.

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Pollinosia-associated gene 795 undergoing significantly low expression in subjects with high cedar pollen-specific IgE levels, useful in diagnosis of allergic diseases and screening drug candidates.

Page 45; Example 6; 73pp; Japanese.

The invention relates to the human pollinosis-associated gene 795 which exhibits significantly reduced expression in the T-cells of individuals with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene was isolated from T-cells from individuals allergic to cedar pollen using the differential display method. Pollinosis-associated gene 795 has homology with the human vimentin gene. The invention also relates also relates to the protein encoded by pollinosis-associated gene 795 to expression constructs and host cells comprising pollinosis-associated gene 795 constructs and host cells comprising pollinosis-associated gene 795 constructs and host cells comprising pollinosis-associated gene 795 nucleic acids; pollinosis-associated gene 795 nucleic acids; and a method of diagnosis of allergic diseases via the detection of pollinosis-associated gene 795 nucleic acids; and a method of companing the expression of pollinosis-associated gene 795 nucleic acids; and a method of sereening drug acudidates for the treatment of allergic diseases with the presence of a llergic disease by measuring the expression of pollinosis-associated gene 795 in pollen antigen-stimulated T-cells in the presence of a test compound relative to antigen-stimulated T-cells in the presence of a test compound relative to allergic diseases and in the screening of drug candidates for the treatment of such diseases. The present sequence represents a PCR primer used in the isolation of human pollinosis-associated gene 795 cDNA 

Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

ö Query Match 0.9%; Score 15; DB 1; Length 17; Best Local Similarity 100.0%; Pred. No. 6.1e+02; Matches 15; Conservative 0; Mismatches 0; Indels

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Gaps

1736 AAAAAAAAAAAAA 1750

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18-MAY-2000; 2000WO-JP003192.
                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pollinosis-associated gene 465 undergoing significantly low expression in subjects after pollen scattering, useful in diagnosis of allergic diseases and screening candidate compounds to regulate response of T cells to antigen stimulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes the human pollinosis-associated gene 465 which has a nucleic acid sequence of 3442 base pairs (bp), given in (AAC92291), that undergoes significantly low expression in subjects after pollen scattering, and its useful in the diagnosis of allergic diseases and screening candidate compounds for remedies capable of regulating the response of T calls to the stimulus by an antigen. The gene is useful in the diagnosis of allergic diseases and screening candidate compounds for remedies capable of regulating the response of T calls to the stimulus by an antigen. The present sequence represents a PCR primer which is used in
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                                                                                                                                                                                                                                   Human pollinosis-associated gene 465 related PCR primer SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kashiwabara T, Oshida T, Obayashi M, Gunji
Yoshida N, Ogawa K, Matsui K, Takahashi E;
                                                                                                                                                                                                                                                                         Human, pollinosis-associated gene 465; pollen scattering; allergy; allergic disease; PCR primer; 88.
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00.0%; Pred. No. 6.1e+02;
ve 0; Mismatches 0; Indels
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100.0%; Pre-
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                                                                                                    AAC92292 standard; DNA; 17
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Matches 15; Conservative
16 AAAAAAAAAAAAA
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, Imai Y,
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Obayashi I,
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                                                                                                                                                AAC92292
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1D AAC9229
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11D AAC9
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The present invention describes the human pollinosis-associated gene 465 which has a nucleic acid sequence of 3442 base pairs (bp), given in (AAC92291), that undergoes significantly low expression in subjects after pollen scattering, and is useful in the diagnosis of allergic diseases and screening candidate compounds for remedies capable of regulating the response of T cells to the stimulus by an antigen. The gene is useful in the diagnosis of allergic diseases and screening candidate compounds for remedies capable of regulating the response of T cells to the stimulus by an antigen. The present sequence represents a PCR primer which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pollinosis-associated gene 465 undergoing significantly low expression in subjects after pollen scattering, useful in diagnosis of allergic diseases and screening candidate compounds to regulate response of T cells to antigen stimulus.
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Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi B;
Yokoi A;
Human; pollinosis-associated gene 465; pollen scattering; allergy; allergic disease; PCR primer; ss.
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100.0%; Pred. No. 6.1e+02;
tive 0; Mismatches 0;
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Les 15; Conservative
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18-MAY-2000; 2000WO-JP003192
       (GENO-) GENOX RES INC. (EISA ) EISAI CO LTD.
                          WPI; 2001-032159/04.
                                                                                                         Best Local Similarity
                                                                                                                                                                       WO200073440-A1
                 Obayashi I,
                                                                                                                                                                   Synthetic.
               Nagasu T,
                                                                                                                                        AAC91719;
                                                                                                      Query Match
                     rokoi A;
                                                                                                           Matches
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The invention relates to the human pollinosis-associated gene 787 which exhibits significantly reduced expression in the T-cells of individuals after the pollen-scattering season, relative to expression levels in T-cells before the pollen-scattering season. The gene was isolated from T-cells from individuals allergic to pollen using the differential display method. The invention also relates to pollen using the differential display primers and probes; methods of detection of pollinosis-associated gene 787 nucleic acids, and a method of diagnosis of allergic diseases via the detection of pollinosis-associated gene 787 nucleic acids. The invention additionally encompasses a method of screening drug candidates for the treatment of allergic diseases by measuring the expression of pollinosis-cassociated gene 787 in pollen antiquen-stimulated T-cells in the presence of a test compound relative to a control. Pollinosis-associated gene 787 is useful in the diagnosis of allergic diseases and in the screening of drug candidates for the treatment of such diseases and in the screening of care sequence represents a PCR primer used in the isolation of human pollinosis-Pollinosis-associated gene 787 undergoing significantly low expressio subjects after pollen scattering, useful in diagnosis of allergic diseases and screening candidate compounds to regulate response of T cells to antigen stimulus. Kashiwabara T, Oshida T, Obayashi M, Gunji Yoshida N, Ogawa K, Matsui K, Takahashi E; Pollinosis; pollinosis-associated gene 441; allergy; T cell; 0.9%; Score 15; DB 1; Length 17; 100.0%; Pred. No. 6.1e+02; lve 0; Mismatches 0; Indels Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other; Human pollinosis-associated gene 441 primer #2. pollen scattering, antigen, primer, ss. Example 6; Page 40; 54pp; Japanese. 100.0%; F1 AAC82875 standard; DNA; 17 BP. 1736 AAAAAAAAAAAAA 1750 18-MAY-2000; 2000WO-JP003190. 99JP-00148783. (first entry) 15; Conservative 16 AAAAAAAAAAAAA Sugita Y, , Imai Y, (EISA ) EISAI CO LTD WPI; 2001-032159/04. Best Local Similarity WO200073435-A1. 27-MAY-1999; Nagasu T, Sı Obayashi I, Homo sapiens 20-MAR-2001 07-DEC-2000. AAC82875; Yokoi A; RESULT 1107 Matches AAC82875/ ð g The invention relates to the human pollinosis-associated gene 787 which exhibits significantly reduced expression in the T-cells of individuals after the pollen-scattering season, relative to expression levels in T-cells before the pollen-scattering season. The gene was isolated from T-cells from individuals allergic to pollen using the differential display method. The invention also relates to pollinosis-associated gene 787 primers and probes; methods of detection of pollinosis-associated gene 787 mucleic acids, and a method of diagnosis of allergic diseases via the 787 mucleic acids, and a method of gene 787 nucleic acids. The invention additionally encompasses a method of screening drug candidates for the treatment of allergic disease by measuring the expression of pollinosis-associated gene 787 in pollen antigen stimulated T-cells in the presence of a test compound relative to a control. Pollinosis—associated gene 787 is useful in the diagnosis of allergic diseases and in the screening of drug candidates for the treatment of such diseases. The present sequence represents a PCR primer used in the isolation of human pollinosis ö Pollinosis-associated gene 787 undergoing significantly low expression in subjects after pollen scattering, useful in diagnosis of allergic diseases and screening candidate compounds to regulate response of T cells to antigen stimulus. ŝ Gaps Kashiwabara T, Oshida T, Obayashi M, Gunji Yoshida N, Ogawa K, Matsui K, Takahashi E; PCR anchor primer, SEQ ID NO:2, used in human gene 787 isolation. ; Human; pollinosis-associated gene 787; pollen allergy; T-cell; reduced expression; detection; diagnosis; drug screening; allergic disease; PCR primer; ss. 0.9%; Score 15; DB 1; Length 17; 100.0%; Pred. No. 6.1e+02; Artive 0; Mismatches 0; Indels Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other; Example 6; Page 40; 54pp; Japanese. 1736 AAAAAAAAAAAA 1750 AAC91719 standard; DNA; 17 BP 27-MAY-1999; 99JP-00148785. 27-MAR-2001 (first entry) 15; Conservative 16 AAAAAAAAAAAAA Sugita Y, Imai Y,

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Gunji

Obayashi M,

Kashiwabara T, Oshida T, Obay Yoshida N, Ogawa K, Matsui K;

Sugita Y, , Imai Y,

Obayashi I,

99JP-00148785

27-MAY-1999;

(GENO-) GENOX RES INC.

Nagasu T,

WPI; 2001-061526/07.

(GENO-) GENOX RES INC

1736 AAAAAAAAAAAAA 1750

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16 AAAAAAAAAAAA 2

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This invention describes a novel nucleic acid molecule comprising a sequence (I) which undergoes significantly low expression in subjects effer pollen scattering, and is useful in diagnosis of allergic diseases and screening candidate compounds for remedies capable of regulating the response of T cells to the stimulus by an antigen
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              Pollinosis-associated gene 441 which undergoes lower expression in usubjects after Pollen scattering, useful in diagnosis of allergic diseases and screening candidate compounds to regulate response of cells to antigen stimulus.
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Yoshida N, Ogawa K, Matsui K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pollinosis; pollinosis-associated gene 441; allergy; T cell;
                                                                                                                                                                                                                                                                           0.9%; Score 15; DB 1; Length 17;
100.0%; Pred. No. 6.1e+02;
ative 0; Mismatches 0; Indels
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rative 0; Mismatches 0; Indels
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                                                                                                      Example 6; Page 35; 42pp; Japanese.
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AAC82874 standard; DNA; 17 BP.
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Imai Y,
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Obayashi I,
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The invention provides a method of diagnosis of allergies that involves: assaying the levels of expression of genes B1001, B1466, B1072 or B1151 in T-cells; and comparing them with the level of expression in healthy T-cells. The method is useful for diagnosing allergies, particularly atopic dermatitis. The present sequence represents a PCR primer used for analysis of the expression of the above genes
                                                                                                                        B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis; human;
PCR primer; 88.
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100.0%; Pred. No. 6.1e+02;
cive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                              Diagnosis of allergies including atopic dermatitis.
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JAPAN GEN NAT CHILDREN'S HOSPITAL.
                                                                                                 Nucleotide sequence of primer GT15C.
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                                                                                                                                                                                                                                        23-FEB-2001; 2001WO-JP001372.
                                                                                                                                                                                                                                                                02-MAR-2000; 2000JP-00061832
                      DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH47126 standard; DNA; 17
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                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-557789/62
                      AAH47127 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                       PCR primer; 88
                                                                                                                                                                                      WO200165259-A1
                                                                        30-NOV-2001
                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-NOV-2001
                                                                                                                                                                                                               07-SEP-2001.
                                                                                                                                                                                                                                                                                                                              Nagasu T,
                                               AAH47127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16
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                                                                                                                                                                                                                                                                                         (GENO-)
                                                                                                                                                                                                                                                                                                      (NIGE-)
RESULT 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1110
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Matches
          AAH47127,
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Best Local Similarity 100. Matches 15; Conservative

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Examining allergic diseases by differential display of gene showing different expression particularly increased expression in remission stage in eosinophils of patients, also applicable in screening candidate compounds for remedies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Diagnosis of allergies including atopic dermatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sugita Y, Hashida R, Ogawa K, Fujishima T,
Takahashi E;
                                                                                                                                                                                                                                    (GENO-) GENOX RES INC.
(NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
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(NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
(EISA ) EISAI CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 6; Page 65; 83pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1736 AAAAAAAAAAAAA 1750
                                                                                                               23-FEB-2001; 2001WO-JP001372
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                                                                                                                                                                         02-MAR-2000; 2000JP-00061832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 AAAAAAAAAAAAA 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15; Conservative
                                                                                                                                                                                                                                                                                                                          Nagasu T, Oshida T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-315738/35.
                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-557789/62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
WO200165259-A1.
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ABK49634/c
XX
AC ABK49634
XX
DY 15-UUL-;
XX
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Human;
KW Himan;
KW differed
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COS Homo saj
XX
COS
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acetyltransferases in the eosinophils of a patient and comparing the expression level with that in the eosinophils of a healthy individual (i.e. differential display). Also included are methods of screening for candidate compounds which affect the expression level of the gene or the activity of the protein encoded by the gene (including related proteins and mutants), the use of probes based on the gene sequence in the examination of allergic diseases, the use of reporter constructs in the screening of candidate compounds, a vector containing a the transcription controlling region of the gene, cells transformed with the vector, an antibody against the protein and a model animal for allergic diseases which is a transgenic non-human vertebrate with lowering of expression intensity of the gene in eosinophils. The method is examining allergic diseases particularly atopic dermatitis which is also applicable in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Examining allergic diseases by differential display of gene showing different expression particularly increased expression in remission stage in eosinophils of patients, also applicable in screening candidate compounds for remedies.
                                                                                                                                                                                                                                                                                                                                                                                                                                      in high throughput, at low cost. The present sequence is a differential display PCR primer for the cDNA encoding the human acetyltransferase-like protein 20-90-05
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                                                                                                                                                                                                                                                                                                                                                                                                                  screening candidate compounds for remedies. Such method can be performed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tsujimoto G;
                                                           The invention relates to a method for examining allergic diseases comprises determining the expression level of a gene containing, the human cDNA appearing as ABK49633 which has homology with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Acetyltransferase-like protein 20-90-05 PCR primer GT15C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.9%; Score 15; DB 1; Length 17; 100.0%; Pred. No. 6.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nagasu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
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(NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
(RISA ) EISAI CO LTD.
                    Example 1; Page 56; 72pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK49635 standard; DNA; 17 BP
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Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hashida R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-315738/35.
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Takahashi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                           The invention provides a method of diagnosis of allergies that involves: assaying the levels of expression of genes B1001, B1466, B1072 or B1151 and T-cells; and comparing them with the level of expression in healthy T-cells. The method is useful for diagnosing allergies, particularly atopic dermatitis. The present sequence represents a PCR primer used for analysis of the expression of the above genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; ss; PCR; acetyltransferase; 20-90-05; allergic disease; primer;
differential display; eosinophil; antiallergic; atopic dermatitis; GTISA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.9%; Score 15; DB 1; Length 17;
100.0%; Pred. No. 6.1e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                         Saito H;
                                                                                                                                                                                                                                         Obayashi I, Matsui K,
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Example 1; Page 56; 72pp; Japanese.

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Gaps

Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

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The invention relates to a method for examining allergic diseases

Comparises determining the expression level of a gene containing, the
human cDNA appearing as ABK49633 which has homology with
acetyltransferases in the eosinophils of a patient and comparing the
expression level with that in the eosinophils of a healthy individual

(i.e. differential display). Also included are methods of screening for
candidate compounds which affect the expression level of the gene or the
activity of the protein encoded by the gene (including related proteins
and mutants), the use of probes based on the gene sequence in the
examination of allergic diseases, the use of reporter constructs in the
controlling region of the gene, cells transformed with the vector, an
antibody against the protein and a model animal for allergic diseases
which is a transgenic non-human vertebrate with lowering of expression
intensity of the gene in eosinophils. The method is examining allergic
diseases particularly atopic dermatitis which is also applicable in
the protein endidate compounds for remedies. Such method can be performed
to high the broad and the protein method is also applicable in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The specification describes a method for examining allergosis. The method comprises measuring the expression level of the gene given in ABL59037, and comparing it with the expression level of the gene in the eosinophils of a healthy person. The method is used for the examination of allergosis. The present sequence represents a PCR primer, which is used in the course of the invention
                                                                                                                                                                                                                                                                                                                                                                    in high throughput, at low cost. The present sequence is a differential display PCR primer for the cDNA encoding the human acetyltransferase-like protein 20-90-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Examining allergosis, involves measuring the expression levels of a specific gene, and comparing it to the levels in the eosinophils of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.9%; Score 15; DB 1; Length 17; 100.0%; Pred. No. 6.1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; allergosis; eosinophil; PCR; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENO-) GENOX SOYAKU KENKYUSHO KK.
(KOKU-) KOKURITSU SHONI BYOIN INCHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 17; 20pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
ses 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL59038;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1113
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                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Examining allergosis, involves measuring the expression levels of a specific gene, and comparing it to the levels in the eosinophils of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;
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                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 15; DB 1; Length 17; Pred. No. 6.1e+02; 0; Mismatches 0; Indels
        Score 15; DB 1; Length 17;
Pred. No. 6.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human allergic disease related PCR primer SEQ ID NO: 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                     Human; allergosis; eosinophil; PCR; primer; ss.
0.9%; Sco...
100.0%; Pred. No. ...
                                                                                                                                                                                                                                           Nucleotide sequence of PCR primer GT15C.
                                                                                                                                                                                                                                                                                                                                                                                                                                     NKYUSHO KK.
BYOIN INCHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 17; 20pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in the course of the invention
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                                                                                                                                                            ABL59039 standard; DNA; 17 BP.
                                                              1736 AAAAAAAAAAAAA 1750
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Matches 15; Conservative
                                    15, Conservative
                                                                                        16 AAAAAAAAAAAAA
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    Aquery Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   healthy control.
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                                                                                                                                 RESULT 1114
ABL59039/c
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                                      Matches
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ID ABN9
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AC ABN9
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KW Hume
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primer; ss.

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The present invention relates to a method for examining allergic diseases which involves determining the expression level of a gene, having one of the 17 nucleotide sequences shown in ABN9812-ABN99812, in the eosinophils in a patient and comparing the expression level with that in the eosinophils of a healthy individual. The method can be used to examine allergic diseases, particularly atopic dermatitis, and its early diagnosis, which is also applicable in screening candidate compounds for remedies. The present sequence is a PCR primer described in the exemplification of the invention
                                                                                                                                                                                                                                                                     Method for examining allergic diseases by differential display of seventeen genes showing different expression particularly significant increase in eosinophils in patients with mild atopic dermatitis, also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.9%; Score 15; DB 1; Length 17; 100.0%; Pred. No. 6.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human allergic disease related PCR primer SEQ ID NO: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                 Ogawa K, Obayashi M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                    (GENO-) GENOX RES INC.
(NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
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(NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
                                                                                                                                                                                                                                                                                                                                             Example 1; Page 109; 165pp; Japanese.
                                                                                                                                                                                                                                                                                                                 applicable in screening compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pre
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                                                                                                             28-SEP-2001; 2001WO-JP008574.
                                                                                                                                          13-OCT-2000; 2000JP-00314093
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                                                                                                                                                                                                               Sugita Y, Hashida R,
                                                                                                                                                                                                                                          WPI; 2002-372311/40.
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                                                      WO200233069-A1.
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                             Ното варіепв.
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The present invention relates to a method for examining allergic diseases which involves determining the expression level of a gene, having one of the 17 nucleotide sequences shown in ABN99812-ABN99828, in the eosinophils in a patient and comparing the expression level with that in the eosinophils of a healthy individual. The method can be used to examine allergic diseases, particularly atopic dermatitis, and its early diagnosis, which is also applicable in screening candidate compounds for remedies. The present sequence is a PCR primer described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; allergy; B1153; differential expression; antiallergic; asthma; antiasthmatic; antiinflammatory; atopic skin inflammation; PCR; primer;
                                                           Method for examining allergic diseases by differential display of seventeen genes showing different expression particularly significant increase in eosinophils in patients with mild atopic dermatitis, also
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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   Nagasu
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                                                                                                                                                                                                                                                                                                                      Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
   Obayashi M,
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(NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
                                                                                                                                     Example 1; Page 109; 165pp; Japanese.
                                                                                                      applicable in screening compounds
                                                                                                                                                                                                                                                                                           exemplification of the invention
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   Ogawa K,
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Hashida R,
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                               WPI; 2002-372311/40.
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 Sugita Y,
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diseases

Saito H;

Nagasu T,

The present invention relates to a method of examining allergic diseases which comprises comparing the expression level of gene B1153 in allergy patients with the expression level in healthy subjects. The method is useful for the treatment, prevention, diagnosis and study of allergic

3xample 6; Page 81; 102pp; Japanese.

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Matches

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The present invention relates to a method for examining allergic diseases with intersectin 2 gene or a gene with equivalent function of intersectin 2 as an indicator gene, which comprises determining the expression level of the gene in the eosinophils in a patient, and comparing the expression level with that in the eosinophils of a healthy individual. The method is for examining allergic diseases, particularly atoppic dermatitis, which is also applicable in screening candidate compounds for remedies. The present sequence is an anchor primer described in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Method for examining allergic diseases by differential display of intersectin 2 gene showing different expression particularly significant increase in eosinophils in patients.
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                                                                                                                      Allergic disease examination method related anchor primer SEQ ID NO:
                                                                                                                                                         Allergic disease; allergy; antiallergic; intersectin 2; eosinophil; atopic dermatitis; human; PCR; primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Allergic disease; allergy; antiallergic; intersectin 2; eosinophil; atopic dermatitis; human; PCR; primer; ss.
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100.0%; Pred. No. 6.1e+02;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Obayashi M,
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(NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
(EISA ) EISAI CO LTD.
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  BP.
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  AAL47234 standard; DNA; 17
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                                                                                                                                                                                                                         Unidentified
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                                                                                22-AUG-2002
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Takahashi E;
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                                          AAL47234;
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AAL47235/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, allergy, B1153, differential expression, antiallergic, asthma,
antiasthmatic, antiinflammatory, atopic skin inflammation, PCR, primer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Examination of allergic diseases comprises detecting gene B1153 over-expressed in T cells of allergy patients for diagnosis treatment and investigation of atopic skin inflammation and asthma.
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diseases including atopic skin inflammation and asthma. The present sequence is a PCR primer described in the exemplification of the
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                                                                                                                      0.9%; Score 15; DB 1; Length 17;
100.0%; Pred. No. 6.1e+02;
tive 0; Mismatches 0; Indels
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                                                                                  Seguence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
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(NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
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ID AAL49949 standard; DNA; 17
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                      Local Similarity 100.
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WO200233122-A1

RESULT 1119 AAL47234/c

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Saito H;

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The present invention relates to a method for examining allergic diseases with intersectin 2 gane or a gane with equivalent function of intersectin 2 as an indicator gene, which comprises determining the expression level of the gene in the eosinophils in a patient, and comparing the expression level with that in the eosinophils of a healthy individual. The method is for examining allergic diseases, particularly atopic dermatitis, which is also applicable in screening candidate compounds for remedies. The present sequence is an anchor primer described in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Method for examining allergic diseases by differential display of intersectin 2 gene showing different expression particularly significant increase in eosinophils in patients.
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                                                                                                                                                                                                                                                     (GENO-) GENOX RES INC.
(NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
(EISA ) EISAI CO LTD.
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                                                                                                                                                                                    13-OCT-2000; 2000JP-00314093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  rakahashi E;
                                      25-APR-2002.
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ABK18190
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AC ABK18191
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DT 09-APR-2
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KW Human; I
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Gaps

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The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for treating conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma, conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma, culgarist, anglodensis, diabetic retinopathy, macular degeneration, culgarist, anglodibroma of tuberous sclerosis, port whise stains, Sturge (Weber syndrome, Paletra Harding a patient having a condition associated with the level of ERG, syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for creating a patient having a condition associated with the level of ERG, by contacting cells of the patient with (I) under conditions suitable for the treatment. Leukaemia or tumour angiogenesis is treated by administering (I) to the patient in conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or call, by contacting the cell with (I). (I) is useful for cleaving RNA of ERG gene, by contacting (I) with RNA, in the presence of advalent callons such as Masz, 1987, and as diagnostic tool to examine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically targeting genes that share homology with ERG gene or ERG fusion genes. ABK, 7354-ABKZ2719 represent nucleic acide, including antisense and enzymatic nucleic acide molecules which regulate expression of ERG, and enzymatic nucleic acide molecules which regulate expression of ERG, and Novel polynucleotide which down regulates expression of Eta-related gene, useful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome. Gaps Von Carlowitz I, Mcswiggen JA, Mclaughlin F, Randi AM; ö 0.9%; Score 15; DB 1; Length 17; 93.3%; Pred. No. 6.1e+02; 0; Indels Sequence 17 BP; 2 A; 13 C; 1 G; 0 T; 1 U; 0 Other; 1; Mismatches related PCR primers of the invention Claim 4; Page 74; 149pp; English. ABK18189 standard; RNA; 17 BP 271 CTCCAGCCCCACCC 285 1 cuccaeccccaccc 15 (RIBO-) RIBOZYME PHARM INC. Query Match 0.9 Best Local Similarity 93.3 Matches 14; Conservative (GLAX ) GLAXO GROUP LTD. WPI; 2002-082995/11. Jarvis T, ABK18189; RESULT 1122 ABK18189 셤 ò

Human, hammerhead ribozyme; cytostatic; antitumour; antidiabetic; ophthalmological; antiarthritic; antipsoriatic; virucide; oeteopathic; vulnerary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis; tumour angiogenesis; diabetic retinopathy; macular degeneration; neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris; angiofibroma of tuberous sclerosis; port-wine stain; wound healing; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss; Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme; Human ERG hammerhead ribozyme target sequence, Seq ID No 836. 09-APR-2002 (first entry) domo sapiens amberzyme 

WO200188124-A2

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 conditions gelected from cancer, lymphoma, Ewing's sarcoma, melanoma, conditions gelected from cancer, lymphoma, Ewing's sarcoma, melanoma, conditions gelected from cancer, lymphoma, Ewing's sarcoma, melanoma, tumour angiogenesis, diabetic retinopathy, macular degeneration, neovascular glaucoma, myopic degeneration, arthritis, psociasis, verruca vilgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge Weber syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for treating a patient having a condition associated with the level of ERG, by contacting cells of the patient with (I) under conditions suitable for the treatment. The method comprises the use of one or more therapies under conditions suitable for the treatment. Leukaemia or tumour angiogenesis is treated by administering (I) to the patient in conjunction with one or more of other therapies such as radiation or chemotherapy treatment. (I) is useful for reducing ERG activity in a cell, by contacting the cell with (I). (I) is useful for cleaving RNA of ERG Gene, by contacting the cell with (I). (I) is useful for cleaving such cation such as Mg2+. (I) is useful for diagnostic tool to examine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically targeting genes that share homology with ERG gene or ERG fusion genes. ABK17354-ABK22719 represent nucleic acids, including antisense and enzymatic nucleic acide, including antisense and enzymatic nucleic acide, including antisense and enzymatic nucleic acide melecules which regulate expression of ERG, and
                                                                                                                                                                                                                                                                                                                                   relates to a nucleic acid molecule (I) which down regulates
                                                                                                                                                                                                                              Novel polynucleotide which down regulates expression of Ets-related genuseful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
                                                                                                                                                               Jarvis T, Von Carlowitz I, Mcswiggen JA, Mclaughlin F, Randi AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17 BP; 2 A; 13 C; 1 G; 0 T; 1 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        related PCR primers of the invention
                                                                                                                                                                                                                                                                                                  Claim 4; Page 74; 149pp; English.
                                              16-MAY-2001; 2001WO-US015866
                                                                               L6-MAY-2000; 2000US-00572021
                                                                                                             (RIBO-) RIBOZYME PHARM INC. (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                             WPI; 2002-082995/11.
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               22-NOV-2001
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ABV90790;
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0.9%; Score 15; DB 1; Length 17; 33.3%; Pred. No. 6.1e+02;
                              0; Indels
                                                                                                                                                                                                                                                               Human POSHL1 scanning oligonucleotide SEQ ID NO 1505.
                              1; Mismatches
                                                                                                                                                                    ABV90792 standard; DNA; 17 BP
                                                             271 CTCCAGCCCCACCC 285
                 93.3%;
                                                                             CUCCAGCCCCACCCC 16
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   Query Match 0.9
Best Local Similarity 93.3
Matches 14; Conservative
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RESULT 1123

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Human, POSHL 1; SH3 domain, POSH-like signalling protein 1; oncogene, Rho GTPase; signal transduction, gene expression; cancer; vaccine;

gene therapy; transgenic; ss.

Homo sapiens

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The invention relates to an isolated SH3 domain (POSH)-like signalling protein 1 (POSHL1) polypeptide (I), comprising a sequence of 730 amino acids (SI, ABB83999), a sequence having 65% sequence identity to (S1), (S1), having 95% deviations, especially conservative substitutions or a fragment of the sequence comprising at least 8 contiguous amino acids. Human POSHL 1 is a proto-oncogene/oncogene product that functions as an adaptor protein that interacts with Rho family small GTPsases as well as commistream components of the signal transduction pathway. (I) is useful for identifying a specific binding partner. (I) and nucleic acids (II) contexting (I) are useful for diagnosing, monitoring disease and treating caused by altered expression of human POSHL1 including diagnosing and treating cancer, they useful in the development of vaccines and (II) is useful for measuring and for surveying gene expression and creating transgenic non-human animals capable of producing the proteins. The present sequence is that of a scanning oligonucleotide useful in examples of the invention. Note: The present sequence difformation supplied to prime by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL-1, useful for treating disorders associated with decreased expression or activity of human POSHL1.
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Rho GTPase; signal transduction; gene expression; cancer; vaccine;
gene therapy; transgenic; ss.
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100.0%; Pred. No. 6.1e+02;
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Local Similarity 100.0%; Pred. No. 6.1
                                                                                  30-JÄN-2001; 2001WO-US000664.
30-JÄN-2001; 2001WO-US000665.
30-JÄN-2001; 2001WO-US000666.
30-JÄN-2001; 2001WO-US000666.
30-JÄN-2001; 2001WO-US000669.
30-JÄN-2001; 2001WO-US000669.
30-JÄN-2001; 2001WS-US000677.
23-MÄY-2001; 2001US-00864761.
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28-JAN-2002; 2002EP-00001165
                                                           2001WO-US000663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-684061/74.
                                                                                                                                                                                                                                                                                                                                                                                                             (AEOM-) AEOMICA INC.
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                                                           30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shannon M;
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The invention relates to an isolated SH3 domain (POSH)-like signalling protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino acids (SL, ABBA399), a sequence having 65% sequence identity to (Sl), (Sl), having 95% deviations, especially conservative substitutions or a fragment of the sequences comprising at least 8 contiguous amino acids. Human POSHL 11s a proto-oncogene/oncogene product that functions as an adaptor protein that interacts with Rho family small GTPases as well as downstream components of the signal transduction pathway. (I) is useful of cor identifying a specific binding partner. (I) and nucleic acids (II) encoding (I) are useful for diagnoshing, monitoring disease and treating caused by altered expression of human POSHL1 including diagnoshing and treating caused by altered expression of human postluming diagnoshing and treating caused by altered expression of numen constructing microarrays which are useful for measuring and for surveying gene expression and creating transgenic non-human animals capable of producing the proteins. The present sequence is that of a scanning oligonucleotide useful in examples of the invention. Note: The present sequence did not form part of the privant by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL-1, useful for treating disorders associated with decreased expression or activity of human POSHL1.
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                                                                                                                                                                                                   30-JAN-2001; 2001WO-US000665.
30-JAN-2001; 2001WO-US000666.
30-JAN-2001; 2001WO-US000667.
30-JAN-2001; 2001WO-US000669.
30-JAN-2001; 2001WO-US000669.
30-JAN-2001; 2001WO-US000670.
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                                                                                                                               28-JAN-2002; 2002EP-00001165
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                                                                                                                                                                                                                                                                                                                                                                           (AEOM-) AEOMICA INC.
                   Homo sapiens.
                                                                                                                                                                  30-JAN-2001;
                                                      EP1239051-A2
                                                                                         11-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                Shannon M;
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ABV90791/c
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The invention relates to an isolated SH3 domain (POSH)-like signalling protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino acids (SI, ABB83999), a sequence having 65% sequence identity to (SI), (SI) having 95% deviations, especially conservative substitutions or a fragment of the sequences comprising at least 8 contiguous amino acids. Human POSHL 1 is a proto-oncogene/oncogene product that functions as an adaptor protein that interacts with Rho family small GTPases as well as downstream components of the signal transduction pathway. (II) is useful for identifying a specific binding partner. (I) and mucleic acids (II) consedubly altered expression of human POSHL1 including disagnosing and creating caused by altered expression of human POSHL1 including disagnosing and treating caused by altered expression of human POSHL1 including macrating caused by altered expression of human POSHL1 including disagnosing and treating caused by altered expression of human POSHL1 including macrating caused by altered expression and creating trensigenic non-human animals capable of producing the proteins. The present sequence is that of a scanning oligonucleotide useful in examples of the invention. Note: The present sequence did not form part of the privated specification, but is based on sequence information supplied to berwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL-1, useful for treating disorders associated with decreased expression or activity of human POSHL1.
Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene; Rho GTPase; signal transduction; gene expression; cancer; vaccine;
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                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-US0006667.
30-JAN-2001; 2001WO-US000667.
30-JAN-2001; 2001WO-US000668.
30-JAN-2001; 2001WO-US000669.
30-JAN-2001; 2001WO-US006670.
13-JAN-2001; 2001US-01864761.
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                                         gene therapy; transgenic; ss.
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ABK49757/c
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Human POSHL1 scanning oligonucleotide SEQ ID NO 1504.

23-DEC-2002 (first entry)

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Human atopic dermatitis cDNA related PCR primer GT15c.
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                                                                                                                                                                                                                                                                                                    Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
                                                                                                           (GENO-) GENOX RES INC.
(NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL
                                                                                                                                                                                       Example 1; Page 55; 74pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                    ABK49756/c
ID ABK49756 standard; DNA; 17 BP
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                                                                                 21-SEP-2001; 2001WO-JP008247.
                                                                                               26-SEP-2000; 2000JP-00293021
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                                                                                                                                              WPI; 2002-330097/36.
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see 15, Conserv
                                                     WO200226962-A1.
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                                                                   34-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                        Synthetic.
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This invention relates to gene sequences that are differentially expressed in eosinophils from patients with atopic dermatitis in the increment stage as compared with those in the remission stage. These sequences are used in a novel method for examining alergic diseases comprising determining the expression levels of these genes and comparing the expression levels of these genes and comparing individual. The method of the invention may have antiallergic or dermatcological activities. The method can be used to diagnose allergic diseases particularly atopic dermatitis, and may also be used to screen candidate compounds for remedies. The method of the invention can be performed in high throughput, at low cost. The present sequence represents the GTISa PCR primer used to amplify the differentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amplified atopic dermatitis related cDNA sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat; polymorphic marker prediction of ubiquitous simple sequences; POMPOI Rep.X; human; genetic disease; drug-treatment; Machado-Joseph; Haw River syndrome; Huntington's disease; fragile-X syndrome; Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia;
                                                                                                                                                                                                                                                         Examining allergic diseases by differential display of genes show different expression particularly increase in remission stage in eosinophils in patients.
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100.0%; Pred. No. 6.10+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                 Nagasu T,
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spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
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                                                                                                                                                                 Ogawa K, Fujishima T,
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                                                                                             (GENO-) GENOX RES INC.
(NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 54; 74pp; Japanese.
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21-SEP-2001; 2001WO-JP008247.
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                                              26-SEP+2000; 2000JP-00293021
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                                                                                                                                                                 Sugita Y, Hashida R,
                                                                                                                                                                                                                WPI; 2002-330097/36.
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Best Local Similarity
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ID ABX7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to gene sequences that are differentially expressed in eosinophils from patients with atopic dermatitis in the increment stage as compared with those in the remission stage. These sequences are used in a novel method for examining allergic diseases comprising determining the expression levels of these genes and comparing the expression level with that in the eosinophils of a healthy individual. The method of the invention may have antiallergic or dermatcological activities. The method can be used to diagnose allergic diseases particularly atopic dermatitis, and may also be used to screen candidate compounds for remedies. The method of the invention can be performed in high throughput, at low cost. The present sequence represents the GTISC PCR primer used to amplify the differentially amplified atopic dermatitis related CDNA sequences of the invention
                                                                    Atopic dermatitis, ss, differential display, primer, PCR; eosinophil; allergic disease, antiallergic; dermatological; GT15c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Atopic dermatitis, 89, differential display, primer; PCR, eosinophil;
allergic disease; antiallergic; dermatological; GT15a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Examining allergic diseases by differential display of genes showing different expression particularly increase in remission stage in eosinophils in patients.
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100.0%; Pred. No. 6.1e+02;
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WPI; 2003-208818/20

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The invention discloses a method for identifying a candidate polymorphic repeat within a coding sequence (expressed sequence tag, EST), which comprises detecting tandem repeats in a target coding sequence, scoring the repeats for polymorphic probability and generating a dataset correlating the repeats with polymorphic probability to identify a candidate polymorphic repeat. The computational methods (polymorphic candidate polymorphic repeat. The computational methods (polymorphic marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are useful for identifying and detecting candidate polymorphic repeats in human genes, which can be used to understand, treat or eliminate genetic diseases, predispositions or adverse drug-treatment reactions. Examples of diseases linked to nucleotide repeats are Machado-Joseph, Haw River Syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis, myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are the polymorphic repeats identified for a search of human ESTS Identifying a candidate polymorphic repeat within a coding sequence, funderstanding or treating genetic disease, comprises detecting tandem repeats in a target coding sequence and scoring the repeats for Sequence 17 BP; 0 A; 2 C; 0 G; 15 T; 0 U; 0 Other; Example; Col 483; 588pp; English polymorphic probability.

DB 1; Length 17; 6.1e+02; 0; Indels Mismatches Score 15; Pred. No. 100.0%; Pre-Query Match
Best Local Similarity 100.0
Matches 15; Conservative

ADB04274 standard; DNA; 17 BP 20-NOV-2003 (first entry) ADB04274;

Human MDZ7 scanning oligonucleotide SEQ ID 5260.

Cytostatic; immunostimulant; gene therapy; vaccine; human; zinc finger protein; MDZ4; MDZ4; MDZ1; chromosome 7q22.1; chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer; developmental disorder; ss.

Homo sapiens

EP1281758-A2

05-FEB-2003.

30-JUL-2002; 2002EP-00016874.

02-AUG-2001; 2001US-00922181

(AEOM-) AEOMICA INC.

Shannon M, Gu Y, Nguyen C;

WPI; 2003-423107/40.

New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7 or MDZ12, e.g. cancer.

Example 8; SEQ ID NO 5260; 103pp; English.

proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is cancoded at chromosome 7921.1, MD24 is encoded at chromosome 6921.3-22.2, MD24 is encoded at chromosome 6921.3-22.2, MD24. MD27, MD24, MD27, and MD21 sequences are useful in therapy. Or in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MD23, MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic acids and proteins are also useful for diagnosing or monitoring a disease caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic acids can also be used as probes to detect and characterize gross alterations in MD23, MD27, or MD212 genetic locus. The probes are useful in constructing microarrays for measuring agene expression. The proteins are useful as therapeutic agents for gene therapy or as vaccines. The present sequence was used to illustrate the invention. present invention relates to novel human zinc finger-containing

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Sequence 17 BP; 1 A; 0 C; 2 G; 14 T; 0 U; 0 Other;

Gaps ö 0.9%; Score 15; DB 1; Length 17; 100.0%; Pred. No. 6.1e+02; tive 0; Mismatches 0; Indels Best Local Similarity 100. Matches 15, Conservative Query Match

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1735 CAAAAAAAAAAAA 1749 15 CAAAAAAAAAAAA

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ADC84469 standard; DNA; 17 BP. ADC84469; RESULT 1130 ADC84469/

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Gaps ö (first entry) 01-JAN-2004 PCR primer for amplifying plant blastogenesis specific gene #SEQ ID 2.

Plant blastogenesis; transformation; gene expression; tissue specific; PCR; primer; ss

Synthetic.

JP2003159071-A 

03-JUN-2003

22-NOV-2001; 2001JP-00358366.

22-NOV-2001; 2001JP-00358366.

(DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH

WPI; 2003-818678/77.

New naturally derived DNA specifically expressed during blastogenesis of a plant, useful for producing a transformed plant and for compulsive expression of a protein.

Example 3; SEQ ID NO 2; 43pp; Japanese.

The invention relates to naturally derived DNA specifically expressed during plant blastogenesis. The DNA of the invention is useful for producing a transformed plant. Methods of the invention are also useful for compulsive expression of this DNA. Methods of the invention are useful for plant tissue specific expression of genes. Also, the growth stage of a plant can be controlled specifically. The current sequence represents a PCR primer for amplifying a plant blastogenesis specific gene of the invention.

Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

0.9%; Score 15; DB 1; Length 17;

Query Match

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(GENO-) GENOX RES INC.
(NIGE-) JAPAN GEN AGENCY NATION
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                                                                            25-FEB-2003; 2003WO-JP002047.
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                                    WO2003083139-A1.
                Unidentified.
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AAV54175/
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                                                                                                                                                                                                                                                                                                                                                                              New naturally derived DNA specifically expressed during blastogenesis of a plant, useful for producing a transformed plant and for compulsive expression of a protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    during plant blastogenesis. The DNA of the invention is useful for producing a transformed plant. Methods of the invention are also useful for compulsive expression of this DNA. Methods of the invention are useful for plant tissue specific expression of genes. Also, the growth stage of a plant can be controlled specifically. The current sequence represents a PCR primer for amplifying a plant blastogenesis specific gene of the invention.
                                                                                                                                                                        PCR primer for amplifying plant blastogenesis specific gene #SEQ ID 1.
                                                                                                                                                                                              Plant blastogenesis, transformation; gene expression; tissue specific;
                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to naturally derived DNA specifically expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ss; allergic disease; B1799; antiallergic; antiinflammatory; dermatological; gene therapy; atopic dermatitis.
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100.0%; Pred. No. 6.1e+02;
ative 0; Mismatches 0; Indels
               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA oligo (SeqID 5) related to the human B1799 gene.
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     Pred. No. 6.1e+02;
                                                                                                                                                                                                                                                                                                                                      (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH
100.0%; Pred. ...
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                                    1736 AAAAAAAAAAAAA 1750
                                                                                                           ADC84468 standard; DNA; 17 BP
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               15; Conservative
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Best Local Similarity
    Best Local Similarity
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                                                                                                                                ADC84468;
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This invention relates to a novel method for screening and examining allergic diseases by the use of B1799 as the indicator gene. Specifically, it comprises determining the expression level of this indicator gene in a biological sample obtained from the patient, and identifying differential expression (increased expression of B1799) in comparison to that observed in a healthy individual. The present invention describes the B1799 protein as antiallergic, antiliclammatory and dermatological. As such, through the use of gene therapy, this method can be used to treat allergic diseases particularly atopic dermatitis. Furthermore, it is useful for determining a diagnosis that is convenient and non-invasive, and is also applicable in high throughput screening to identify candidate compounds for additional remedies. This oligomucleotide sequence is the DNA oligo (SeqID 5) related to the human B1799 gene of the invention.
                                                                                                                                                      Examining allergic diseases, such as atopic dermatitis, comprises comparing the expression levels of gene B1799 in T cells in a patient and a healthy individual.
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    Saito
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100.0%; Pred. No. 6.1e+02;
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    Sugita Y,
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    Oshida T,
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                                                                                                                                                                                                                                                                                                                         Example 1; SEQ ID NO 5; 87pp; Japanese.
Matsumoto Y, Imai Y, Yoshida N,
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Gaps

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Indels

100.0%; Pred. No. 6.4e+02; tive 0; Mismatches 0;

15; Conservative 1736 AAAAAAAAAAAAA 16 ААААААААААААА

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                                                                                                                                                          This is the nucleotide sequence of a PCR primer used in the method of the invention, involving the use of novel apoptosis-related DNAs and proteins. The inventions can be used as diagnostic reagents for apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent in immunohistological staining, as a spoptosis inhibitors. It can also be used for treatment of apoptosis-related diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is the nucleotide sequence of a PCR primer used in the method of the invention, involving the use of novel apoptosis-related DNAs and proteins. The inventions can be used as diagnostic reagents for apoptosis e.g. (monoclonal) antibodies for the protein, as a reagent in immunohistological staining, as apoptosis inhibitors. It can also be used for treatment of apoptosis-related diseases
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                                                                                    Novel apoptosis-related DNAs and proteins - for diagnosis, preventing treating diseases associated with apoptosis.
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100.0%; Pred. No. 6.4e+02;
ative 0; Mismatches 0; Indels
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                                                                                                                                Example 1; Page 51; 70pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence PCR primer 10.
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(KYOW ) KYOWA HAKKO KOGYO KK.
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                                                                                                                                                                                                                                                                                                                          15; Conservative
                                                          WPI; 1998-495844/42
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV54173;
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0.9%; Score 15; DB 1; Length 18;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypervariable region; ENV protein; vaccinia virus; gag gene; retrovirus; vaccines; infection; protection; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                          Novel apoptosis-related DNAs and proteins - for diagnosis, preventing treating diseases associated with apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                  PCR; primer; amplification; apoptosis; antibody; inhibition; ss; immunohistological staining.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 0.9%; Score 15; DB 1; Length 18; Local Similarity 100.0%; Pred. No. 6.4e+02; les 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 48; 70pp; Japanese.
                                                                                                       Nucleotide sequence PCR primer 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIV-1 gag protein DNA primer #4.
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                                                                                                                                                                                                                                                                                  97JP-00050302.
                                                                                                                                                                                                                                                                                                            (KYOW ) KYOWA HAKKO KOGYO KK.
                       AAV54166 standard; cDNA; 18
                                                                             (first entry)
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                                                                                                                                                                                                  WO9839437-A1
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                                                                             21-DEC-1998
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                                                                                                                                                                         Synthetic
                                                   AAV54166;
                                                                                                                                                                                                                                                                                                                                      Sakaki Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
RESULT 1135
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Gaps

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The invention relates to identification of genes and proteins of adipose tissue relating to obesity, particularly complications of visceral obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the proteins (AAY67598-V67600) are used in the genetic diagnosis, prevention and treatment of adipose tissue related diseases. Sequences AAZ90640-51 represent PCR primers amplifying the human adipose tissue genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue relating to obesity, particularly complications of visceral obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633 and the proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention and treatment of adipose tissue related diseases. Sequences AAZ90640-51 represent PCR primers amplifying the human adipose tissue genes
                                            A physiologically active protein specifically derived from mammal tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A physiologically active protein specifically derived from mammal tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adipose tissue, obesity, diabetes; hyperlipemia, hypertension, human, arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
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100.0%; Pred. No. 6.4e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                         / Match 0.9%; Score 15; DB 1; Length 18;
Local Similarity 100.0%; Pred. No. 6.4e+02;
les 15; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human adipose tissue gene amplifying primer #9
                                                                                          Example 2; Page 18; 50pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Page 18; 50pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ90648 standard; DNA; 18 BP.
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WPI; 2000-306578/27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV35388-V35414 are primers used in a method which results in a recombinant vaccinia virus comprising of a gag gene from a retrovirus such as HIV-1 or HIV-2, fused to a DNA fragment containing an epitope region (30-300 bases in length) of a retroviral gene other than the gag gene may be altered so as to produce a gag protein modified from the natural sequence by the addition, deletion or substitution of at least 1 amino acid residue. The fusion gene is inserted into a recombinant vaccinia virus vector which is used to transform a host cell (such as the La, Vero, VEF, rabbit kidney RK13 or human myeloma TK-143 cells). Upon culturing the host cell produces particulate structures containing the protein page protein. The recombinant varus or the fusion gag protein. The recombinant vaccinia virus or the fusion gag protein. The recombinant vaccinia virus or the fusion gag protein particles may be used in the production of vaccines for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant vaccinia virus containing fusion HIB gag gene -
production in host cells of gag protein for use as vaccine.
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Mismatches 0; Indels
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                                                                                                                                                                                                                                   (NINA-) JAPAN NAT INST INFECTIOUS DISEASES.
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                                                                                                                                                                                    96JP-00323412
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Matches 15; Conservative
                                                                                                                                                                                                                                                           (JAPG ) NIPPON ZEON KK
                                                                                                                                                                                                                                                                                                       Kojima A, Kurata T,
                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-312481/27.
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                                              WO9822596-A1
                                                                                                                                        19-NOV-1997;
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                                                                                          28-MAY-1998
Synthetic.
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Query Match

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RESULT 1137

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The present invention relates to functionalised nanocrystals for use in nonisotopic detection systems for biomolecules e.g. nucleic acids, proteins, lipids or drugs. The nanocrystals have polymucleotide strands attached to their surfaces with one end of the polymucleotide extending outwardly from the nanocrystal. The present sequence is one such nanocrystals, which have polymucleotides complementary to the first polymucleotides, so that the respective complementary to the first polymucleotides, so that the respective complementary strands hybridise to each other and form a dendrimer. This enditimer produces a signal which can then be detected e.g. fluorescence. The present sequence is composed mainly of Adenine bases. This sequence may therefore be used
                                                                                                                                                                                                Functionalized nanocrystal carrying polynucleotide, used for detecting target analyte, forms dendrimers with complementary nanocrystals to amplify the fluorescent signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Functionalized nanocrystal carrying polynucleotide, used for detecting target analyte, forms dendrimers with complementary nanocrystals to amplify the fluorescent signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nanocrystal; biomolecule detection; nonisotopic detection system; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     with a polynucleotide composed mainly of Thymine bases (AAA58386)
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100.0%; Pred. No. 6.4e+02;
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                                                                                                 Castro S;
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                                                                                                                                                                                                                                                                                                    Example 3; Page 68; 72pp; English.
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                                                                                                 Nelson MB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP
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99US-00437076.
99US-00437076
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                                               (BIOC-) BIOCRYSTAL LTD.
                                                                                                                                                WPI; 2000-376593/32
                                                                                                 Barbera-Guillem E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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09-NOV-1999;
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09-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A physiologically active protein specifically derived from mammal tissue.
                                                                                                                                                                                                                                                                                                 Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human; arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 15; DB 1; Length 18;
Pred. No. 6.4e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18 BP; 0 A; 2 C; 1 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                  Human adipose tissue gene amplifying primer #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 18; 50pp; Japanese.
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                                                                                                 В.
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                                                                                                 AAZ90651 standard; DNA; 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA58385 standard; DNA; 18
                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NISB ) JAPAN TOBACCO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
ses 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-306578/27
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                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-NOV-1998;
                                                                                                                                                                                                13-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-2000
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                                                                                                                                              AAZ90651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA58385
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AAA58385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                    AAZ90651/
LD AAZ9
XX AAZ9
XX AAZ9
XX AAZ9
XX Adip
NB Huma
NB Homo
NB H
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Gaps

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0; Indels

us10008789-3.rng

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The present invention relates to functionalised nanocrystals for use in nonisotopic detection systems for biomolecules e.g. nucleic acids, proteins, lipids or drugs. The nanocrystals have polynucleotide strands attached to their surfaces with one end of the polynucleotide extending outwardly from the nanocrystal. The present sequence is one such polynucleotide. These nanocrystals are used with a second series of nanocrystals, which have polynucleotides complementary to the first polynucleotides, so that the respective complementary to the first polynucleotides, so that the respective complementary strands hybridise to each other and form a dendrimer. This dendrimer produces a signal which can then be detected e.g. fluorescence. The present sequence is composed mainly of Thymine bases. This sequence may therefore be used with a polynucleotide composed mainly of Adenine bases (AAAS8385)
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Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 U; 0 Other;

Gaps ö Query Match 0.9%; Score 15; DB 1; Length 18; Best Local Similarity 100.0%; Pred. No. 6.4e+02; Matches 15; Conservative 0; Mismatches 0; Indels

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1736 AAAAAAAAAAAAA 1750 18 АААААААААААА

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025/c AAT06025 standard; cDNA; 20 AAT06025

13-APR-1996 (first entry)

Oligonucleotide based on consensus from saponin glycosyl hydrolase

saponin glycosyl hydrolase, tomatinase, plant pathogenic fungi, avenacinase, deglycosylation, pore formation, cell death, primer, probe, consensus; ss.

Synthetic.

WO9530009-A2

09-NOV-1995

95WO-GB000592 17-MAR-1995; 94GB-00008573 29-APR-1994; (GATS-) GATSBY CHARITABLE FOUND.

Daniels MJ; Bowyer P, Osbourn AE,

WPI; 1995-393080/50.

New isolated saponin glycosyl hydrolase enzymes - used to develop prods. for the modification of microbial organisms and plants or plant prods.

Claim 35; Page 59; 113pp; English

AAT06025-26 are oligonucleotides useful as probes or primers designed from sequences conserved between saponin glycosyl hydrolases, especially avenacinase, tomatinase and ALP's (T06021-24). The enzymes are isolated from plant pathogenic fungi. The enzymes detoxify saponins by deglycosylation, which is sufficient to destroy the ability of the saponin to complex with membrane sterols. Saponin/sterol complexes in eukaryotic membranes results in pore formation and leakage of cell contents, with subsequent cell death. The DNA and proteins of the invention are useful in identification of related enzymes, structural studies of saponins and also for development of agents which can modulate SGH activity, e.g. for reducing pathogenicity of SGH-producing pathogens for specific hosts AATO6025/ NX AATO AXC AATO XX AATO XX AATO XX BADO XX COBS XX Synt XX Synt XX Synt XX Synt XX COBS XX CATO 
Sequence 20 BP; 3 A; 6 C; 5 G; 0 T; 0 U; 6 Other;

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                                                                                                                                                                                                                                                                                              Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; PCR primer; bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ORFS) of the genome of Chiamydia trachomatis (see AAZ01425). These ORPS encode polypeptides (see AAX36754-Y37949) which can be used as vaccines against Chiamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microoraganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal utertitis, epical diseases such as nongonococcal utertitis, epidymitis, cervicitis, salpingitis, perihepatitis, batholinitis; pneumopathy in breast feeding infants; and veneral lymphogranulomatosis. The polypeptides of the invention may be of use in treating these
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR primers AAZ01426-Z06209 were used to amplify open reading frames
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                                                                                                                                                                                                                                                               PCR primer used to amplify an ORF of Chlamydia trachomatis.
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100.0%; Pred. No. 6.9e+02;
ive 0; Mismatches 0; Indels
DB 1; Length 20;
                             1; Indels
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 Score 15; DB 1; I
Pred. No. 6.9e+02;
                              6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome sequence of Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 1464; 1755pp; English.
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100.0%; Fr.
0;
                                                             355 CCGCCGTGGGTGGGGTCCC 373
                                                                                           CCKGMRTGGGTRGCGKMCC 1
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97FR-00016034.
98US-0107077P.
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 0.9%;
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                                                                                                                                                                       AAZ01703 standard; DNA; 20
                                                                                                                                                                                                                                     (first entry)
 Query Match 0.9
Best Local Similarity 63.2
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-371125/31.
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es 15; Conserv
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04-NOV-1998;
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                                                                                                                                                                                                       AAZ01703;
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RESULT 1144

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Gaps

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0.9%; Score 15; DB 1; Length 20; 100.0%; Pred. No. 6.9e+02; ive 0; Mismatches 0; Indels

907 CAGCCTCCAGAGGAT 921

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15 CAGCCTCCAGAGGAT

Local Similarity 100.

Best Loca Matches

Query Match

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Human; epidermal growth factor receptor; hyperproliferative disease,
Herl; antisense; prophylaxis; psoriasis; phosphorothioate backbone;
                                                                                                                                                                                                                                                                    /mod_base= OTHER
/note= "2'methoxyethyl nucleotides"
                                                Human Her-1 antisense oligonucleotide ISIS #128464.
                                                                                                                                                           /mod_base= OTHER
/note= "2'methoxyethyl nucleotides"
                                                                                                                               /mod_base= OTHER
/note= "Phosphorothioate backbone'
                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           Freier SM;
                                                                                                                                                          base= OTHER
                                                                                                                                                                                                                                     _ag= g
/mod_base= m5c
16. .20
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/mod_base= m5c
                                                                                                                                                                                                         mod_base= m5c
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       AAD36602 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                   28-SEP-2001; 2001WO-US030551.
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                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                             (ISIS-) ISIS PHARM INC
                                                                                                                                /mod
                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-394234/42.
                                                                            tumour; cancer; ss.
                                                                                                                                                                                                                                                                                         WO200226758-A1
                                                                                                                  modified_base
                                                                                                                                            modified base
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                                                                                                                                                                                                               modified base
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                                                                                                                                                                                                                                                       modified_base
                                  09-AUG-2002
                                                                                        Homo sapiens
                                                                                               Synthetic
                      AAD36602;
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Molecular beacon; fluorophore; nanoparticle; nucleic acid detection; ss.

Molecular beacon target sequence.

(first entry)

22-JUL-2002

ABL57070

ABL57070 standard; DNA; 20 BP.

1145

**ABL57070** 

Location/Qualifiers

misc\_binding

Synthetic

/\*tag= a //bound moiety= "Molecular beacon" /note= "forms double-stranded region with bases 1-20 of sequence in ABL57069"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of a perfectly matched target sequence for a molecular beacon comprising an oligonucleotide probe (see ABL57069) covalently attached at the 3' end to fluorescent dye and at the 5' end to a nanoparticle. In the native state, the probe forms a hairpin conformation with hybridised termini. The proximity of the fluorophore and quencher (gold nanoparticle) in the molecular beacon results in little or no detectable fluorescence. Upon hybridisation of the central complementary stretch of the probe to a target sequence, such as the present sequence, the hairpin undergoes a conformational change resulting in an increase in fluorescence, the extent of which is proportional to the amount of target sequence present. Single mismatches can be detected. The invention relates generally to the use of metal surface quenchers such as particles or films for high sensitivity applications in, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 BP; 15 A; 3 C; 1 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        detection and diagnostic systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        example,
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The invention relates to an antisense oligonucleotide targetted to a nucleic acid molecule encoding human epidermal growth factor receptor (Herl) to inhibit its expression. The antisense compounds are useful for treating diseases or conditions associated with Her-1 such as hyperproliferative diseases especially cancer (lung, ovarian, colon or prostrate cancer) and psoriasis. They are also useful as research reagents, diagnostics, therapeutics, kits and prophylactically e.g. to prevent or delay tumour formation. The present sequence is an antisense oligonucleotide targetted to human Her-1

Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;

Novel antisense oligonucleotide that specifically hybridizes with and inhibits nucleic acid encoding epidermal growth factor receptor, useful for treating hyperproliferative disease such as cancer or psoriasis.

Claim 1; Page 46; 169pp; English.

Sensitively detecting proximity changes in a system that utilizes an interacting fluorophore and quencher, for high sensitivity applications, involves utilizing a metal surface as quencher.

Example 2; Page 26; 62pp; English.

Libchaber A;

(UYRQ ) UNIV ROCKEFELLER. Dubertret B, Calame M, WPI; 2002-404569/43.

29-AUG-2001; 2001WO-US041941. 29-AUG-2000; 2000US-0228728P. 30-MAR-2001; 2001US-0280350P.

WO200218951-A2.

07-MAR-2002.

Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiaathmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

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New X-chromosome gene expressed in haploid cells of the testis, useful for gene diagnosis, discrimination of sex, separation of sperm, infertility treatment and chromosomal manipulation.
                                                                                                                                                              Mouse; X-chromosome; germ cell less gene; gcl gene; gene diagnosis; sex discrimination; infertility treatment; chromosomal manipulation; sperm separation; gene therapy; PCR; primer; ss.
                                                                                                                                           HT15-C downstream PCR primer used for identification of genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 2 A; 2 C; 1 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                       (LIVE-) LIVESTOCK IMPROVEMENT ASSOC JAPAN INC.
(UYGU-) UNIV GUNMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 4; 28pp; English
                                                                                                                                                                                                                                                                                                                                                           Kondo T;
                                                                          AAD35095 standard; DNA; 20 BP
1736 AAAAAAAAAAAAA 1750
                                                                                                                                                                                                                                                                               02-OCT-2001; 2001EP-00123259.
                                                                                                                                                                                                                                                                                                    03-OCT-2000; 2000JP-00303994
                      15
                                                                                                                      25-JUL-2002 (first entry)
            AAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                           Aizawa A, Kawakami A,
                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-354153/39.
                                                                                                                                                                                                                                  EP1195382-A2
                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                         10-APR-2002
                                                                                                AAD35095
                                                      RESULT 1146
                                                                요
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Pharmaceutical composition for treating ailments associated with impaired

Katz E, Pabalan J, Aguilar D;

Li Y, Sandrasagra A, Ka , Tang L, Shahabuddin S;

Nyce JW, I Miller S,

WPI; 2003-229219/22.

23-APR-2002; 2002WO-US013135. 24-APR-2001; 2001US-0286137P. (EPIG-) EPIGENESIS PHARM INC.

WO200285308-A2

31-OCT-2002.

Homo sapiens

The present invention relates to genes located on the X-chromosome of mammals. These genes are specifically expressed in haploid cells of the testis and encoded amino acid sequences having homology with the amino acid sequences by a descriptions of the invention are used for gene diagnosis, discrimination of sex, sequences especially in livestock. They are also used in gene therapy. The present DNA sequence is a PCR primer which is used for the identification of sex primer which is used for the identification of genes by differential display method

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Gaps
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  Score 15; DB 1; Length 20;
Pred. No. 6.9e+02;
                      0; Indels
                       Mismatches
   100.08; PA
Query Match
Best Local Similarity 100.(
Matches 15; Conservative
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1736 AAAAAAAAAAAAA 1750 AAAAAAAAAAAA S 13

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ABZ87313 standard; DNA; 20 BP
                       ABZ87313;
RESULT 1147
      ABZ87313,
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Human oligonucleotide sequence 17-OCT-2003 (first entry)

Human ICAM oligonucleotide sequence.

(first entry)

17-OCT-2003

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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' or 3' end genomic flanking regions, 5' or 3' end genomic flanking regions, 5' or 2' egions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nacal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention of has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a cuse in antisense gene therapy. The composition may have a cuse in antisense gene therapy. The composition may have a cuse in antisense gene therapy. The composition may have a cuse in antisense gene therapy. The composition may have a cuse in antisense gene therapy. The composition may have a cust in antisense or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing levels of adenosine or receptor, producing bronchodilation, increasing levels of adenosine cut in a subject stissue, or treating bronchodomostriction, unus allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 2555; 872pp; English
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Best Local Similarity
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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5 or 3 end genomic flanking regions, 5 and 3' intron-exon junctions, or regions within 2-10 mucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an entiinflammatory steroid and ubjquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing levels of denosine of the confidence of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lung surfactant in a subject's tissue, or treating bronchoconstriction, ung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO
                              antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antialtasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Katz E, Pabalan J, Aguilar D;
   Human; antisense; lung dysfunction; nasal airway dysfunction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 13777; 872pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li Y, Sandrasagra A, Ke
Tang L, Shahabuddin S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-APR-2001; 2001US-0286137P.
                                                                                                                                                                                                                                                                                                                                                                                                                               23-APR-2002; 2002WO-US013135.
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Miller S,
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ö Gaps ; 0 0.9%; Score 15; DB 1; Length 20; 100.0%; Pred. No. 6.9e+02; iive 0; Mismatches 0; Indels Sequence 20 BP; 4 A; 10 C; 4 G; 2 T; 0 U; 0 Other; CCCACGGAGCAGCAC 271 257 ઠે

cccacedadcadcac 19 ABZ89440 standard; DNA; 20 17-OCT-2003 (first entry) ABZ89440; S RESULT 1149 ABZ89440 ID ABZ8 XX ABZ8 AC ABZ8 XX I7-C XX I7-C XX Hume 셤

Human oligonucleotide sequence.

Human, antisense, lung dysfunction, nasal airway dysfunction, antiinflammatory, antiallergic, antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, cytostatic, gene therapy, antisense gene therapy, respiratory, lung, adenosine sensitivity, adenosine receptor, bronchodilation, bronchoconstriction, lung allergy, lung inflammation; respiratory disease; ds.

Homo sapiens.

WO200285308-A2

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC.

Katz E, Pabalan J, Aguilar D; Li Y, Sandrasagra A, K. Tang L, Shahabuddin S; Miller S, Nyce JW,

WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

Disclosure; SEQ ID NO 4682; 872pp; English.

preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of undiquinted tung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5 or 3 end genemic flanking regions, 5 and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiaschmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a new in antisense gene therapy. The composition is useful for treating or antisense gene therapy. The composition is useful for treating or accounting the composition is useful for treating or accounting the composition is useful. 

Sequence 20 BP; 14 A; 2 C; 2 G; 2 T; 0 U; 0 Other;

Gaps ö 0.9%; Score 15; DB 1; Length 20; 100.0%; Pred. No. 6.9e+02; 0; Indels 100.0%; Prec. ... 15; Conservative Similarity Query Match Local Matches

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1735 CAAAAAAAAAAAA 1749 6 CAAAAAAAAAAAAA

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BP 20 ABZ90649 standard; DNA; 20 (first entry) 17-OCT-2003 ABZ90649; RESULT 1150 ABZ90649

Human oligonucleotide sequence

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The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation coodon, coding region, 5 or 3 and genomic flanking regions, 5 and 3 intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction as pecced active agent comprising an entinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of edenosine receptor, producing bronchodilation, increasing levels of ubiquinone or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pharmaceutical composition for treating ailments associated with impaired
Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodiation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.
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                                                                                                                                                                                                                                                                                                                                                                                                             Katz E,
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Tang L, Shahabuddin S;
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lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed Sequence 20 BP; 14 A; 3 C; 1 G; 2 T; 0 U; 0 Other;

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                 Length 20;
                                              0; Indels
              0.9%; Score 15; DB 1; L
100.0%; Pred. No. 6.9e+02;
ttive 0; Mismatches 0;
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Query Match
Best Local Similarity luv...
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Gaps

CAAAAAAAAAAA 20

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RESULT 1151

Human p53 exon 5 PCR primer 1. ABZ25524 standard; DNA; 20 28-MAR-2003 (first entry) ABZ25524; ABZ25524/c
1D ABZ2555.
X AC ABZ255:
XX DT 28-MAR
X X

ö The invention relates to a novel method for detecting a cell with a neoplastic or pre-neoplastic phenotype, comprising testing a sample cell for the presence of loss of heterozygosity at one or more loci on one or more chromosomes. The chromosomes are selected from a group of chromosome 1-22, where a loss of heterozygosity at one or more of the loci is indicative of a neoplastic or pre-neoplastic phenotype. The method of the invention has cytostatic activity. Detecting a cell with a neoplastic or pre-neoplastic confirmations, monitoring or treating the progression of neoplastic or pre-neoplastic conditions, e.g. PCR; primer, ss; neoplastic; pre-neoplastic; heterozygosity; cytostatic; urothelial neoplasia; p53; human. Detecting a cell with a neoplastic or pre-neoplastic phenotype, useful for diagnosing or treating neoplasia or pre-neoplastic conditions, comprises testing the cell for the presence of loss of heterozygosity at urothelial neoplasia. The present sequence represents a PCR primer used in the invention to amplify exon 5 of the p53 gene Gaps ö Target oligonucleotide #1 used in nonlinear optical technique. 0.9%; Score 15; DB 1; Length 20; 100.0%; Pred. No. 6.9e+02; ive 0; Mismatches 0; Indels Sequence 20 BP; 2 A; 8 C; 2 G; 8 T; 0 U; 0 Other; Nonlinear optical technique; screening; ss Example 6; Page 113; 248pp; English. AAD57844 standard; DNA; 20 BP 11-JUN-2002; 2002WO-US018427. 12-JUN-2001; 2001US-0297813P. 857 CTGCAGGAAGAGAA 871 CTGCAGGAAGAGAA 1 (TEXA ) UNIV TEXAS SYSTEM 20-NOV-2003 (first entry) Query Match 0.9 Best Local Similarity 100. Matches 15; Conservative Johnston D; WPI; 2003-156900/15. one or more loci WO2002100246-A2 Homo sapiens Zzerniak B, 19-DEC-2002 15 AAD57844; RESULT 1152 AAD57844 ઠે g

2001US-0306040P. 2001US-0347821P. 2002US-0354668P. 17-JUL-2002; 2002WO-US022681 WO2003064991-A2 17-JUL-2001; 23-OCT-2001; 206-FEB-2002; 2 Jnidentified 07-AUG-2003. 

(SALA/) SALAFSKY J

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The present invention relates to a method for detecting interactions between biological components using a nonlinear optical technique. The invention is used for screening candidate binding partner(s) for binding to test molecule. It can also be used to detect changes in orientation or conformation of the probe and/or target. The present sequence is a target oligonucleotide used in nonlinear optical technique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequences given in AAQ73325-81 represent oligonucleotides which hybridise specifically with DNA or RNA from a herpes virus gene corresponding to one of the open reading frames U15, -8, -9, -20, -27, 29, -30, -42, -52 or IE175 of herpes simplex virus type I (HSV-1). These oligos pref. hybridise with a translation initiation site, a coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New oligonucleotide(s) hybridising with DNA or RNA of herpesvirus gene are used in the treatment and diagnosis of herpes simplex virus, cytomegalovirus, Epstein Barr virus and varicella zoster infections.
                                                                                                                                                                                         Screening candidate binding partner(s) for binding to test molecule by applying external force field to sample in homogeneous phase, alluminating sample with light beam(s) at fundamental frequencies, and measuring physical properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hybridise; herpes simplex virus; HSV; open reading frame; translation initiation site; coding region; 5' UTR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 20;
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100.0%; Pred. No. 6.9e+02;
iive 0; Mismatches 0;
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Brown-Driver VL, Wyatt JR;
                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 20B; 146pp; English.
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1es 15, Conservative
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                                                                                                                               WPI; 2003-646172/61
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Anderson KP,
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02-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New modified oligo-nucleotide contg guanine quartet - inhibits activity of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
                  infection,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Inhibition; replication; herpes simplex virus; HSV; HIV; retard; human cytomegalovirus; influenza virus; influenza virus; influenze length; neurological disorders; phospholipase Activity; hyperproliferation; malignancy; cardiovascular disease; snake bite; malignancy; aging; ss.
region or a 5' untranslated region. These oligos may be used in compositions for the treatment and diagnosis of herpes viral infectic by contacting the virus or the animal, or its cells, tissues or body fluids with the oligo. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brown-Driver VL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Phosphorothionate intersugar linkages"
                                                                                                             Score 14.8; DB 1; Length 18;
Pred. No. 6.8e+02;
0; Mismatches 2; Indels
                                                                               Sequence 18 BP; 0 A; 0 C; 12 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bennett CF, Chiang M,
att JR, Imbach JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 18 BP; 0 A; 0 C; 12 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                       Guanine quartet containing oligomer, #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 105; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wyatt JR,
                                                                                                                                                                              1019 TTGGGGATGGGGCTGGGG 1036
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                                                                                                                                                                                                                                                                                           BP
                                                                                                             0.8%;
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                                                                                                                                                                                                                                                                                          AAQ61992 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                       (revised)
(first entry)
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J, Vickers TA, W
                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1994-135613/16.
                                                                                                               Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of chromosomes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
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04-NOV-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                         AAQ61992;
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Gaps

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DB 1; Length 18;

0.8%; Score 14.8;

Query Match

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AAQ61913 standard; DNA; 18 BP

RESULT 1156

AAQ61913

(revised)
(first entry)

25-MAR-2003 04-NOV-1994

AAQ61913

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequences given in AAQ61825-50 and AAQ61886-906 are oligonucleotides which contain a G4 or two G3 stretches and which may be used for inhibiting replication of herpes simplex virus (HSV). Oligonucleotides such as these may also be used for inhibiting activity of HIV, human cytomegalovirus or influenza virus, or for treating inflammatory and neurological disorders caused by phospholipase A2 activity in cases of hyperproliferation, malignancy, cardiovascular disease and snake bite. They may also be used for inhibiting division of malignant cells by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modualting telomere length, which may also retard aging. (Updated on 25-
MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                           Inhibition; replication; herpes simplex virus; HSV; HIV; human cytomegalovirus; influenza virus; influenzameation; neurological disorders; phospholipase A2 activity; hyperproliferation; malignancy; cardiovascular disease; snake bite; malignancy;
                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chiang M, Brown-Driver VL;
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/note= "Phosphorothionate intersugar linkages"
88.9%; Pred. No. 6.8e+02;
iive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18 BP; 0 A; 0 C; 12 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                            HSV replication inhibiting oligomer, ISIS no 5653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 14.8; DB 1;
Pred. No. 6.8e+02;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bennett CF, Chian
att JR, Imbach JL;
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                                                                                                                                                                                                                                                                                                                                           malignancy; cardiovascular disease;
telomere length; retard; aging; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; Page 19; 144pp; English.
                                              1019 TTGGGGATGGGGCTGGGG 1036
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                                                                                                                                                     AAQ61897 standard; DNA; 18
                                                                                                                                                                                                                  (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anderson KP,
                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vickers TA,
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Best Local Similarity
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04-NOV-1994
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                16;
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                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
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                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New modified oligo-nucleotide contg guanine quartet - inhibits activity of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
                                                                                                                                 human cytomegalovirus; influenza virus; inflammation;
neurological disorders; phospholipase A2 activity; hyperproliferation;
malignancy; cardiovascular disease; snake bite; malignancy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brown-Driver VL;
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                                                                                                                                                                                                                                                                           /*tag= a
/note= "Phosphorothionate intersugar linkages"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                    Inhibition; replication; herpes simplex virus; HSV; HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18 BP; 0 A; 0 C; 12 G; 6 T; 0 U; 0 Other;
                                                                                      HIV replication inhibiting oligomer, ISIS no 5666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 14.8; DB 1;
Pred. No. 6.8e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anderson KP, Bennett CF, Chiang Vickers TA, Wyatt JR, Imbach JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 23; 144pp; English.
                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                 celomere length; retard; aging; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1019 TTGGGGATGGGGCTGGGG 1036
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ses 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1994-135613/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of viruses, e.g of chromosomes.
                                                                                                                                                                                                                                                            misc feature
                                                                                                                                                                                                                                                                                                                         WO9408053-A1
                                                                                                                                                                                                                                                                                                                                                                                    29-SEP-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RC,
                                                                                                                                                                                                                                                                                                                                                        14-APR-1994
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                                                                                                                                                                                                                Synthetic
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Gaps

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2; Indels

1019 TTGGGGATGGGGCTGGGG 1036

Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative (

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DB 1; Length 18;

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WPI; 1995-082179/11
                                                    29-JUL-1993;
                       misc_feature
                                          WO9504068-A1
                                                 28-JUL-1994;
   25-MAR-2003
19-OCT-1995
                                             09-FEB-1995,
                  Synthetic.
                                                            Ecker DJ;
AAQ97983;
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Vascular endothelial growth factor receptor; VBGF receptor; flt-1; flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage; tumour angiogenessis; psoriasis; rheumatoid arthritis; ocular disease; fms-like tyrosine kinase 1; kinase insert domain containing receptor; foetal liver kinase 1; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (VGGF). A parient (preferably human) having a condition associated with the level of the fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient. AAX67275 to AAX75752 represent specific examples of nucleic acid molecules from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes nucleic acid molecules which modulate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.8%; Score 14.8; DB 1; Length 18; 88.9%; Pred. No. 6.8e+02; .ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                     Human flt1 VEGF receptor hairpin ribozyme substrate #61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escobedo J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 BP; 5 A; 9 C; 2 G; 0 T; 2 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stinchcomb D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 94; 218pp; English.
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                                                         ВР.
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96US-00584040.
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                                                         AAX70293 standard; RNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ25595 standard; DNA; 18
                                                                                                                                                                  (first entry)
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Best Local Similarity 88.9
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-OCT-1995;
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                                                                                                                                                                  28-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1997.
                                                                                                               AAX70293;
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     RESULT 1158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New peptide nucleic acid (PNA) oligomers are provided which (a) consist of naturally occurring nucleobases covalently bound to a polyamide backbone and (b) hybridise to the translation initiation AUG region, 5' untranslated region (5' UTR), 3' untranslated region (3' UTR), splice intranslated region (5' UTR), splice junctions or coding sequence of a human immunodeficiency virus gene consent from env, gag, pol, rev and tar. The PNAs can be used to trarget RNA and single stranded DNA (ssDNA) to produce antiseise-type gene regulation moieties. They have utility as gene-targetted drugs for modulating HIV processes. Hence they can be used to treat AIDS and other viral infections. They are also useful in diagnostic applications and as stranded DNA. They are also bable to form triple helices in which a first PNA strand binds with RNA or sbDNA and a second PNA strand binds with the first PNA strand binds with the significant charge and are water soluble, which facilitates callular uptake. Further, since they contain amides of non-biological amino acids, they are biostable and resistant to enzymatic degradation by proteases.

The present sequence is a specifically claimed PNA sequence (represented by the sequence of nucleobases) targetting HIV genes. (Updated on 25-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                               /*tag= a hotology at least one (and preferably all) of the backbone subunits are composed of N-acetyl N-(2-aminoethyl)glycine peptide residues, the mucleobase being attached covalently to the acetyl group and the peptide linkage being formed by condensation of the glycine carboxy group of one residue with the amino group of the 2-aminoethyl moiety in the next residue."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligomer hybridisable to HIV sequence and contg. peptide nucleic acid sub:unit - binds in complementary manner to DNA and RNA, and useful for modulating HIV viral activity, e.g. in treating AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                   Peptide nucleic acid; PNA; HIV; human immunodeficiency virus; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 14.8; DB 1; Length 18;
Pred. No. 6.8e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18 BP; 0 A; 0 C; 12 G; 6 T; 0 U; 0 Other;
                                                                             Peptide nucleic acid oligomer targetting HIV gene.
                                                                                                                                                               antiviral; antisense; triple helix; ss
                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 176; 186pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1019 TTGGGGATGGGGCTGGGG 1036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94WO-US008517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93US-00099718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.8%;
88.9%;
(revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16; Conservative
                                                                                                                                                                                                                                                                                                        1. .18
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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Gaps ö

Human RhoG antisense phosphorothioate oligonucleotide #36.

TIGGGGTIGGGGTIGGGG 18

Matches

8 셤

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AAZ25553 to AAZ25582 represent specifically claimed antisense
oligonucleotides targeted to, and capable of inhibiting the expression of
nucleic acids encoding human RhoG. RhoG is a member of the Rho subfamily
of small GTPases the expression of which is associated with the induction
of mitosis by mitogens. RhoG is thought to be required for entry into the
coff mitosis by mitogens. RhoG is thought to be required for entry into the
coff mitosis by mitogens. RhoG is thought to be required for entry into the
coff mitosis and the actin cytoskeleton which regulates changes during
cell cycle progression (e.g. cell cycle. It also effects the dynamic
cell cycle progression (e.g. cell counding and pinching off during
mitosis) and with determining the density to which cells will proliferate
(RhoG affects an actin-dependent signal transduction pathway mediating
the level of contact inhibition through surface signals). Additionally,
RhoG is associated with the development of cancers (RhoG participates in
ca signalling pathway involving ras-mediated transformation). Antisense
compounds from the present invention may be used for inhibiting the
expression of human RhoG in cells and tissues in vitro and may be used
diagnostically to determine the role of RhoG in various biochemical
cycoskeleron and in cancer development). AAZ25590 to AAZ2559 represent
concernment when RhoG antisense oligonuclectides, but they do not inhibit RhoG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
          Human; RhoG; inhibition; antisense; phosphorothioate; expression; GTPase; mitosis; mitogen; DNA synthesis; cell cycle; cancer; dynamic organisation; actin cytoskeleton; ras-mediated transformation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antisense oligonucleotides useful for inhibiting the expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.8%; Score 14.8; DB 1; Length 18; 88.9%; Pred. No. 6.8e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                     /*tag= a
/note= "phosphorothioate linkages"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as strongly as the specifically claimed sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18 BP; 5 A; 5 C; 6 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 15; Col 27; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1507 CCGCTGGATGGGCACATC 1524
                                                                                                                                                                                                                                                                                                                                                         98US-00161015
                                                                                                                                                                                                                                                                                                                                                                                                98US-00161015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ52631 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-579906/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human RhoG gene
                                                                              diagnosis; ss
                                                                                                                                                                              Key
modified_base
                                                                                                                                                                                                                                                                                                                                                           25-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                25-SEP-1998;
                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                               US5965370-A
                                                                                                                                                                                                                                                                                                                    12-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cowsert LM;
                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ52631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ52631/C
ID AAZ526
XX
AC AAZ526
XX
DT 29-FEB
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polynucleotides obtained from adult testes, foetal brain, adult brain, brain (foetal and adult), foetal kidney, adult spleen, and adult thymus brain (foetal and adult), foetal kidney, adult spleen, and adult thymus convail in the stress. The polynucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Suggested activities include nutritional activity, yerokine and cell proliferation/differential activity, yerokine and cell proliferation/differential activity, hamone stimulating (e.g. as vaccines) or suppressing activity, haematopoiesis regulating activity, tissue growth activity, and tunnour inhibition activity, The polynucleotides ignaphressor activity, and tunnour inhibition activity. The polynucleotides are also presently valuable for yeterinary applications. AAZSSSSS compositions are also presently valuable for veterinary applications. AAZSSSS compositions are also present human secreted proteins, and AAYY3300 to AAXSSSSS concepted proteins, and AAYY3300 to AAXSSSSS concepted proteins, given in the present invention.

AAZSSSSS concepted proteins given in the present invention.

AAZSSSSS concepted proteins given in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polynucleotides and proteins having biological activities which make them suitable for treating, preventing or ameliorating medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                              Human, secreted protein; immunostimulatory; haemostatic; cytokine; proliferative; differentiative; chemotactic; chemokinetic; vaccine; thrombolytic; antiinflammatory; cytostatic; immunosuppressive; gene therapy; hybridisation; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes human secreted proteins encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 14.8; DB 1; Length 18; Pred. No. 6.8e+02;
Human secreted protein clone yk261_1 probe SEQ ID NO:264.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18 BP; 1 A; 11 C; 1 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wong GG, Clark HF, Fechtel K, Agostino MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 729; 730pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conditions in humans or animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             879
                                                                                                                                                                                                                                                                                      98US-0095472P.
98US-0096824P.
98US-0099843P.
                                                                                                                                                                                                                                                                                                                                                              98US-0100424P.
98US-0102329P.
98US-0103615P.
                                                                                                                                                                                                                                                      99WO-US010843.
                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0111799P.
98US-0112159P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0114415P
99US-00248059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-00287150
99US-00311021
                                                                                                                                                                                                                                                                                                                                           98US-0099950P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             862 GGAAGAGGAAGAGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 GGAGGTGGAAGAGGAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-053095/04
                                                                                                                                             Homo sapiens
                                                                                                                                                                                 409958642-A2
                                                                                                                                                                                                                                                                                                                                                                                 29-SEP-1998;
09-OCT-1998;
11-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                     14-DEC-1998;
31-DEC-1998;
10-FEB-1999;
                                                                                                                                                                                                                                                      14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-MAY-1999;
                                                                                                                                                                                                                                                                                                                                             11-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                15-SEP-1998
                                                                                                                                                                                                                  18-NOV-1999
                                                                                                                                                                                                                                                                                                                            11-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-APR-1999
                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Location/Qualifiers

Synthetic

8. .9 /\*tag= a /label= RNA

misc\_RNA

WO200206531-A2

24-JAN-2002

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This invention relates to an antisense compound targeted to a nucleic acid molecule encoding a member of the human Rho family of small GTP binding pycteins, where the antisense compound inhibits the expression of the member of the human Rho family. The invention includes antisense oligonucleotides AAF94580 - AAF94637 which target a RhoA nucleotide sequence, AAF94645 - AAF94684 which target a RhoA nucleotide sequence, AAF946575 - AAF94686 - AAF94758 which target a RhoC nucleotide sequence, AAF947090 which target a Rac 1 nucleotide sequence and AAF94795 - AAF94809 which target a Rac 1 nucleotide sequence and AAF94795 - AAF94809 which target bycerpiclecative conditions, especially cancer, abnormal wound healing or clotting conditions and ischemia/reperfusion or recoxygenation injury. The compound may also be used to diagnose the above conditions
                                                                                                                                                                                           Rho; GTP binding protein; phosphorothioate antisense oligonucleotide;
RhoA; RhoB; RhoC; RhoG; Rac 1; cdc42; hyperproliferative condition;
cancer; wound healing; clotting; ischaemia; reperfusion; reoxygenation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An antisense compound targeted to a nucleic acid molecule encoding a member of the human Rho family of small GTP binding proteins useful for
                                                                                                                                                         Rho G antisense phosphorothioate oligonucleotide SEQ ID 169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 0.8%; Score 14.8; DB 1; Length 18; Local Similarity 88.9%; Pred. No. 6.8e+02; les 16; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18 BP; 5 A; 5 C; 6 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 18; Page 81; 156pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treating e.g. cancer and ischemia.
                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                18-AUG-2000; 2000WO-US022808
                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-00387341
                                      AAF94745 standard; DNA; 18
                                                                                                                23-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roberts ML, Cowsert LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-191677/19.
                                                                                                                                                                                                                                                                                                                                  WO200115739-A1.
                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                           08-MAR-2001.
                                                                             AAF94745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
RESULT 1161
                      AAF94745
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Probes for detecting target nucleotide sequence in sample, has sequence that forms hairpin structure having a double-stranded segment and singlestranded loop collectively forming region complementary to target

Example 4; Page 49; 72pp; English.

seguence

(GENE-) APPLIED GENE TECHNOLOGIES INC.

WPI; 2002-171819/22.

Dattagupta N;

14-JUL-2000; 2000US-00616761. 30-MAR-2001; 2001US-00823647.

12-JUL-2001; 2001WO-US022166

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The present sequence is that of DNA-RNA-DNA hybrid oligonucleotide
AGT02013. This is one of a set of oligonucleotides (see ABA91527-30) used
to assess the minimum number of ribonucleotides in DNA-RNA chimeric
coligonuclectides required for RNase H cleavage. Each oligonucleotide of
the set had a different number of ribonucleotides, 2 in the present case.
The oligonucleotides were mixed with target DNA oligonucleotide AGT02009
(see ABA91531) and incubated with RNase H (5 U/ml) at 37 degrees C for 30
minutes. The results showed that 4 ribonucleotides were the minimum
number for RNA cleavage. The invention provides probes for nucleic acid
hybridisation. The probes form a hairphin structure comprising a double-
stranded stem and a single-stranded loop, and are capable of both
intramolecular and intermolecular hybridisation. The double-stranded stem
may comprise a methylphosphonate DNA:RNA hybrid that is resistant to
RNASE H cleavage. When the probe hybridises with a target DNA, the RNA
strand in the DNA:RNA duplex becomes sensitive to RNAse H treatment and
can be removed. Arrays and methods for nucleic acid hybridisation using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; colon cancer; tumour; abnormal cell growth; melanoma;
cervical cancer; colorectal adenocarcinoma; Wilms' tumour; leukaemia;
lymphoma; antisense therapy; CATX; probe; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.8%; Score 14.8; DB 1; Length 18; 88.9%; Pred. No. 6.8e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Colon cancer associated cDNA CATX-8, 5' PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18 BP; 2 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1736 AAAAAAAAAAAAAA 1753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK27450 standard; DNA; 18 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the probes are provided
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1163
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Gaps

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1507 CCGCTGGATGGGCACATC 1524

à 셤

Matches

1 CAGCAGGATGGGCACATC 18

ABA91529 standard; DNA; 18

RESULT 1162

ABA91529

ABA915297 ID ABA9 XX XX ABA9 XX DT 23-A XX XX XX XX DNA-

23-APR-2002 (first entry)

DNA-RNA-DNA oligonucleotide AGT02013 used to test RNase H cleavage.

DNA-RNA hybrid; RNase H; nucleic acid detection; ss.

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Shimizu T, Nakayama I, Nagayama K, Fukuda A, Tanaka Y, Kaku K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid (I) involved in growth regulation in human colonic epithelial cells, termed CATX. (I) is useful as a probe/primer for detecting tumours, preferably colon cancer. The nucleic acid, encoded polypeptide and antibody are useful in diagnosis and treatment of abnormal cell growth (such as cervical and anomas). Colorectal adenocarcinomas, Wilms' tumour, leukaemias and prymphomas), in screening assays for the treatment of abnormal cell growth, for raising antibodies, and to screen for peptide analogues and antagonists. (I) is useful as a biomarker for human tumour cells, e.g., colon cancer cells, for generating probes and primers designed for identifying and/or cloning homologues in other cell types, in antisense therapy, and in tissue profiling. (I) identifies cancer cells at an early stage of development, so that premalignant cells can be identified prior to their spreading throughout the human body. (I) allows early detection of potentially cancerous conditions, and treatment of the cancerous conditions prior to spread of the cancer cells throughout the body, or prior to development of an irreversible cancerous condition. ABK27456.

ABK27465 represent human colon cancer associated coding sequences and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                   New isolated nucleic acid involved in growth regulation in human colonic epithelial cells, termed CATX, for diagnosing and treating abnormal cell growth, and for use as a probe/primer for detecting tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.8%; Score 14.8; DB 1; Length 18; Best Local Similarity 88.9%; Pred. No. 6.8e+02; Matches 16; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human chromosome 1p36-35 PCR primer SEQ ID NO:507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18 BP; 6 A; 1 C; 8 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                       Sxample; Page 91; 130pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1617 CTCAGTTCCAGTTCCCAT 1634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCAGTTCCATTCCCCAT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-MAR-2001; 2001JP-00068285.
                                                                          38-AUG-2000; 2000WO-US021606
                                                                                                  99US-0147933P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL43463 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-APR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   primers of the invention
                                                                                                                                                                             WPI; 2002-121548/16.
                                                                                                                                                   Wang K;
                                                                                                                          (FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR primer; 88.
                       WO200111047-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JP2001321190-A
 Homo sapiens.
                                                                                                  09-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-NOV-2001
                                                 15-FEB-2001
                                                                                                                                                   Bowman BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL43463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL43463
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The present invention describes a method of arraying genome clones. The method comprises: (a) clones of the genomic libraries contained in method comprises: (a) clones of the genomic libraries contained in comprises numbered for discrimination are mixed in each of the multiwell plates numbered for discrimination are mixed from the areaction; (c) a signal corresponding to the marker is detected from the resultant amplified product to specify the discrimination Nos. of the multiwell complified product to specify the discrimination Nos. of the multiwell plates containing the clones having said marker sequence; (d) the order of the maximum in the specified discrimination Nos. to array the multiwell completes; (e) the clones in the multiwell plates of the specified discrimination Nos. are mixed respectively in each wells of longitudinal and lateral directions; (f) the mixed lones are cultured and the constituted are specified from the detected result; and (i) the clones are reconstituted as the positions on the chromosome and arrayed. The microarray is useful for gene analysis. ABL42357 to ABL45322 represent per primers for human chromosome and ABL45322 represent propresent PCR primers for human chromosome 21q22.1, which are specifically claimed for use in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rice, Oryza sativa var. Kinmaze, acetolactic acid synthase, enzyn
herbicide resistance, pyrimidinylcarboxy-based herbicide, plant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 14.8; DB 1; Length 18;
Pred. No. 6.8e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rice acetolactic acid synthase PCR primer SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18 BP; 3 A; 4 C; 7 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NAAG-) NAT INST AGROBIOLOGICAL SCI.
                                                                                                                                                                                                                                                                                                 Claim 4; Page 14; 528pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18
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10-MAR-2000; 2000JP-00066716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-NOV-2001; 2001WO-JP010014.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-NOV-2000; 2000JP-00362630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 683 CACAGCCAGTGAGGGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CACAGCTTGTGAGGGGCT
                                                           (RIKA ) RIKAGAKU KENKYUSHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16; Conservative
                                                                                                                                                                                                                                  Arraying genome clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                   WPI; 2002-144136/19
                                                                                                 (GENO-) GENOTEX YG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VO200244385-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza Bativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABN89400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABN89400/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Gape

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Sequence 18 BP; 5 A; 9 C; 0 G; 4 T; 0 U; 0 Other;
                                         Example 6; Page 32; 96pp; Japanese.
                                                                                                                                                                                                              Human microsatellite repeat M2_3_4.
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                                                                                                                                                                                                                                                                                                                                                                          Example 2; Page 5; 20pp; English.
                                                                                                                                  1010 AAGATGTGGTTGGGGATG 1027
                                                                                                                                                                                                                                                                                                                           Matsuzaka
                                                                                                                                              18 AAGAGGTGGTTGGTGATG 1
                                                                                                                                                                             BP
                                                                                                                                                                                                                                                                                      06-DEC-2002; 2002US-00314405.
                                                                                                                                                                                                                                                                                                  15-NOV-2000; 2000US-00713616
                                                                                                                                                                           ADA27360 standard; DNA; 18
                                                                                                                                                                                                   20-NOV-2003 (first entry)
                                                                                                                Local Similarity 88.9
hes 16; Conservative
      WPI; 2002-490301/52
                                                                                                                                                                                                                                                                                                                         Inoko H, Tamiya G,
                                                                                                                                                                                                                                                                                                                                      WPI; 2003-616782/58
                                                                                                                                                                                                                                                                                                              (INOK/) INOKO H.
                                                                                                                                                                                                                                                              US2003108940-A1
                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                          12-JUN-2003.
                                                                                                           Query Match
                                                                                                                                                                                        ADA27360
                                                                                                                                                                RESULT 1166
                                                                                                                      Matches
                                                                                                                                                                      ADA27360
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synthase (ALS) gene encoding ALS resistant to pyrimidinyl carboxy herbicides. Plants which may be transformed with the mutant gene include rice, and also maize, barley, wheat, soya, cotton and tobacco. The mutant gene may be useful in the production of herbicide-resistant plants which can be cultivated in the presence of the herbicide. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rice acetolactate synthase related oligonucleotide ALS-Rsp6 SEQ ID NO:13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genes of rice origin encoding pyrimidinyl carboxy herbicide resistant acetolactate synthase for production of herbicide resistant strains or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88; rice; acetolactate synthase; ALS; pyrimidinyl carboxy herbicide;
herbicide-resistance; herbicide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to novel mutant forms of the rice acetolactate
       present sequence represents the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.8%; Score 14.8; DB 1; Length 18; Best Local Similarity 88.9%; Pred. No. 6.8e+02; Matches 16; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                      2; Indels
                                                                                                                               0.8%; Score 14.8; DB 1; Length
88.9%; Pred. No. 6.8e+02;
iive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fukuda A,
                                                                                Sequence 18 BP; 7 A; 0 C; 11 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence 18 BP; 5 A; 9 C; 0 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaku K, Shimizu T, Kawai K, Nagayama K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; SEQ ID NO 13; 96pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TSUB ) KUMIAI CHEM IND CO LTD.
(NAAG-) NAT INST AGROBIOLOGICAL SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1010 AAGATGTGGTTGGGGATG 1027
                                                                                                                                                                                                                                  863 GAAGAGGAAGAGGCG 880
                                                                                                                                                                                                                                                                                   18
                                                                                                                                                                                                                                                                                                                                                                                                           ADD42032 standard; DNA; 18 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
disequilibrium studies. The p
microsatellite repeat M2_3_4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-FEB-2003; 2003WO-JP001917.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAR-2002; 2002JP-00095721.
                                                                                                                                                                                                                                                                                 1 GAGGAGGAAGAGGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGAGGTGGTTGGTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA82914 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                         Local Similarity 88.9
1es 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rice and other plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-902935/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003083118-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADD42032;
                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18
                                                                                                                                                                                                                                                                                                                                                         RESULT 1167
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ID AAA8
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                                                                                                                                                                                                                                                                                                                                                                                                             8x88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                     The present invention describes acetolactic acid synthase (I) isolated from Oryza sativa var. Kinmaze (rice). (I) has resistance against pyrimidinylcarboxy (PC)-based herbicides as well as acetolactic acid synthase activity. (I) can be used for providing plants with high resistance against PC-based herbicides. The present sequence represents a PCR primer for (I) which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an oligonuclectide primer capable of specifically hybridising to a DNA having the sequence of the flanking regions of a microsatellite selected from M2-4-9, M2-2-9, M2-2-12, M2-3-11, M2-2-20, M2-2-21, M2-2-23, M2-2-24, M2-4-25, M2-4-36, M2-2-39, M2-2-32, M2-2-32, M2-3-32, M2-3-32, M2-3-36, M2-2-46. The primer is useful for determining the number of repeat units of the microsatellite cited above. The primer is useful in HLA-related research, such as genetic mapping of HLA class II-associated diseases, transplantation matching, population genetics, and diseases, transplantation hot spots as well as linkage
                                                                           Gene encoding acetolactic acid synthase, useful in providing new breeds of plannts with high resistance against pyrimidinylcarboxy-based herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New oligonucleotide primer capable of specifically hybridizing to a DNA having the sequence of the flanking regions of a microsatellite (e.g. M249), useful for HLA-related research, e.g. transplantation matching.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ds; HLA-related research; HLA class II-associated disease; transplantation matching; recombination hot spot identification; linkage disequilibrium study; human; microsatellite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.8%; Score 14.8; DB 1; Length 18; 88.9%; Pred. No. 6.8e+02; iive 0; Mismatches 2; Indels
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Tanaka Y;

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Gaps

AAA82914;

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Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme; recognition site; target; ribozyme binding site; eye disease; vulnerary; proliferative disease; skin disease; psoriasis; diabetic retinopathy; cytokine; inflammartion; cell-cycle dependent kinase; cyclin; MMP; antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide; antisickling; ophthalmological; keratolytic; gene therapy; viral wart; atopic dermatitis; actinic keratosis; squamous cell carcinoms; seborrheic wart; vitreoretinopathy; scar; sickle cell retinopathy; ss.
                                                                                                                                                                                                                      Diagnosing patients predisposed to autoimmune disease, lipopolysaccharide -induced shock or inflammatory conditions.
                                                                                                                                                                                                                                                                                                                             A method has been developed for identifying an individual predisposed to autoimmune disease, a condition mediate by tumour necrosis factor (TNF) autoimmune disease, a condition or an inflammatory condition or infection. The method comprises detecting a mutated CD7 gene, which causes a predisposition, in a DNA-containing sample from the individual. The method is used to identify or treat a patient predisposed to or suffering from an autoimmune disease, especially rhemmatoid arthritis, a condition mediated by TNF-alpha or IFN-gamma, particularly lipopolysaccharide-induced shock, an inflammatory condition or an infection, and asthma. The present sequence represents a PCR primer used in the construction of a probe for detecting a disrupted mouse CD7 gene fragment in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell-cycle dependent kinase cdk4 ribozyme binding site SEQ ID NO:500.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.8%; Score 14.8; DB 1; Length 19;
18.9%; Pred. No. 7e+02;
ve 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19 BP; 4 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                            Example 1; Page 16; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1576 ACCACTGACTGCTGAGTC 1593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AGCACTGCCTGCTGAGTC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAHS8076 standard; DNA; 19 BP.
99WO-US013210.
                                                                                                                                   Lee D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-OCT-2000; 2000WO-US029500
                                          98US-0088800P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16; Conservative
                                                                                                                                   Haynes BF, Patel DD,
                                                                                                                                                                              WPI; 2000-116595/10.
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                                                                                       UYDU-) UNIV DUKE.
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  10-JUN-1999;
                                            10-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse, CD7; autoimmune disease; lipopolysaccharide induced shock; asthma; infection; tumour necrosis factor alpha; TNF-alpha; IFN-gamma; interferon gamma; septic shock; inflammation; immunosuppressant; antirheumatic; antiarthritic; antiinflammatory; vasotropic; antiarthratis; PCR primer ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1. Representative examples of ribozyme recognition sites are given in AAA81415 to AAA86777. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in
                                                                                                                                   Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1, PCNA and Cyclin B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse CD7 gene fragment detection probe construction PCR primer #2
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88.9%; Pred. No. 7e+02;
tive 0; Mismatches 2; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19 BP; 3 A; 5 C; 8 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Robbins JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 53; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tritz R, Welch PJ, Barber JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              905 GCCAGCCTCCAGAGGATG 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTGCCTCCAGAGGATG 19
                                                                                       cdk4 ribozyme binding site #95
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                                                                                                                                                                                                                                                                                                                 99WO-US028772.
                                                                                                                                                                                                                                                                                                                                                              98US-0110954P.
                                          (first entry)
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Best Local Similarity 88.9
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                           (IMMU-) IMMUSOL INC
                                                                                                                                                                                                                          WO200032765-A2.
                                                                                                                                                                                                                                                                                                                 06-DEC-1999;
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                                          04-DEC-2000
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Synthetic.

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AAZ57557;

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Gaps

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Query Match
                                                   RESULT 1171
                                          Matches
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WPI; 2002-479562/51. RESULT 1172 ADE36879 g δ The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a ribozyme (1) which cleaves RNA encoding a cytckine involved in inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle dependent kinase, growth factor or a reductase, or administering a nucleic acid molecule (II) comprising a promoter operably linked to a nucleic acid segment encoding (1). (1) can have antipsoriatic, and emacological, cytostatic, antiseborrheic, antidiabetic, antisickling, ophthalmological, cytostatic, antiseborrheic, antidiabetic, antisickling, cleaves RNA encoding cytokine involved in inflammation. (1) can be used in gene therapy. (I) and (II) are useful for treating proliferative skin diseases such as psoriasis, atopic dermatitis, actinic keratosis, also be used for treating proliferative eye diseases such as diabetic retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of prematurity and retinal detachment, and for treating and preventing carring such as keloid, adhesion and hypertrophic or hypertrophic burn scar. AAH57877 to AAH62099 sepresent sequences used in the companion of the present invention ö Treating proliferative skin or eye diseases and scarring, using ribozymes that cleave RNA encoding cytokines involved in inflammation, matrix metalloproteinases, growth factors and cell-cycle dependent kinases. Gaps Human; 88; antisense; inhibitor of apoptosis; HIAPI; HIAP2; XIAP; cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP; pancreatic cancer; embryonic development; viral pathogenesis; autoimmune disorder; neurodegenerative disease; multiple sclerosis; lupus erythematosus; herpes virus infection; pox virus infection; adenovirus infection; proliferative disease. Human inhibitor of apoptosis, XIAP, antisense oligonucleotide #2. .; 0 0.8%; Score 14.8; DB 1; Length 19; 18.9%; Pred. No. 7e+02; ve 0; Mismatches 2; Indels Sequence 19 BP; 3 A; 5 C; 8 G; 3 T; 0 U; 0 Other; Example 1; Page 108; 408pp; English. 905 GCCAGCCTCCAGAGGATG 922 (UYOT-) UNIV OTTAWA. (AEGE-) AEGERA THERAPEUTICS INC 2 GGCTGCCTCCAGAGGATG 19 27-SEP-2001; 2001WO-CA001379. 28-SEP-2000; 2000US-00672717. 88.98; ABK93655 standard; DNA; 19 26-AUG-2002 (first entry) Local Similarity 88.9 nes 16; Conservative Robbins JM, Tritz R; WPI; 2001-300427/31 WO200226968-A2 Homo sapiens 04-APR-2002 ABK93655; 

Young S;

Holcik M,

Lacasse E, Baird S,

Korneluk RG,

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The invention relates to an inhibitor of apoptosis (IAP) antisense

nucleic acid (I) that inhibite IAP biological activity, regardless of
length of the antisense nucleic acid, the IAP proteins may be mouse or
thuman XIAP, HIAPI or HIAP2. Also included are a pharmaceutical
composition comprising a mammalian IAP antisense molecule and a method of
composition comprising a mammalian IAP antisense molecule and a method of
enhancing apoptosis in a cell, comprising administering a negative
cregulator of the IAP anti-apoptotic pathway to the cell. The IAP
antisense inhibitor is useful for enhancing apoptosis in a cell in a
mammal diagnosed with a proliferative disease. The method is useful for
treating a patient diagnosed with a proliferative disease like cancer.
The IAP antisense molecule is useful to treat, ameliorate, improve,
sustain or prevent proliferative diseases (e.g. ovarian cancer,
adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
conditions where apoptosis is involved or implicated (e.g. embryonic
development, viral pathogenesis, lupus erythematosus and infection by herpes
virus, pox virus and adenovirus). The present sequence is an IAP
Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing apoptosis in a cell, for treating cancer and other proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rhesus rotavirus; RRV; rhesus:human reassortant virus; virucide; antidiarrhoeic; gene therapy; vaccine; immune response; human rotavirus; diarrhoeal gastroenteritis; reverse-transcription; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid molecule comprising a gene segment from a rhesus rotavirus or from one of 3 rhesus:human reassortant viruses, useful for eliciting protective immune responses to human rotaviruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhesus rotavirus (RRV) reverse transcription PCR primer SEQ ID NO:145.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.8%; Score 14.8; DB 1; Length 19; 88.9%; Pred. No. 7e+02; tive 0; Mismatches 2; Indel8
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em SA, Zamb TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19 BP; 4 A; 3 C; 8 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antisense molecule of the invention
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Rappaport RS, 'Sidhu MS, Udem SA,
                                                                                                   Claim 8; Page 32; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   900 CCTGAGCCAGCCTCCAGA 917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADE36879 standard; DNA; 19
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Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhesus rotavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003072716-A2
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                                                        diseases
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comprising a gene segment from a rhesus rotavirus (RRW) or from one of the three rhesus human reassorant viruses. Also described: (1) a vector comprising (1); (2) a recombinant bost cell comprising the vector; and (3) a method of producing a polypeptide encoded by (1), comprising culturing the recombinant host cell under conditions suitable for expression of the nucleic acid molecule. (1) has virucide and antidarkhoeic activities, and can be used in gene therapy and vaccines. The nucleic acid (1), or its variant, can be used in eliciting protective immune responses to human rotaviruses, which are major causes of diarrhoeal gastroenteritie in infants and young children. The present sequence represents a reverse transcription PCR primer which is used in
                                                                              The present invention describes an isolated nucleic acid molecule (I),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 19 BP; 6 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
                          2; SEQ ID NO 145; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                    an example from the present invention.
                             Example
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0.8%; Score 14.8; DB 1; Length 19; 88.9%; Pred. No. 7e+02; tive 0; Mismatches 2; Indels 1678 GICACCAAAIGCIGICIT 1695 Grcacaaaargcrgrcar 18 16; Conservative Local Similarity Query Match Matches 셤 ò

ВP. ABK32799 standard; DNA; 15 ABK32799; RESULT 1173 ABK32799

Human APPBP1 gene, allele-specific oligonucleotide #29. 23-APR-2002 (first entry) Нощо варіепв 

Human, amyloid beta precursor protein binding protein 1, APPBP1; probe, Alzheimer's disease, transgenic animal; platelet aggregation; single nucleotide polymorphism; SNP; allele-specific oligonucleotide; ss.

WO200202820-A1.

10-JAN-2002

30-JUN-2000; 2000US-0215511P

32-JUL-2001; 2001WO-US020951.

(GENA-) GENAISSANCE PHARM INC.

Sausker EA; Choi JY, Kazemi A, Koshy B, Chew A, Anastasio AE, Stephens CJ;

WPI; 2002-164539/21.

Amyloid beta precursor protein binding protein 159 kD (APPBP1) gene polymorphic variants, useful e.g. in studying the expression and function of APPBP1 and screening candidate drugs for treating Alzheimer's disease.

Claim 17; Page 13; 104pp; English.

The invention relates to an isolated polypeptide comprising a sequence beta precursor protein to a reference sequence for the amyloid beta precursor protein binding protein 1, 59kD (APPBPI) protein or its fragment. The polymorphic variants are useful in studying the expression and function of APPBPI, in expressing APPBPI protein for use in screening for candidate drugs to treat diseases related to APPBPI activity, in studying the effect of the variation on the biological activity of APPBPI, and the binding affinity of candidate drugs targeting APPBPI for

methods are useful in validating APPRP1 as a candidate target for treating a specific condition or disease predicted to be associated with APPBP1 activity, or in the design of clinical trials of candidate drugs for treating a specific condition or disease associated with APPBP1 activity. The transgenic animals are useful for studying expression of the APPBP1 isogenes in vivo, for in vivo screening and testing of drugs targeted against APPBP1 protein, and for testing the efficacy of therspeutic agents and compounds for disorders related to platelet aggregation in a biological system. ABK32771-ABK32327 represent human invention 88888888888888

Sequence 15 BP; 13 A; 1 C; 0 G; 0 T; 0 U; 1 Other;

Gape . 0 0.8%; Score 14.6; DB 1; Length 15; 93.3%; Pred. No. 6.3e+02; tive 1; Mismatches 0; Indels 14; Conservative Local Similarity Query Match Matches

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Gaps

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AAV08586 standard; DNA; 16 AAV08586;

BP.

15-FEB-1999 (first entry)

Primer ACE/118FT for human ACE gene.

PCR primer; human; ACB; angiotensin converting enzyme; angiotensinogen; cardiovascular status; AGT; ATI; type 1 angiotensin II receptor; stroke; polymorphic pattern; blood pressure; electrocardiographic profile; cardiac condition diagnosis; myocardial infarction; atherosclerosis; hypertension; cardiovascular disease; ss.

Homo sapiens. Synthetic

WO9845477-A2

15-OCT-1998.

98WO-IB000475. 01-APR-1998;

97US-0042930P 04-APR-1997;

(EURO-) EURONA MEDICAL AB.

Norberg LT, Andersson MK, Lindstroem PHR;

WPI; 1998-568361/48

Assessing cardiovascular status in humans by polymorphic analysis - of genes for angiotensin converting enzyme, angiotensinogen and angiotensin II receptor, used to diagnose predisposition to disease and to predict effect of therapy.

Example 1; Page 27; 71pp; English

This sequence represents a PCR primer for the human ACE (angiotensin converting enzyme) gene, and can be used in the method of the invention. The method is for assessing cardiovascular status in humans by determining the sequence of at least one polymorphic site in the ACE (angiotensin converting enzyme), AGT (angiotensinogen) and/or ATI (type 1 angiotensin II receptor) genes, and comparing the polymorphic pattern with that in patients with predetermined markers of status. The method is used to assess blood pressure or electrocardiographic profile, to diagnose a cardiac condition such as (silent) myocardial infarction (MI), 

RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

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RT-PCR primer of the invention SEQ

Synthetic.

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(first entry)

11-MAY-1999

AAX18368;

AAX18368 standard; DNA; 16 BP.

RESULT 1176 AAX18368/c

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This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-dalta-N3'; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, dalta = V or N; V = adenine, gamma e thymine; N = adenine, guanine, cytosine or thymine; gamma = thymine; k = natural number of 3 or over indicating the repetition of gamma; in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene
                 response to treatments with ACB inhibitors, angiotensin II receptor antagonists, divetics, alpha- or beta-adensers/or receptor antagonists, etc. It is also used to identify susceptibility to cardiovascular disease. Libraries of nucleic acids containing polymorphic positions in the 3 genes, and libraries of targets corresponding to the peptides from the genes are used to screen for cardiovascular agents. The nucleic acids contained in the library can be is used as source of probes
 They can also be used to predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptides having at least two new nucleotides - useful as primers in RT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                             0.8%; Score 14.4; DB 1; Length 16; 93.8%; Pred. No. 7e+02;
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                                                                                                                                                                       Sequence 16 BP; 1 A; 8 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                     0; Mismatches
hypertension, atherosclerosis or stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RT-PCR primer of the invention SEQ ID 1.
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                                                                                                                                                                                                                                                                                         1385 AGCCAGGTCAGGAGGA 1400
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                                                                                                                                                                                                                                                                                                                            16 AGCCAGGTCAGGGGGA 1
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                                                                                                                                                                                                                                                   15, Conservative
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This sequence represents a primer of the invention. The invention relates to sequences of at least two nuclectides of formula: (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma) K-delta-N3'; where X = a labelled compound and/or a nuclectide with voluntary sequence; m = 0 or 1; alpha = thywine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, quanine or cytosine; N = adenine, quanine, cytosine or thymine; gamma = thymine; k = thymine expressed by gamma is composed of repetition of gamma, in which thymine expressed by gamma is composed of 1;3 or less of adenine, quanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene
                                                                                                                                                                                                                                                                                                                                                    Peptides having at least two new nucleotides - useful as primers in RT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA sequence determination; gene sequence analysis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.8%; Score 14.4; DB 1; Length 16; 93.8%; Pred. No. 7e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16 BP; 1 A; 0 C; 1 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RT-PCR primer of the invention SEQ ID 4.
                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 10; 19pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1735 CAAAAAAAAAAAA 1750
                                                                                                                                                                                                                                                                97JP-00208312.
                                                                                                                                                                                                                                   97JP-00208312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX18363 standard; DNA; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 93.8
les 15, Conservative
                                                                                                                                                                                                                                                                                            (TAKI ) TAKARA SHUZO
                                                                                                                                                                                                                                                                                                                         WPI; 1999-183822/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RT-PCR primer;
                                                                                                                                                                                                                                                                18-JUL-1997;
                                                                                                                                                                        JP11032765-A.
                                                                                                                                                                                                                                   .8-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JP11032765-A.
                                                                                                                                                                                                       09-FEB-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sednences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Gaps

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1; Indels

Score 14.4; DB 1; Pred. No. 7e+02; 0; Mismatches 1;

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15; Conservative

Matches

Local Similarity

Query Match Best Local S

0.84;

1735 CAAAAAAAAAAAAA 1750

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16 CGAAAAAAAAAAAA 1

Length 16;

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This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)*, delta-N3'; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, gamaine or cytosine; N = adenine, guanine, cytosine or thymine; samma = thymine; a natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene
                                                                                                                                                                   Peptides having at least two new nucleotides - useful as primers in RT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human angiotensin-converting enzyme (ACE) PCR primer, SEQ ID NO:12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polymorphic marker; cardiovascular disease; myocardial infarction; unstable angina; hypertension; atherosclerosis; stroke; prognosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assessing cardiovascular status in humans involves comparing test polymorphic pattern comprising polymorphic positions within genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     drug screening; treatment outcome; human; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jonsson L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Angiotensin-converting enzyme gene; ACE; polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16 BP; 0 A; 1 C; 0 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

0.8%; Score 14.4; DB 1
Best Local Similarity 93.8%; Pred. No. 7e+02;
Matches 15; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Norberg LT, Andersson MK, Lindstrom PHR,
                                                                                                                                                                                                                    Disclosure; Page 10; 19pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1734 ACAAAAAAAAAAAA 1749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1212/c
AAA38212 standard; DNA; 16 BP.
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                                 97JP-00208312
                                                                 97JP-00208312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 AGAAAAAAAAAAA 1
                                                                                                (TAKI ) TAKARA SHUZO CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EURO-) EURONA MEDICAL AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-318010/27.
                                                                                                                                  WPI; 1999-183822/16.
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14-OCT-1998;
                                                                 18-JUL-1997;
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09-FEB-1999
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The invention relates to a novel method of assessing the cardiovascular status in an individual and to newly identified polymorphisms in the genes encoding amplotensin-converting enzyme (ACE), angiotensin II receptor type 1 (ATI) and type 2 (ATI), angiotensinogen (AGI), renin, andotensinogen (AGI), renin, caceptor type 1 (ATI) and type 2 (ATI), angiotensinogen (AGI), renin, caceptor type 1 (ATI) and type 2 (ATI), angiotensinogen (AGI), renin, caceptor type 1 and beta-adensergic andotensinogen (AGI), renin, caceptor type A and beta-adensergic caceptor type A and comparing the setplement at the method comprises determining the sequence at one or more polymorphic positions within these genes, and comparing the predetermined cardiovascular disease status. The polymorphic markers are useful for determining the predisposition of an individual to cardiovascular disease status of a patient given a predicting the likely cardiovascular status of a patient given a predicting the likely cardiovascular status of a patient given a predicting the likely cardiovascular status of a patient given a predicting the likely cardiovascular status of a patient given a predicting the likely cardiovascular status of a patient given a predicting the likely cardiovascular status of a patient given and prodes for factorising administration of cardiovascular drugs (e.g., ACE inhibitors), beta-adrenergic receptor antagonists (beta and prodes for detecting genetic polymorphic site may be used as privates and probes for detecting genetic polymorphic site may be used as privates and probes for detecting genetic polymorphisms or in molecular chyquents of the genes comprising a polymorphic gates and the proteins comparation of the reading of patients from clinical trials who are predicted to be noncreated with a sub-population of the treatment group betained for use in the appropriate population, partial and error in adverse response, to a particular calmined patient propulation of the treatment group patients are given be approved for use in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ACE, AGT and AT1 genes polymorphisms PCR primer SEQ ID NO: 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, genetic polymorphism, disease diagnosis, treatment; cancer,
cardiovascular system, nervous system, glaucoma, PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
encoding specific proteins, with reference polymorphic pattern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.8%; Score 14.4; DB 1; Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16 BP; 1 A; 8 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                               Example 1; Page 48; 126pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1385 AGCCAGGTCAGGAGGA 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC61212 standard; DNA; 16 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.8%;
Best Local Similarity 93.8%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 AGCCAGGTCAGGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence determination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MO200056922-A2.
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23-MAR-2000; 2000WO-GB001102.

Gaps

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(UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
                                                                                                                                                                                                                                                                                                  97US-00943162
97US-0108152P
                           (GEMI-) GEMINI GENOMICS AB.
                                                                                                                                                                                                    AAD44143 standard; DNA; 16
                                                                                                                                                                                                                       13-DEC-2002 (first entry)
                                                                                                                                                                                                                                                                                                                          Broaddus W,
                                              WPI; 2000-638268/61.
                                                                                                                                                                                                                                                                                                                                   WPI; 2002-412824/44.
                                                                                                                                                      Local Similarity
                                     Lindstrom PHR,
                                                                                                                                                                                                                                                            Unidentified
     23-MAR-1999;
23-MAR-1999;
                   23-DEC-1999;
                                                                                                                                                                                                                                                                                         30-SEP-1998;
                                                                                                                                                                                                                                                                                                  03-OCT-1997;
                                                                                                                                                                                                                                                                                                       03-OCT-1997;
             24-MAR-1999;
                                                                                                                                                                                                                                                                      US6277571-B1
                                                                                                                                                                                                                                                                                                                         Fillmore H,
                                                                                                                                                                                                                                                                               21-AUG-2001
                                                                                                                                                                                                                                                    primer; ss.
                                                                                                                                                                                                              AAD44143;
                                                                                                                                                 Query Match
                                                                      regime.
                                                                                                                                                          Matches
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The present invention describes nucleic acids (A) that interact stably with a target sequence and contain at least one phosphoro(di)thicate link, having endouclease activity. (A), and more generally any catalytic nucleic acid (A') that modulates expression of the cestrogen receptor gene, are used to treat cancer (particularly of breast or endometrium), in vivo or by transforming cells ex vivo and implanting treated cells, or for other conditions associated with levels of cestrogen receptor. Because of the high selectivity for targeted RNA, (A) can also be used to correlate inhibition of gene expression with alterations in phenotype, particularly for identification of therapeutic targets, and as research reagents (for RNA, in the same way that restriction endonucleases are
                                                                                        The invention relates to a method of sequential consensus region-directed amplification for sorting a mixture of DNAs into 2 or more subsets or distinguishing gene expression patterns in 2 samples. The methods, kits and oligonucleotides are useful for sorting a mixture of DNAs into 2 or more subsets or distinguishing gene expression patterns in 2 samples e.g. for disease disgnosis and gene expression patterns in 2 samples e.g. for disease diagnosis and gene analysis. The present sequence is oligo dT PCR primer used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acids that interact, and optionally cleave, target sequences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage; hammerhead trbozyme; bhairpin ribozyme; antisense oligonucleotide; gene expression modification; cancer; phosphorothioate; endonuclease; anticancer; breast cancer; endometrium cancer; ss.
                                                                                                                                                                                                                                                                                                                        0.8%; Score 14.4; DB 1; Length 16; 93.8%; Pred. No. 7e+02; ive 0; Mismatches 1; Indels
samples, useful for disease diagnosis and gene analysis.
                                                                                                                                                                                                                                                                                                                                                                          1; Indels
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Haeberli P;
                                                                                                                                                                                                                                                                               Sequence 16 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thompson JD, Beigelman L, Mcswiggen JA, Reynolds M, Zwick M, Jarvis T, Woolf T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 77; Page 80; 148pp; English.
                                             Example; Fig 1C; 19pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                     1736 AAAAAAAAAAAAA 1751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US008547.
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98US-00103636.
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AAA25458 standard; DNA; 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                          15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       used to treat cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-013248/01.
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reynolds M, Zwic
Matulic-Adamic J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9954459-A2
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Matches
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                                                                                                                                                                                                                                                                        Assessing disease status in individual by determining sequence(s) at one or more polymorphic positions within the human genes encoding the protein(s) involved in physiological pathway associated with treatment
                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention is related to methods for determining the polymorphic pattern of an individual and using the results to determine their risk of a number of diseases, including cancer, cardiovascular diseases, glaucoma and nervous system disorders such as depression and neurodegenerative diseases. In addition, the methods can be used to determine the effects of different types of treatment for individuals, and thus enables appropriate therapies to be prescribed. The PCR primers shown in sequences AAGGI101-C61371 were all used to demonstrate the methods of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequential consensus region-directed amplification; gene expression; disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligo-dT PCR primer #3 used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                      Sanders R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 16;
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                                                                                                                                                                                    Olaisson E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16 BP; 1 A; 8 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 14.4; DB 1
Pred. No. 7e+02;
0; Mismatches
                                                                                                                                                                                      Jonsson L,
                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 55; 141pp; English.
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                   99US-0126046P.
99WO-IB000497.
99US-0126243P.
99US-00471890.
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                                                                                                                                                                                 Norberg LT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 AGCCAGGTCAGGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15; Conservative
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Bellon L;

Sequential consensus region-directed amplification for sorting mixture of DNAs into 2 or more subsets or distinguishing gene expression patterns in

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Gillies

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Human; 88; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; D20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNAzyme; inozyme; G-oleaver; amberzyme; zinzyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; Parkinson's disease; ataxia; Huntington's disease; creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
used with DNA). The combination of modifications in (A) improves resistance to nucleases, binding affinity and/or activity. AAA23503 to AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their corresponding target sequences. AAA25993 to AAA26105 represent their corresponding target sequences. sequences, and AAA26107 to AAA26218 represent their corresponding target sequences. AAA26419 to AAA26711 represent other ribozyme sequences and antisense oligonucleotides used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury.
                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                              0.8%; Score 14.4; DB 1; Length 17; 93.8%; Pred. No. 7.3e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                             Seguence 17 BP; 2 A; 1 C; 1 G; 13 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 30; Page 155; 200pp; English
                                                                                                                                                                                                                                                                                                              1729 AGTTTACAAAAAAA 1744
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28-FEB-2000; 2000US-0185516P.
06-MAR-2000; 2000US-0187128P.
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(BLAT/) BLATT L.
(MCSW/) MCSWIGGEN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                               ABK03501 standard; RNA; 17
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                                                                                                                                                                                                                                                  Best Local Similarity 93.8 Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human CD20 Zinzyme #52
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                                                                                                                                                           invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABK03501;
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                                                                                                                                                                                                                                  Query Match
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The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NGGO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a nucleic acids may be enzymatic nucleic acid cleaving a an RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) proposessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) proposessing an NCH motif). The CD20-targetting nucleic acid is used to cleave RNA with a YGY motif). The CD20-targetting nucleic acid as used to cleave RNA cc C CD20 in the presence of a divalent cation that is preferably Mg^27+.

Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targetting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, leukaemia, HIV (human immunodeficiency virus) associated NHL, lymphocytic loukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell lymphoma (MLL), immunocycoma (IMC), small B-cell lymphocytic lymphoma, immune thrombocytopaenia, and inflammatory arthropathy. The NOGO crasence of a divalent cation that is preferably Mg^2+ Furthermore, the nucleic acid may be contacted with a cell lymphomy and cell may be contacted with a cell act of one or more contacted may be contacted with a cell contact NOGO. The treatment may further compation that is preferably Mg^2+ Furthermore, the nucleic acid may be contacted with a cell contact NOGO-targetting nucleic acid may be contacted with a cell contact a patient having a condition associated with the level of the contact central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke). Alzheimer's disease, muscul
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The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NGO). The nucleic acids and the control of a neurite growth inhibitor gene (NGO). The nucleic acids and the control of a nucleic acids (e.g. a ribozyme or a DNazyme) an Inozyme (an andolytic nucleic acid cleaving a an RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NCH motif), a G-cleaver (cleaving RNA with a NCH motif), a G-cleaver (cleaving RNA with a YCY motif). The CD20-targetting nucleic acid is used to cleave RNA with a YCY motif). The CD20-targetting nucleic acid is used to cleave RNA of CC of CD20. The treatment may further comprise the use of one or more corrected with a YCY motification of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targetting nucleic acid may be used to treat lymphoma, leukaemia, B-call lymphoma, low-grade or follicular non-cleakaemia, HLV (human immunodeficiency virus) associated WHL, mantle-cell lymphoma (MCL), immunocytoma (MCL), small B-call lymphocytic lymphoma, cleaved with a cell to reduce NOGO gene in the presence of a divalent cation that is preferably Mg^2 t. Furthermore, the creatment may further comprise the use of one or more cell and treat a patient having a condition associated with the level of the cell and treat a patient having a condition associated with the level of the treatment may further comprise the use of one or more cell and treat a patient having a condition associated with the level of the treatment may further comprise the use of one or more cell and treat a patient having a condition associated with the level of therapies. In particular, the NGGO-argetting nucleic acid may be used to treat central nervous system (NS) injury and celebrovaried (CVA, stroke), Alzheimer's disease, dementherapy-induced neuropathy, amyotrophic lateral sclenal energence of states which response to the respect o
                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
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                                                                                                                                                                                                                                                                                   Chowrira BM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             central nervous system injury.
                                               11-FEB-2000; 2000US-0181797P.
28-FEB-2000; 2000US-0185516P.
06-MAR-2000; 2000US-0187128P.
  09-FEB-2001; 2001WO-US004273
                                                                                                                                                       RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                   Blatt L, Mcswiggen J,
                                                                                                                                                                                                                              (CHOW/) CHOWRIRA B M.
                                                                                                                                                                                 (BLAT/) BLATT L.
(MCSW/) MCSWIGGEN J.
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Gaps . 0 0.8%; Score 14.4; DB 1; Length 17; 33.8%; Pred. No. 7.3e+02; ve 0; Mismatches 1; Indels Sequence 17 BP; 7 A; 0 C; 10 G; 0 T; 0 U; 0 Other; 93.8%; Local Similarity 93.8 nes 15; Conservative Matches

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861 AGGAAGAGGAAGAGGA 876 

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ABN07886 standard; DNA; 17 ABN07886; RESULT 1184
ABN07886
ID ABN07886
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AC ABN07886
AC ABN07886
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DT 29-MAY-2
XX

29-MAY-2002 (first entry)

Human, genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss. Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7878. 2000US-0234687P. 2000US-0236359P. 2000GB-00024263. 2001WO-US000663. 2001WO-US000663. 2001WO-US000664. 2001WO-US000665. 2001WO-US000666. 2001WO-US000668 2001WO-US000669 25-MAY-2001; 2001WO-US016981 2001WO-US000661 2001WO-US000667 2001WO-US000670 05-FEB-2001; 2001US-0266860P WO200192524-A2 30-JAN-2001; 30-JAN-2001; 30-JAN-2001; 30-JAN-2001; Homo sapiens 30-JAN-2001; 30-JAN-2001; 06-DEC-2001 

Shannon ME Chen W, Rank DR, Hanzel DK, Gu Y, Ji Y, Penn SG,

WPI; 2002-179446/23.

(AEOM-) AEOMICA INC.

New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.

Disclosure; SEQ ID NO 7878; 214pp; English.

The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunospens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as the rapeutic supplement in parients having specific deficiency in hGDMLP-1 capture probes for surface-enhanced having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production and in vaccines or for replacement therapy. The concentration and skeletal muscle disorders hGDMLP-1 is localised to chromosome 22.

The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence data for this patent did not form part of the printed concentration. The sequence capture patent of the printed concentration and selection in the exemplification of the present invention. N. B. specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequence

Sequence 17 BP; 2 A; 3 C; 9 G; 3 T; 0 U; 0 Other;

Gaps ö Query Match 0.8%; Score 14.4; DB 1; Length 17; Best Local Similarity 93.8%; Pred. No. 7.3e+02; Matches 15; Conservative 0; Mismatches 1; Indels

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834 GGAAGCTGCTGGGGTC 849

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1 GGGAGCTGCTGGGGTC 16

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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 can be used as probes to detect, characterise and quantify nucleic acids in samples, as amplification substrates, to hGDMLP-1 nucleic acids in samples, as amplification substrates, to protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specific blomolecule capture probes for surface-enhanced laser desorption ionisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production disorders hGDMLP-1 may be used for disorders associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence in the exemplification of the present invention. N.B. The present for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         recognize hGDMLP-1 proteins,
                                                                                                                                                                           Human, genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
skeletal muscle disorder; amplicon; screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptide, for raising antibodies that recognize hGDMLP-1 prote or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
                                                                                                                                             Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7877.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 7877; 214pp; English.
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                                 ABN07885 standard; DNA; 17 BP
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2001WO-US000664.
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2001WO-US000669.
2001WO-US000669.
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2001WO-US000662
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                                                                                                         (first entry)
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30-JAN-2001;
30-JAN-2001;
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                                                                     ABN07885;
RESULT 1185
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The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for treating conditions selected from cancer, lymphoma, Ewing's sarcoma, metanoma, tumour angiogenesis, diabetic retinopathy, macular degeneration, conditions alected from cancer, lymphoma, Ewing's sarcoma, metanoma, wypic degeneration, arthritis, psoriasis, verruca ungaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge weber syndrome, Rippel-Trenaunay-Weber syndrome, Osler-Weber-rendu syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for treating a patient having a condition associated with the level of ERG, by contexting calls of the patient with (I) under conditions suitable for the treatment. Leukaemia or tumour conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or chemotherapy treatment. (I) is useful for reducing ERG activity in a cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic; ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic; vulnerary; cancer; lymphoma; Ening's sarcoma; melanoma; psoriasis; tumour angiogenesis; diabetic retinopathy; macular degeneration; neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris; angiofibroma of tuberous sclerosis; port-wine stain; wound healing; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss; Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;
specification, but was obtained in electronic format directly from WIPO
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useful for treating cancer, diabetic retinopathy, macular degeneration,
arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human ERG hammerhead ribozyme target sequence, Seq ID No 835.
                                                                                                        Length 17;
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                                                                 Sequence 17 BP; 1 A; 4 C; 9 G; 3 T; 0 U; 0 Other;
                                                                                                           0.8%; Score 14.4; DB 1;
93.8%; Pred. No. 7.3e+02;
tive 0; Mismatches 1;
                       at ftp.wipo.int/pub/published_pct_sequence
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                                                                                                                                                                                                   834 GGAAGCTGCTGGGGTC 849
                                                                                                                                                                                                                                                                                                                                                           ABK18188 standard; RNA; 17 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-APR-2002 (first entry)
                                                                                                      Query Match
Best Local Similarity 93.8°
Matches 15, Conservative
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Novel enzymatic nucleic acid molecules which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B useful for treating cancer, inflammatory disorders and autoimmune diseases.
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ERG gene, by contacting (I) with RNA, in the presence of a divalent cation such as Mg2+. (I) is useful for diagnosis of conditions and diseases related to the expression of ERG, and as diagnostic tool to examine genetic drift and mutations within diseased calls or to detect the presence of ERG RNA in a cell. (I) is useful for specifically targeting genes that share homology with ERG gene or ERG fusion genes. ABK17354-ABK22719 represent nucleic acids, including antisense and enzymatic nucleic acid molecules which regulate expression of ERG, and related PCR primers of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                            0.8%; Score 14.4; DB 1; Length 17; 87.5%; Pred. No. 7.38+02; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                            Sequence 17 BP; 2 A; 11 C; 3 G; 0 T; 1 U; 0 Other;
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94US-00245466.
94US-00291932.
96US-00777916.
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23-DEC-1996;
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regurances expression or a sequence encouring a summing the regular configuration. The enzymatic nucleic acid molecule is adapted to treat cancer and is useful for down-regularing REL-A activity in a cell, for treating a patient having a condition associated with the level of REL-A. (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in the presence of a divalent cation, especially MG'2+. The enzymatic and antisense nucleic acid molecules are useful for treating breast, lung, prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic, cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or multidrug resistant cancer. The method involves use of other drug theraphes such as monoclonal antibodies, REL-A-specific inhibitors or cyclophosphamide, doxorubin, fluorouracil carboplatin, edarrexate, gencitabine or radiation therapy. The enzymatic and antisense nucleic acid molecules are also useful for treating inflammatory disease such as expection, gene therapy applications, ischaemia/reperfusion injury central nervous system (CRS) and myocardial), glomerulonephritis, ceterion, airway inflammation, inflammatory bowel disease, infection. This sequence represents the substrate of a novel enzymatic nucleic acid molecule
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of nuclear factor
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13.8%; Pred. No. 7.3e+02;
ve 0; Mismatches 1; Indels
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94US-00245466.
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96US-00777916.
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Best Local Similarity
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15-AUG-1994;
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(STIN/) STINCHCOMB D T.

The invention describes an enzymatic nucleic acid molecule (I) which down

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Novel enzymatic nucleic acid molecules which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B useful for treating cancer, inflammatory disorders and autoimmune diseases.
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                                                                                                                                                                                                                                                                                                                                                                   regulates expression of a sequence encoding a subunit of nuclear factor kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme configuration. The enzymatic nucleic acid molecule is adapted to treat cancer and is useful for down-regulating REL-A activity in a cell, for treating a patient having a condition associated with the level of REL-A. (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in the presence of a divalent cation, especially MG'2+. The enzymatic and antisense nucleic acid molecules are useful for treating breast, lung,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prostate, colorectal, brain, ossophageal, stomach, bladder, pancreatic, cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or multidrug resistant cancer. The method involves use of cother drug therapies such as monoclonal antibodies, REL-A-specific inhibitors or chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate, gencitabine or radiation therapy. The enzymatic and antisense nucleic acid molecules are also useful for treating inflammatory disease such as
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                                                                          Stinchcomb DT, Mcswiggen J, Draper KG;
                                                                                                                                                                                                                                                                                        Claim 3; Page 33; 72pp; English.
(MCSW/) MCSWIGGEN J. (DRAP/) DRAPER K G.
                                                                                                                                 WPI; 2003-340953/32
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0; Gaps 0.8%; Score 14.4; DB 1; Length 17; 93.8%; Pred. No. 7.3e+02; tive 0; Mismatches 1; Indels Sequence 17 BP; 2 A; 7 C; 7 G; 0 T; 1 U; 0 Other; Ouery Match 0.89 Best Local Similarity 93.89 Matches 15; Conservative

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704 GCCCACCCAGGCGGGG 719 1 GCCCACCCAGGCUGGG 16 유 ઠે

ACA06578 standard; RNA; 17 BP (first entry) 03-JUN-2003 ACA06578; RESULT 1189

NFKB sub-unit modulating inozyme substrate #397.

Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme; G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human; lung cancer; prostate cancer; colorectal cancer; brain cancer; cosphageal cancer; atomach cancer; bladder cancer; pancreatic cancer; cervical cancer; head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor; chemotherapy; paclitacati, docetaxel; cisplatin; methotraxate; cyclophosphanide; doxorubin; fluorouracil carboplatin; edatrexate; gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes; rheumatoid arthritis; restenoàsi; Crohn's disease; obesity; ischaemia; gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis; transplant/graft rejection; reperfusion injury; glomerulonephritis; allergic airway inflammation; inflammatory bowel disease; infection; ss. 

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regulates expression of a sequence encoding a subunit of nuclear factor kappa B (NREB), where (I) is an inosyme, zinzyme, G-cleaver or ambersyme configuration. The enzymatic nucleic acid molecule is adapted to treat cancer and is useful for down-regulating REL-A activity in a call, for treating a patient having a condition associated with the level of REL-A. (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in the presence of a divalent cation, especially MG 2+. The enzymatic and antisense nucleic acid molecules are useful for treating breast, lung, prostate, colorectal, brain, oesophagal, stoomach, bladder, pancreatic, cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or multidrug resistant cancer. The method involves use of other drug chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate, cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate, gemeitabine or radiation therapy. The enzymatic and antisense nucleic gemeitabine or radiation therapy. The enzymatic and antisense nucleic caid molecules are also useful for treating inflammatory disease such as rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 33; 72pp; English.
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94US-00245466.
94US-00291932.
96US-00777916.
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                                        US2002177568-A1
  Homo sapiens.
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Human MDZ7 scanning oligonucleotide SEQ ID 5254. ADB04268 standard; DNA; 17 BP 704 GCCCACCCAGGCGGG 719 2 GCCCACCCAGGCUGGG 17 20-NOV-2003 (first entry) Local Similarity 93.8 nes 15, Conservative ADB04268; RESULT 1190 Matches ADB04268/ ò 요 

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The invention relates to a novel short interfering RNA (siRNA) nucleic acid molecule, that modulates expression of a nucleic acid molecule encoding HBR2, K-Ras, H-Ras, N-Ras, human immunodeficiency virus (HIV) or a component of HIV. The nucleic acid molecules are useful for reducing thematic activity. The nucleic acid molecules are useful for reducing HBR2, K-Ras, H-Ras, and HIV acid molecules are useful for reducing HBR2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are also useful for treating breast, ovarian, colorectal, lung, prostate, bladder, or pancreatic cancer, and HIV infection, and AlDS. The sequences shown in ABZ59889 - ABZ66216, ABZ66531, ABZ66520 - ABZ66524, ABZ66530 - ABZ66531, ABZ65531, ABZ66531, ABZ66531,
                                                                                                                                                                                                                                                                                                                                        Novel short interfering RNA and enzymatic nucleic acid useful for treating cancer, modulates the expression of a nucleic acid encoding HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
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enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
anti-rheumatic; cancer; AIDS; ss.
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06-JUN-2001; 2001US-0296249P.
10-SEP-2001; 2001US-0318471P.
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06-JUN-2001; 2001US-0296249P.
10-SEP-2001; 2001US-0318471P.
                                                  29-MAY-2002; 2002WO-US016840.
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                                                                                                                                                                                            (RIBO-) RIBOZYME PHARM INC.
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                                                                                                                                                                                                                                                                                              WPI; 2003-140484/13.
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                                                                                                                                                                                                                                              Mcswiggen J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2003
  05-DEC-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is corocted at chromosome 6p21.3-22.2, MD27 is encoded at chromosome 6p21.3-22.2, MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome 16p12.2 and MD212 is encoded at chromosome 16p12.2 and MD212 is encoded at chromosome 16p12.2 and MD24, MD27, or MD214, MD27, or MD212. And MD214. MD24, MD27, or MD212. The nucleic caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic acids can also be used as probes to detect and characterize gross atterations in MD23, MD24, MD27, or MD212. The probes are useful in constructing microarrays for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as the present sequence was used to illustrate the invention.
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Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
developmental disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7 or MDZ12, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
anti-rheumatic; cancer; AIDS; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17 BP; 1 A; 1 C; 0 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 8; SEQ ID NO 5254; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human HER2 DNAzyme substrate #593.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1736 AAAAAAAAAAAAAA 1751
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                                                                                                                                                                                                                                                                  30-JUL-2002; 2002EP-00016874
                                                                                                                                                                                                                                                                                                               02-AUG-2001; 2001US-00922181
                                                                                                                                                                                                                                                                                                                                                                                                               Nguyen C;
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                                                                                                                                                                                                                                                                                                                                                                                                               Gu Y,
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                                                                                                                     Homo sapiens
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Mcswiggen J;

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                                                                                                                                                                                                                                                                                  acid molecule or an enzymatic nucleic acid molecule, that modulates expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras, human immunodeficiency virus (HIV) or a component of HIV. The nucleic acid molecule of the invention has cytostatic, anti-HIV, and anti-HER2, K-Ras, H-Ras, and HIV acid molecules are useful for reducing HER2, K-Ras, H-Ras, and HIV acid molecules are useful for caducing are also useful for cancer, on HIV acid molecules are shown in ABZ59899 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ65244, ABZ65530 - ABZ65520 - ABZ65524, ABZ65530 - ABZ65520 - ABZ655
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                                                                                                                                                                                                                                                          The invention relates to a novel short interfering RNA (siRNA) nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                Novel short interfering RNA and enzymatic nucleic acid useful for treating cancer, modulates the expression of a nucleic acid encoding HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
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enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
anti-rheumatic; cancer; AIDS; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.8%; Score 14.4; DB 1; Length 17;
18.8%; Pred. No. 7.3e+02;
ve 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17 BP; 1 A; 10 C; 2 G; 0 T; 4 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human K-Ras DNAzyme substrate #1031
                                                                                                                                                                                                 Claim 58; Page 129; 185pp; English
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06-JUN-2001; 2001US-0296249P.
10-SEP-2001; 2001US-0318471P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ribozymes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 68.8*
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                             WPI; 2003-140484/13
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expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras, human immunodeficiency virus (HIV) or a component of HIV. The nucleic acid molecule of the invention has cytostatic, anti-HIV. and anti-rheumatic activity. The nucleic acid molecules are useful for reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are also useful for treating breast, ovarian, colorectal, lung, prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences shown in ABZ59889 - ABZ62216, ABZ64944 - ABZ65531, ABZ66520 - ABZ65244, ABZ65530 - ABZ65530 - ABZ65534, ABZ65530 - ABZ65534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human leukocyte antigen; HLA; probe; tissue transplantation; MHC gene; major histocompatibility complex; paternity test; forensic medicine; haematological malignancy; inherited disorder; adoptive immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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probes each recognising a sequence motif present in some allele(s)
useful for donor matching in tissue transplantation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  0.8%; Score 14.4; DB 1; Length 17; 93.8%; Pred. No. 7.38+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human leukocyte antigen class I gene URSTO probe 350-367.
                                                                                                                                                                                                                                                                                                                                                                        Sequence 17 BP; 6 A; 6 C; 3 G; 0 T; 2 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1603 GTACCTGCTGGGTTCT 1618
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                                                                                                                                                                                                                                                                                                    ribozymes of the invention
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Sequence 18 BP; 5 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
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                                                                               CAGCCTCCAGAGGATG 922
                                                           0.8%;
                                                                                                                                                                                                     98US-00161244
                                                                                         CACCCTCCAGAGGATG 17
                                                                                                                                                                                                              98US-00161244
                                                                                                                AAZ65420 standard; DNA; 18
                                                                                                                                    10-APR-2000 (first entry)
                                                                Local Similarity 93.8
nes 15; Conservative
                                                                                                                                                                                                                                 Cowsert LM;
                                                                                                                                                                                                                        (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                           WPI; 2000-105082/09.
                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                US6004814-A.
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                                                                                                                                                                                                                                 Bennett CF,
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                                                           Query Match
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                                                                                                       RESULT 1195
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nucleotide polymorphisms (SNPs) which the inventors identified in human genes. These SNPs can be used in disease diagnosis and prediction of an individual's susceptibility to disease, in forensic and paternity testing and in genetic mapping. In particular, the SNPs of the invention can be used to diagnose susceptibility to diseases of the cardiovascular,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single nucleotide polymorphism; SNP; human; genetic disease; disease susceptibility; cardiovascular system; endocrine system; neurological system; forensic testing; paternity testing; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid selected from one of 106 genes comprising single nucleotide polymorphisms, allele-specific oligonucleotides to the genes are useful for phenotypic correlations, forensics, paternity testing, medicine and genetic analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     endocrine and neurological systems, such as coronary artery disease, schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
  cells, due to the development of mutations in CD71 which altered the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention is concerned with a number of human single
                                                                                                                                0.8%; Score 14.4; DB 1; Length 18; 93.8%; Pred. No. 7.6e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ireland JS, Lander ES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.8%; Score 14.4; DB 1; Length 18; 93.8%; Pred. No. 7.6e+02; Live 0; Mismatches 1; Indels
                                                                                 Sequence 18 BP; 0 A; 7 C; 4 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 BP; 3 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Single nucleotide polymorphism PCR primer #1406.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (WHED ) WHITEHEAD INST BIOMEDICAL RES
                              epitope recognised by the antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cargill M, Daley GQ,
Patil N, Sklar P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Fig 5; 214pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
                                                                                                                                                                                                                                             729 GGCTTCTGGGCCCCTC 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         391 ACGCAGGGCTCCCTG 406
                                                                                                                                                                                                                                                                         3 GCTTCTGGTCCCCTC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2000; 2000WO-US008440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0127248P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 ACGCAGGGGATCCCTG 2
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC72279 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                   Query Match
Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AFFYMETRIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-611722/58.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200058519-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Altshuler D,
Lipshutz RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-OCT-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC72279;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AFFY-)
                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1196
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequences AA265197-265440 represent novel phosphorothioate antisense oligonucleotides targetted against the human CD71 gene, which encodes the CD71 transferrin receptor. Upon uptake in the small intestine, iron immediately combines with the ubiquitous serum protein transferrin, the primary vehicle by which iron is transported around the body. The uptake of circulating iron-transferrin complexes is mediated by the transferrin receptor, CD71. The requirement of both iron-transferrin complexes and CD71 for cell proliferation suggests that inhibition of iron utilisation could represent a strategy for the treatment of cancer. The could represent a strategy for the treatment of an animal suspected of having a disease or disorder which can be treated by inhibition of CD71 expression. Use of the antisense compounds and methods of the invention may also be useful prophylactically to prevent or delay infection, inflammation or tumour formation. The antisense compounds may also be useful for research and as diagnostic tools. The antisense oligonucleotides provide a tool for effectively downregulating CD71 expression. Prior art methods utilised antibodies specific for CD71 proteins; however, this resulted in the development of resistant tumour
                                                                                                                                                                                                                                                                                                                                                                              ö
                   the alleles of the HLA genes in a prospective donor and a prospective recipient in tissue or organ transplantations. The method can also be used in paternity testing, in forensic medicine, as a follow up technique in treatment of haematological malignancies or inherited disorders, in adoptive immunotherapy, and in identification of bacteria and viruses. The method can provide for the identification of alleles of the polyallelic genes using a limited number of selected recurring motif
method is particularly useful for matching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antisense oligonucleotides targeted to genes encoding CD71, useful for preventing, diagnosing and treating inflammatory disorders and tumors.
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human CD71 phosphorothioate antisense oligonucleotide SEQ ID NO:71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; CD71; transferrin receptor; antisense; phosphorothioate;
antiproliferative; anticancer; anti-inflammatory; gene therapy; 88.
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                                                                                                                                                                                                                                                                                                                      Score 14.4; DB 1; Length 18;
Pred. No. 7.6e+02;
); Mismatches 1; Indels
chromosomes and viral DNA. The
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Gaps

Mon Aug 16

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WPI; 2001-290930/30
                                                                          WO200129262-A2.
                                                     Homo sapiens.
                                                                                                                                          15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-SEP-2002
                                                                                                                                                                                                                                                     acid sample.
                                                                                               26-APR-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 1199
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                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention is concerned with a number of human single nucleotide polymorphisms (SNPs) which the inventors identified in human genes. These SNPs can be used in disease diagnosis and prediction of an individual's susceptibility to disease, in forensic and paternity testing and in genetic mapping. In particular, the SNPs of the invention can be used to diagnose usceptibility to diseases of the cardiovascular, endocrine and neurological systems, such as coronary artery disease, echizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
                                                                                                                Single nucleotide polymorphism; SNP; human; genetic disease;
disease susceptibility; cardiovascular system; endocrine system;
neurological system; forensic testing; paternity testing; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
                                                                                                                                                                                                                                                                                                                                                              Nucleic acid selected from one of 106 genes comprising single nucleotide polymorphisms, allele-specific oligonucleotides to the genes are useful for phenotypic correlations, forensics, paternity testing, medicine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                         , Daley GQ, Ireland JS, Lander ES;
Sklar P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.8%; Score 14.4; DB 1; Length 18; 93.8%; Pred. No. 7.6e+02; ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 BP; 3 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                               Single nucleotide polymorphism PCR primer #1398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP specific lower PCR primer SEQ ID 346.
                                                                                                                                                                                                                                                                         (WHED ) WHITEHEAD INST BIOMEDICAL RES (AFFY-) AFFYMETRIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Fig 5; 214pp; English
                              AAC72267 standard; DNA; 18 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     391 ACGCAGGGCTCCCTG 406
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                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                        Altshuler D, Cargill M,
Lipshutz RJ, Patil N, S
                                                                                                                                                                                                                                                                                                                                         WPI; 2000-611722/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                genetic analysis.
                                                                                                                                                                                    WO200058519-A2.
                                                                                                                                                                                                                                                     31-MAR-1999;
                                                                          09-FEB-2001
                                                                                                                                                                                                         05-0CT-2000
                                                    AAC72267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11
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         RESULT 1197
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Sequences AAH17205 - AAH40944 represent PCR primers, single nucleotide polymorphisms SNPs. The present invention false is single nucleotide polymorphisms SNPs. The present invention includes kits for determining the presence or absence of a SNP, using the includes kits for determining the presence or absence of a SNP, using the oligonucleotides of the invention. The PCR primers are used to amplify a SNP primer is used as a genotyping primer. The oligonucleotides are useful for genotyping a nucleic acid sample by performing a single-nucleotide primer extension reaction. The oligonucleotides are useful for determining the presence, absence or identity of a SNP and for genotyping nucleic acid samples, for e.g. to assess by association analysis the genotype of an individual or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic trait suspected of being caused by one or more SNPs. Phenotypic trait suspected of being caused by one or more and acute intermittent pophyria. Phenotypic traits also include symptomes of or susceptically to multifactorial cisease of which a component is or may be genetic such as autoimmune disease of which a component is or may be genetic such as autoimmune microorganism. The method is also useful in forensic investigations and microorganism. The method is also useful in forensic investigations and patenting and patentity analysis. The present sequence represents a PCR primer specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenesis imperfects; autofimune disease; acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polynucleotide polymorphism in a nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.8%; Score 14.4; DB 1;
33.8%; Pred. No. 7.6e+02;
1ve 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 51; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORCH-) ORCHID BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD38936 standard; DNA; 18
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Best Local Similarity 93.8
Matches 15; Conservative
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Novel antisense compound useful for treating diseases associated with Cyclin D2 expression, comprises an oligonucleotide comprising up to 50 nucleobases in length, which inhibits expression of Cyclin D2 in cells or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes a compound (I) of up to 50 nucleobases in length, which inhibits the expression of Cyclin D2. (I) is useful for inhibiting the expression of Cyclin D2 in cells or tissues in vitro. (I) is thus useful for treating disease associated with Cyclin D2 expression. (I) is useful for diagnostics, therapeutics, prophylaxis and as research reagents and kits. This sequence represents human cyclin D2 inhibition
                                                         Antisense inhibition of human cyclin D2 related oligonucleotide #48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Downstream PCR primer recognising the 5'' region of betal-AR DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.8%; Score 14.4; DB 1; Length 18; 93.8%; Pred. No. 7.6e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alpha-myosin heavy chain promoter; alpha-MHC;
human betal-adrenergic receptor; betal-AR; transgene;
heart tissue-specific promoter; transgenic animal model;
heart muscle disease; heart failure; PCR primer; ss.
                                                                                              diagnostic; therapeutic; prophylaxís;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18 BP; 3 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 15; Col 45-46; 40pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              associated oligonucleotide
                     11-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.8
Best Local Similarity 93.8
Matches 15; Conservative
                                                                                            Human, cyclin D2, diagno
cyclin 2 inhibition, ss
                                                                                                                                                                                                                                                                                                                                                                                                               NPI; 2003-361492/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissues in vitro.
                                                                                                                                                                                                                                                                                                                                        SISI (-SISI)
                                                                                                                                                                                       US6492173-B1
                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-APR-1998;
                                                                                                                                                                                                                            10-DEC-2002.
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                                                                                                                                                                                                                                                                                                                                                                              Cowsert LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV65956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to antisense compounds targetted to a nucleic acid molecule encoding Her2 (human Epidermal Growth Factor receptor 2) that specifically hybridises with and inhibits the expression of Her2. Antisense compounds of the invention are used for treating diseases or conditions associated with Her2 such as hyperproliferative diseases or lung, breast, gastric, oesophageal, colon, bladder, salivary, neural or cardiac cancer. They are also useful prophylactically e.g. to prevent or delay infection, inflammation and tumour formation. The invention is also used in gene therapy. The present sequence is an antisense oligonucleotide targetted to human Her-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel antisense oligonucleotide which modulates the expression of Human Epidermal Growth Factor receptor, Her2, is useful for treating tumors inflammation or to prevent infection in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
hyperproliferative disorder; prophylaxis; inflammation; antisense; tumour; gene therapy; phosphorothioate backbone; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.8%; Score 14.4; DB 1; Length 18; 93.8%; Pred. No. 7.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                             /mod_base= OTHER
/note= "2'methoxyethyl nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "2'methoxyethyl nucleotides"
                                                                                                                                                                    /mod_base= OTHER
/note= "Phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 BP; 4 A; 2 C; 8 G; 4 T; 0 U; 0 Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                              .ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                 mod_base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 89; 116pp; English
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0
                                                                                                                                                                                                                                                                                                                                                                           /mod_base≈ m5c
L5. .18
                                                                                                                                                                                                                                                                                                                      mod_base= m5c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1665
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ACA60611 standard; DNA; 18 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-SEP-2001; 2001WO-US028572.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1650 TCTCCCTGACATCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bennett CF, Cowsert LM;
                                                                                                                                                                                                                            *tag=
                                                                                                                                   ....18
/*tag=
                                                                                                                                                                                                                                                                                                 *tag=
                                                                                                                                                                                                                                                                                                                                                                                                               *tag=
                                                                                                                                                                                                                                                                                                                                                           *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-471192/50.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200222636-A1
                                                                                                              Key
modified_base
                                                                                                                                                                                                        modified_base
                                                                                                                                                                                                                                                                                modified base
                                                                                                                                                                                                                                                                                                                                        modified base
                                                                                                                                                                                                                                                                                                                                                                                            modified_base
                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-2002
                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Matches

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ACA60611/c ID ACA60 XX AC ACA60

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Hayden MR,
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                                                                     cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ94997/
 X8XXXXXXXXXXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                           PCR primers AAV65954-57 were used to screen for the transgene of the invention. The upstream primers recognise the alpha-myosin heavy chain promoter (alpha-MfC) and the downstream primers recognise 5' region of the human betal-adrenergic receptor (betal-AR) coding region. The specification describes a transgenic animal, especially a mouse, which has incorporated into its genome a transgene comprising a heart tissuebecific promoter operatively linked to a coding sequence comprising betal-IAR, the transgenic animal. The transgenic animal can be used as a model for heart muscle disease and heart failure in a mammal. The transgene can also be used for treating heart failure in a mammal. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human ABC1 cholesterol transporter; chromosome 9q31;
ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;
                                                                                         Transgenic mice as models for heart disease - having incorporated in their genome a heart tissue-specific promoter operatively linked to DNA coding for a beta-1-adrenergic receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cardiovascular disease; coronary artery disease; coronary restenosis; cerebrovascular disease; peripheral vascular disease; Alzheimer's disease; Niemann-Pick disease; Huntington's disease; X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis; prognosis; prophylaxis; drug screening; transgenic animal; PCR primer;
                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                               0.8%; Score 14.4; DB 1; Length 19; 33.8%; Pred. No. 7.8e+02; ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ABC1 gene exon 40 5' PCR primer, SEQ ID NO:148.
                                                                                                                                                                                                                                                                                                        Sequence 19 BP; 2 A; 6 C; 7 G; 4 T; 0 U; 0 Other;
                                                                                                                                         Example 1; Page 18; 40pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0124702P.
99US-0138048P.
99US-0139600P.
99US-0151977P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYBR-) UNIV BRITISH COLUMBIA.
(XENO-) XENON BIORESEARCH INC.
                                                                                                                                                                                                                                                                                                                                                                               110 CAGAGGCTCGGGGCTT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC69249 standard; DNA; 19 BP
 97US-0041966P.
                       (UYTE-) UNIV TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-MAR-2000; 2000WO-IB000532.
                                                                                                                                                                                                                                                                                                                                    0.8%;
Local Similarity 93.8%;
hes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                             Bristow MR;
                                                                    WPI; 1998-557104/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200055318-A2.
03-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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08-JUN-1999;
17-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC69249;
                                              Port JD,
                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1202
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Matches
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The invention relates to the human ABCI cholesterol transporter protein

(B18082) and to nucleic acid sequences (G5120) which encode it. ABCI is
a member of the ATP-binding casettee (G5120) which encode it. ABCI is
a member of the ATP-binding casettee (G5120) which encode it. ABCI is
a member of the ATP-binding casettee (ABC transport. particularly
concerns, and plays a crucial role in cholesterol transport, particularly
cinvolved in cholesterol efflux from the cell. The gene encoding ABCI is
involved in cholesterol efflux from the cell. The gene encoding ABCI is
conversed on chromosome 931, and mutations in this gene are associated
with two genetic HDL (high density lipoprocein) deficiency disorders.

CC carditogushable in that TD is an autosomal recessive disorder. While
CFHA is inherited as an autosomal dominant trait. Low levels of HDL ("good
corelate as an autosomal dominant trait. Low levels of HDL ("good
corelate as an autosomal dominant trait. Low levels of HDL ("good
corelate as an autosomal dominant trait. Low levels of HDL ("good
corelates, particularly coronary artery disease.

CC cholesterol") in the blood correlate with a high risk of cardiovascular
disease, coronary restenosis, and peripheral vascular disease.

CC conversely, a high level of HDL has protective effects against
cardiovascular disease. The invention provides genetic constructs and
cardiovascular disease comprising the administration of an expression
cardiovascular disease comprising the administration of an expression
cc cardiovascular disease comprising the administration of an expression
cc cardiovascular disease, coronary restenosis or peripheral vascular
cuther relates for cardiovascular disease, especially coronary artery disease,
crebrovascular disease, coronary restenosis or peripheral vascular
crebrovascular disease, Alinked de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                        New ABC1 polypeptide is useful for treating diseases associated with ABC1
biological activity, e.g. Alzheimer's disease, Huntington's disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T cell receptor; single chain; scTCR; TCR; single chain antibody; scFv; polyspecific binding molecule; cancer; infection; tumour; graft rejection; immunosuppressive; antitumour; therapy; mouse; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide KC295/KC296 used in scTCR-scFv fusion construction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19 BP; 5 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
Pimstone SN;
                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 10; 229pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1184 GCTCCCAGCCCATCCT 1199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.8%;
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    Wilson AR,
                                                                                         WPI; 2000-587528/55
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(IMMU-) IMMUSOL INC.
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                                                                                                                                                                                                                                                                                                                      Double-stranded oligonucleotide KC295/KC296 codes for a G4S peptide linker that was used to connect a single chain T cell receptor (scTCR) and a single chain antibody (scPv) in the construction of a single chain polyspecific binding molecule (sc-PBM) of the invention. Such sc-PBMs can associated antigon (HLAA) and for preventing or treating cancer in a patient in which the cancer features HLA-expressing tumour cells (claimed). Targets include tumour cells or virally infected cells. The sc-PBM can be used to selectively control T-cell mediated immune responses such as T-cell proliferation, differentiation, activation or B lymphocyte stimulation. This can be used to reduce or eliminate an immune response
                                                                                                                                                                                                                                             treating
                      /*tag= a
/note= "single-stranded overhang on complementary strand
of sequence 5'-CCGG-3'"
                                                                                                                                                                                                                                        Single-chain polyspecific binding protein used for preventing or treatin
a cancer comprising human-leukocyte-associated antigen-expressing tumor
cells comprises a single-chain T-cell receptor linked to a single-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.8%; Score 14.4; DB 1; Length 19; 93.8%; Pred. No. 7.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                            Wong HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19 BP; 4 A; 3 C; 9 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                            Klinman NR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            e.g. in patients undergoing transplant surgery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                    Example 5; Fig 21B-3; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cyclin D2 ribozyme binding site #50.
Location/Qualifiers
                                                                                                                                                                                            Sherman LA,
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                                                                                                                     99WO-US024645
                                                                                                                                             98US-0105164P
                                                                                                                                                                    (SUNO-) SUNOL MOLECULAR CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          527 ATGAGCCCCCGCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15; Conservative
                                                                                                                                                                                            Card K,
                                                                                                                                                                                                                  WPI; 2000-339516/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200032765-A2
                                                                     WO200023087-A1
             misc feature
                                                                                                                                             21-OCT-1998;
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                                                                                                                     21-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-DEC-1999;
                                                                                                                                                                                           Weidanz JA,
                                                                                              27-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-JUN-2000
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                                                                                                                                                                                                                                                                             antibody
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ij
                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
Representative examples of ribozyme recognition sites are given in AAARASIS to AAA6787. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in
                                                                                                                                                        New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1, PCNA and Cyclin B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19 BP; 5 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cyclin D2 ribozyme binding site SEQ ID NO:1939.
Robbins JM;
                                                                                                                                                                                                                                                                                                                              Disclosure; Page 75; 109pp; English.
    Barber JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1518 GCACATCTTGTGCAAG 1533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0161532P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH59515 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       restenosis treatment
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Welch PJ,
                                                                                WPI; 2000-412314/35.
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ses 15, Conserv
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Tritz R,
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RESULT 1207
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                                            The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a ribozyme (1) which cleaves RNA encoding a cytokine involved in inflammation, matrix metalloprotainse (MMP), cyclin, cell-cycle dependent kinase, growth factor or a reductase, or administering a nucleic acid melecule (II) comprising a promoter operably linked to a nucleic acid segment encoding (I). (I) can have antipsoriatic, copthalmological, cytostatic, antiseborrheic, antidiabetic, antisickling, copthalmological, vunearary, keratolytic and virucide activities, and cleaves RNA encoding cytokine involved in inflammation. (I) can be used in gene therapy. (I) and (II) are useful for treating proliferative skin diseases such as psoriasis, atopic dermatitis, actinic keratosis, aguamous or basal cell carcinoma and viral or seborrheic wart. They can also be used for treating proliferative eye diseases such as diabetic retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of prematurity and retinal detachment, and for treating and preventing scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New oligonucleotides, useful for detecting bacteria that may contaminate drinking water, provide quick results for many species in parallel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detection, probe, contaminant, drinking water, Legionella, coliform; faecal streptococci, soil; sputum, biopsy, urine, food, pharmaceutical, cosmetic, fluorescent in situ hybridisation, FISH, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes novel oligonucleotide probes used to detect contaminant bacteria that may be present in drinking water. The probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                            0.8%; Score 14.4; DB 1; Length 19; 93.8%; Pred. No. 7.8e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19 BP; 5 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                          exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23S/16S rRNA detecting probe SEQ ID 4.
                 Example 1, Page 213; 408pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Page 12; 53pp; German
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Best Local Similarity 93.8
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
can detect bacteria (especially Legionella, faecal streptococci and coliforms) that may contaminate drinking water in environmental samples (water or soil), clinical samples (sputum, biopsies, urine etc.), in bathing and drinking water and in foods, pharmaceuticals and commetics, in by in situ hybridisation. The probes combine the advantages of fluorescent in situ hybridisation with those of culture methods only a relatively short culture step is required; analysis takes 24-48 hours (contrast many days for conventional methods) and all relevant bacteria ean be tested simultaneously. The oligonucleotides can differentiate between species of the same genus and are easy to use, allowing simple analysis of a large number of samples. ABX94532-ABX94578 represent the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour; OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis; inflammation; therapy; hyperproliferative disorder; infection; cancer; chromosome 7q22; ZRP-1; phosphorothioate; ss.
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/note= "2'-methoxyethyl (2'-MOE) nucleotides"
16. .20
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/note= "2'-methoxyethyl (2'-MOB) nucleotides"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                              oligonucleotide probes described in the invention
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modified_base
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                                                              The invention relates to antisense compounds targetted to a nucleic acid encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22. Antisense compounds of the invention are useful for modulating the expression of TRIP6 such as hyperproliferative disorders (e.g. with the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as research reagents and kits and in distinguishing between functions of various members of a biological pathway. The are also useful in antisense therapy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dimethylarginine dimethylaminohydrolase; DDAH; DDAH1; DDAH2; arginine deaminase; hyperlipidemia; renal failure; hypertension; restenosis; atherosclerosis; schizophrenia; multiple sclerosis; cancer; ischemia repertusion injury; septic shock; multi organ failure; arthritis; skin disorders; inflammatory cardiac disease; migraine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               used to identify e.g. cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotides encoding methylarginase polypeptides, vectors comprising these mucleotides and the polypeptides themselves can be used in medicaments for the treatment of hyperlipidemia, renal failure, hypertension, restenosis after angioplasty, atherosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                               Length 20;
                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel methylarginase polypeptides and polynucleotides, modulators of them, which are used in the treatment of hypertension, and bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Charles IG;
                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 7 A; 9 C; 3 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                               Score 14.4; DB 1;
Pred. No. 8.1e+02;
hyperproliferative disorders, such as cancer
                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Whitley GSJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligo d(T) primer for human DDAH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 33; 68pp; English.
                                Claim 3; Page 76; 111pp; English.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP
                                                                                                                                                                                                                                                                                                                                                                                                                   477
                                                                                                                                                                                                                                                                                                                                                 0.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JAN-2000; 2000WO-GB000226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99GB-00001705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACCACACTGGCCAAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA47676 standard; cDNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UNICO ) UNIV COLLEGE LONDON
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 93.0.
The 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leiper JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-543392/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200044888-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vallance PJT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infection; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                   462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method of sequential consensus region-directed amplification for sorting a mixture of DNAs into 2 or more subsets or distinguishing gene expression patterns in 2 samples. The methods, kits and oligonucleotides are useful for sorting a mixture of DNAs into 2 or more subsets or distinguishing gene expression patterns in 2 samples e.g. for disease disgnosis and gene expression patterns in 2 samples e.g. For primer used to illustrate the method of the invention
             cancer. Modulators of the enzyme can be used in medicaments for the treatment of ischemia-reperfusion injury of the brain or heart, cancer, lethal hypertension in severe inflammatory conditions such as septic shock or multi-organ failure, or local and systemic inflammatory disorders including arthritis, skin disorders, inflammatory cardiac disease, migrafine, or microbial or bacterial infection. The sequence of human DDAH was obtained by data base searching. The EST's used in the process are given in GENESEQ records AAA47661-A47677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequential consensus region-directed amplification; gene expression;
disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligo-AT PCR primer #1 used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
complications of heart failure, schizophrenia, multiple sclerosis or
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                                                                                                                                                                                                                           0.8%; Score 14.2; DB 1; Length 15; 93.3%; Pred. No. 7.1e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.8%; Score 14.2; DB 1; Length 15; 93.3%; Pred. No. 7.1e+02; ive 1; Mismatches 0; Indel8
                                                                                                                                                                                     Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gillies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example, Fig 1D; 19pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
                                                                                                                                                                                                                                                                                                      1735 CAAAAAAAAAAAAA 1749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-00163485.
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97US-0108152P.
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD44150 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                            15 BAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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Best Local Similarity 93.33
Matches 14; Conservative
                                                                                                                                                                                                                                               Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Broaddus W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-412824/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US6277571-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fillmore H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD44150;
                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1209
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1734 ACAAAAAAAAAAA 1748

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The present sequence represents a PCR primer which is used in an example from the present invention for the isolation of human TSA7005 gene. The human TSA7005 protein shares 32% homology with human and mouse Reg proteins, and 34% homology with the rat Reg protein. TSA7005 mas pancreatic beta cell growth activity and hypoglycaemic activity. The TSA7005 protein can be used for the diagnosis and treatment of diseases associated with the gene and its expression product
                                                                                                                                                                                                                        TSA7005 gene, encoding a polypeptide useful for the diagnosis and treatment of diseases associated with its expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O.8%; Score 14.2; DB 1; Length 16; Local Similarity 93.3%; Pred. No. 7.4e+02; No. 7.4e+02; No. 14; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16 BP; 1 A; 0 C; 0 G; 14 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                             Example 1; Page 24; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1736 AAAAAAAAAAAA 1750
                                                                                                                    99JP-00201279.
                                                                                 99JP-00201279.
                                                                                                                                                      (SAKA ) OTSUKA PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 DAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Conservative
                                                                                                                                                                                         VPI; 2001-303742/32
                JP2001025389-A.
                                                                                 15-JUL-1999;
                                                                                                                    15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-AUG-2001
                                                 30-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH27758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta -N3'; or (X)m5'-(alpha)a-beta a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, guanine, crytosine; N = adenine, guanine, cytosine or thymine; gamma = thymin; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of repetition of gamma, in which thymine expressed by gamma is composed of 13 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptides having at least two new nucleotides - useful as primers in RT-
                                                                                                                                                                                                                                            RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 2 Other;
                                                                                                                                                                                                         RT-PCR primer of the invention SEQ ID 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 12; 19pp; Japanese
                                                                                                  AAX18387 standard, DNA, 16 BP
                                                                                                                                                                                                                                                                                                                                                                                                                       97JP-00208312
                                                                                                                                                                                                                                                                                                                                                                                   97JP-00208312
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TAKI ) TAKARA SHUZO CO LID
                51.
                                                                                                                                                                         11-MAY-1999 (first entry)
                1 AVAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-183822/16.
                                                                                                                                                                                                                                                                                                                                                                                                                       18-JUL-1997;
                                                                                                                                                                                                                                                                                                               JP11032765-A
                                                                                                                                                                                                                                                                                                                                                  09-FEB-1999
                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                      AAX18387
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Gaps

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This invention relates to the human LUNX protein and the polynucleotide sequence encoding it. The invention includes a vector containing a LUNX golynucleotide, a host cell transformed with the vector, and an antibody that binds to LUNX. The gene can be used for cancer diagnosis and diagnosis of micrometastatic cancer and for the production of the LUNX
                                                                                                                                                                                                                                                                                                                                   Polynucleotide encoding LUNX gene product useful for the detection of cancer especially micrometastatic cancer.
                                                                                                           UNIX; human; cancer; micrometastatic cancer; primer; ss.
                                                                                 Primer used in human LUNX cDNA isolation.
                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 27; 30pp; Japanese.
BP
                                                                                                                                                                                                                                                     99JP-00253186.
                                                                                                                                                                                                                         99JP-00253186
                                                                                                                                                                                                                                                                               (SAKA ) OTSUKA PHARM CO LID.
AAH27758 standard; DNA; 16
                                                     (first entry)
                                                                                                                                                                                                                                                                                                         WPI; 2001-313367/33
                                                                                                                                                                    JP2001078772-A.
                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                         37-SEP-1999;
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0.8%; Score 14.2; DB 1; Length 16; 93.3%; Pred. No. 7.4e+02; ive 1; Mismatches 0; Indels

1735 CAAAAAAAAAAAA 1749

Conservative

Local Similarity hes 14; Conserv

Matches

Query Match

15 BAAAAAAAAAAAA 1

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Human, TSA7005; Reg; pancreatic beta cell growth, hypoglycaemic; diagnosis; PCR primer; ss.

Homo sapiens

Human TSA7005 gene isolation related PCR primer SEQ ID NO:4.

(first entry)

27-JUN-2001

AAF82119

AAF82119 standard; DNA; 16 BP

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Gaps

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The sequence is that of a bovine microsatellite sequence obtd. by
screening a genomic library of bovine MboI DNA fragments of between 250
and 500 bp with an (ACI)5 and a (TCI)5 oligomuclectice probe. One out of
50 clones cross-hybridised. Assuming independent distribution of
microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
in the bovine genome is estimated at >100, 000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequences upstream and
commiscream of the microsatellite sequence were used to generate the
required PCR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTTRRIM). The microsatellites may be
used to identify individuals, for parentage testing, and in the genetic
mapping of economic trait loci, or genes involved the determinism of
economically important traits esp. in cattle, to allow selective
breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN

    used in genetic identification, gene

gene product. The present sequence represents a primer used in the isolation of cDNA encoding human LUNX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                          Query Match 0.8%; Score 14.2; DB 1; Length 16; Best Local Similarity 93.3%; Pred. No. 7.4e+02; Matches 14; Conservative 1; Mismatches 0; Indels
                                                       Sequence 16 BP; 1 A; 0 C; 0 G; 14 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence of microsatellite from clone AGLA206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Table 7; Page 131; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymorphic bovine DNA markers - mapping, and selective breeding.
                                                                                                                                                                                                                                                                                              AAQ33508 standard; DNA; 14 BP.
                                                                                                                                                                   1735 CAAAAAAAAAAA 1749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92WO-US000340
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                                                                                                                                                                                                                                                                                                                                                                     (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Georges M, Massey JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1992-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENM-) GENMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09213102-A1
                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus
                                                                                                                                                                                                                                                                                                                                     AAQ33508;
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DUBS enzymes are ubiquitin-specific thiol proteases or Deubiquitinating forms.

(DUB) enzymes. The DUB enzymes are induced by at least one cytokine and include two conserved domains (CYS and HIS domains). DUB-1 is interleukin (LI)-3, IL-5 and/or GM-CSF induceble and is expressed in haematopoietic cells and induces growth arrest of the cell in the GO/GI phase of the cell cycle. The enzymes of the invention can be used to arrest preventing e.g. cancer especially leukaemias or lymphomas. The enzymes an also be used to arrest preventing e.g. cancer especially leukaemias or lymphomas. The enzymes can also be used to stimulate preferably haematopoietic cell proliferation e.g. to produce blood cells for replacing blood cell depletion due to disease or condition e.g. immune suppression from AIDS or therapy such as chemotherapy or dialysis. The enzymes may also be used to suppress the immune system e.g. during organ or cell transplantation. The nucleic acid can be used to transform cells for screening agents
                                                                                                                                                                                                                                   DUB; ubiquitin-specific; thiol protease; deubiquitinating enzyme; murine; cytokine-induced; conserved domain; CYS; HIS; haematopoietic cell; cell growth arrest; proliferation; cancer; leukaemia; lymphoma; PCR primer; amplify; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding deubiquinating enzymes - useful for inhibiting or stimulating growth of haematopoietic cells, e.g. for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primers AAT91860-61 were used for PCR amplification of DUB-1 (T14) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14 BP; 0 A; 0 C; 1 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                 3' primer for DUB-1 (T14) cDNA amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DAND ) DANA FARBER CANCER INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 39; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      which inhibit DUB enzyme activity
                                                                                          AAT91861 standard; DNA; 14 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95US-0002066P.
96US-0019787P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       96WO-US012884
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1 AAAAAAAAAAA 14
                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-154255/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhu Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                               WO9706247-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-AUG-1995;
                                                                                                                                                               20-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                   20-FEB-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dandrea AD,
                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                           AAT91861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                      RESULT 1214
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                                                                         AAT91861,
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Matches 14; Conservative

Query Match Best Local Similarity

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14 ACAAAAAAAAA 1

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RESULT 1215 AAV09227/c

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Gaps

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0.8%; Score 14; DB 1; Length 14; 100.0%; Pred. No. 7.1e+02; Live 0; Mismatches 0; Indels

us10008789-3.rng

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PolyT oligonucleotides (see AAV12217-28) were used in reverse transcription reactions on polyA+ RNA isolated from the fins of control or retinoic acid-treated zebrafish (Danio rerio). Several combinations of AAV12229-33) for differential display PCR. Bands demonstrating reproducible differential amplifications were found using the primers given in AAV12221 and AAV12231. The PCR product was reamplified (see AAV1224-35). A differential display product (see AAV12213) which exhibited a dependence on the presence of retinoic acid for its exhibited a dependence on the was used to isolate a full-length clone (see AAV1223) coding for a novel retinoid metabolising protein (see AAV1223), designated zP450RAI
                                                                                                                                                                                                                                                                                                                                            Retinoid metabolising protein – useful to develop products to treat, e.g.
cancer, actinic keratosis, oral leukoplakia, acne, psoriasis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HPPD; barley; hydroxyphenylpyruvate dioxygenase; plant; transformation; transgenic; plant cell; callus tissue, protoplast; electroporation; particle bombardment; soya; barley; wheat; oilseed rape; maize; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.8%; Score 14; DB 1; Length 14; 100.0%; Pred. No. 7.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14 BP; 0 A; 0 C; 1 G; 13 T; 0 U; 0 Other;
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Best Local Similarity 100.0%; Pred. No. /...
Annearvative 0; Mismatches
                                                                                                                                                                                                                                                          Beckett BR,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 14; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX02698 standard; DNA; 14 BP
                                                                                                       97WO-CA000440.
                                                                                                                                                96US-00667546
96US-00724466
                                                                                                                                                                                                               (TOOH ) UNIV QUEENS KINGSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1734 ACAAAAAAAAAAA 1747
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                                                                                                                                                                                                                                                          Petkovich PM, White JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 ACAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sunflower; tobacco; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barley HPPD primer #4.
                                                                                                                                                                                                                                                                                                     WPI; 1998-077178/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hordeum vulgare.
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                      WO9749815-A1
                                                                                                       3-JUN-1997;
                                                                                                                                                21-JUN-1996;
                                                                                                                                                                         01-OCT-1996;
                                                        31-DEC-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JAN-1999.
                                                                                                                                                                                                                                                                                                                                                                                         ichthyosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is a 3' poly(T) PCR primer used in the amplification of the inducible cytochrome P450RAI gene which specifically metabolises a derivative of the retinoic acid (RA). The cytochrome P450 gene in general produces enzymes involved in the oxidative metabolism of endogenous and exogenous compounds. The cytochrome P450 nucleotide sequence can be used to induce or suppress the expression of its protein. P450RAI is highly induced by RA in cell lines and tissues. This allows for the development of a drug screen using promoters and nucleotide sequences to identify drugs which are useful for reducing the catabolism of RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Retinoid metabolising protein; P450RAI; retinoid oxidase; retinoic acid; zebrafish; inhibitor; antisense; cancer; actinic keratosis; oral leukoplakia; head tumour; neck tumour; non-small call lung carcinoma; asal cell carcinoma; acute promyelocytic leukaemia; skin cancer; acne; psoriasis; ichthyosis; therapy; diagnosis; screening; differential display; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying DNA encoding inducible or suppressible cytochrome P450 - by screening for drugs which reduce the catabolism of retinoic acid, useful in cancer chemotherapy and the treatment of acne and psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                     3' poly(T) primer, PCR; amplification; cytochrome P450 gene;
oxidative metabolism; P450RAI; retinoic acid; RA; promoter; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.8%; Score 14; DB 1; Length 14; 100.0%; Pred. No. 7.1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Poly(T) oligonucleotide used in differential display PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14 BP; 0 A; 0 C; 1 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 50; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV12219 standard; DNA; 14 BP
                                                                                                                                                                                                                                                                                                                                                                     97WO-CA000488.
                                                                                                                                                                                                                                                                                                                                                                                                             96US-00667546
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AAV09227 standard; DNA; 14
                                                                                   07-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 ACAAAAAAAAAA 1
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                                                                                                                              3' poly(T) primer 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-077193/07
                                                                                                                                                                                                                                                                                                                                                                  23-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Petkovich PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996;
                                                                                                                                                                                                                                                                                 409749832-A2
                                                                                                                                                                                                                                                                                                                                                                                                                21-JUN-1996;
                                                                                                                                                                                                                                      Synthetic.
                                      AAV09227;
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Gaps .. 0

97DE-01030066

14-JUL-1997; 14-JUL-1997;

97DE-01030066

(BADI ) BASF AG

Synthetic

RESULT 1216

ઠે 셤 DNA, attached to a solid support, and reporter DNA, where either a part of the anchor DNA or reporter DNA is designed to form a triple-strand structure with part of the test sequence. Triple-x formation results in displacement of the reporter DNA which is detected as an indication of the presence of the DNA test sequence. The method is used to detect DNA genes for ribosomal RNA) in clinical samples, but also detecting oncogenes and Hepatitis B virus

sequences to an aqueous medium containing at least one

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Gaps

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0.8%; Score 14; DB 1; Length 14; 100.0%; Pred. No. 7.1e+02; ive 0; Mismatches 0; Indels

1736 AAAAAAAAAAAA 1749

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Local Similarity 100.04

Best Loc Matches

Query Match

Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;

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AAX02695-X02708 are primers used in the isolation of a novel barley (Hordeum vulgare) hydroxyphenylpyruvate dioxygenase (HPPD) protein. This protein is useful for plant transformation to produce transgenic plants especially where an expression cassette is introduced into a plant cell. callus tissue, a whole plant or protoplasts by Agrobacterium tumefaciens transformation, electroporation or particle bombardment and where the plants are selected from soya, barley, wheat, oilseed rape, maize and sunflower, or where the DNA is expressed in tobacco plants, especially in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Triplex formation; DNA detection; triple helix; identification; bacteria;
                                                                                       DNA encoding barley hydroxyphenylpyruvate dioxygenase - for producing plants with increased vitamin E content, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Triple helix third strand of Esterase D gene nucleotides 962-975.
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  Falk J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.8%; Score 14; DB 1; Length 14; 100.0%; Pred. No. 7.1e+02; ive 0; Mismatches 0; Indels
  Schmidt R, Kurpinska K,
                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 14 BP; 0 A; 0 C; 1 G; 13 T; 0 U; 0 Other;
                                                                                                                                                     Example 1; Page 9; 26pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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18 14; Conservative
Lerchl J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oncogene; virus; ss.
                                           WPI; 1999-096742/09
                                                                                                                                                                                                                                                                                                                                                                                  leaves or seeds
  Seulberger H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-MAR-1999
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The present sequence represents a potential triple-helix forming region. It can be used to demonstrate the assay of the invention. The assay comprises adding a sample containing double-stranded DNA test sequences, e.g. containing the present sequence, to an aqueous medium containing at least one complex of anchor DNA, attached to a solid support, and reporter DNA, where either a part of the anchor DNA or reporter DNA is sequence. Triplex formation results in displacement of the test sequence. Triplex formation results in displacement of the reporter DNA which is detected as an indication of the presence of the DNA test sequence. The method is used to detect DNA sequences, particularly for identification of bacteria (by detecting genes for ribosomal RNA) in clinical samples, but also detection of oncogenes and Hepatitis B virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assay of genetic sequences based on triplex formation from double stranded analyte - and hybrid of anchor and reporter sequences, with reporter released if triplex formation occurs, used e.g. to identify
                                                                                                                                                                                                                                         Triple-helix forming region; Triplex formation; DNA detection; identification; bacteria; oncogene; virus; ds.
                                                                                                                                                                                                       Triple helix forming nucleotides 962-975 of Esterase D gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Col 15-16; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PROF-) PROFILE DIAGNOSTIC SCI INC.
                                                                                                 AAX14688 standard; DNA; 14 BP
                                                                                                                                                                                                                                                                                                                                                                                                        93US-00173489.
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                                                                                                                                                                    (first entry)
14 AAAAAAAAAAAA 1
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                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                        22-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                       29-OCT-1992;
                                                                                                                                                                      24-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                    19-JAN-1999.
                                                                                                                                    AAX14688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bacteria
                                                           RESULT 1219
                                                                                  AAX14688
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0.8%; Score 14; DB 1; Length 14;

Query Match

The present sequence represents a polymucleotide that is able to form a triple helix with a double stranded sequence. Cytosine bases in the present can be replaced with 5-methylcytosine for increased triplex stability. The present sequence is used in the assay of the invention, where it can be part of the anchor DNA or reporter DNA sequence. The assay comprises adding a sample containing double-stranded DNA test

Assay of genetic sequences based on triplex formation from double stranded analyte - and hybrid of anchor and reporter sequences, with reporter released if triplex formation occurs, used e.g. to identify

93US-00173489. 92US-00968436, Disclosure; Col 15-16; 168pp; English.

bacteria

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Homo sapiens.
                                                                        WO9907893-A1
                                                                                                             05-AUG-1998;
                                                                                                                                 38-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-NOV-2000
                                                                                           18-FEB-1999.
                                             Synthetic
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Matches
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                                                                                                                                                                                                                                                                                                                                                                  Optical detection of hybridization complexes for specific target nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                        target nucleic acid presence in a sample. A preferred target is a Mycobacterium complex nucleic acid sequence. The detection method uses visual detection of a change in the hybridization without aid of instrumentation. Multiple copies of a target nucleic acid sequence are mixed with first and second detectable probes under hybridizing conditions favouring particle agglutination via a bridging molecule allowing for visual detection of the target nucleic acid sequence. The bridging molecule enhances or inhibits formation of a hybridization
                                                                                                                                                                              target; hybridisation; probe; primer;
                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel method for the visual detection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human senescence factor p23 T12 anchor primer SEQ ID NO:17.
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                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;
      Pred. No. 7.1e+02; Mismatches 0;
                                                                                                                                                                                                                                                                                                                              Reshatoff MR;
                                                                                                                                                                              Visual; nucleic acid detection; targe
agglutination; bridging molecule; ss
                                                                                                                                                             WO9923258 oligonucleotide primer 1.
                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 40; 46pp; English
100.0%; Pre
                                                                                                    AAX57019 standard; DNA; 14 BP
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                                   1736 AAAAAAAAAAAA 1749
                                               1 AAAAAAAAAAAAA 14
                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 AAAAAAAAAAA 1
      Local Similarity 100.
1es 14; Conservative
                                                                                                                                                                                                                                                                                                                            Weisburg WG, Stull PD,
                                                                                                                                                                                                                                                                                                         (GENP-) GEN-PROBE INC
                                                                                                                                                                                                                                                                                                                                                WPI; 1999-326994/27
                                                                                                                                                                                                                                                                                                                                                                            acid sequences.
                                                                                                                                                                                                                                                                    30-OCT-1998;
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                                                                                                                                          19-JUL-1999
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                                                                                                                                                                                                            Synthetic.
                                                                                                                       AAXS7019
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                 Matches
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The present invention describes human senescence factor p23. An expression vector for p23 is useful for inducing a senescent phenotype in expression vector for p23 is useful for inducing a senescent phenotype in a cell (preferably eukaryotic). This may help in regulating diseases, including cancer, persistent inflammation, and various proliferative and degenerative disorders. These transgenic cells are useful in gene therapy of for treating cancer, particularly where antisense oligonucleotides are useful for blocking normal or mutant p23 expression in cancer cells or other proliferating cells. Transgenic cells are also useful for producing the p23 polypeptide in large quantities. The antibodies are useful for culture and tissue biopsies. The p23 polymocleotides are useful for modulating the whole gene encoding p23, and variants of p23. Assays based on p23 elements, which detect p23 levels and activity are useful as clasolating the whole gene encoding p23, and variants of p23. Assays based on p23 elements, which detect p23 levels and activity are useful as clasolating the whole gene encoding p23, and activity are useful as clasolating the whole gene encoding p23, and variants of p23. Assays based con p23 elements for staging tumours, determining prognosis, and/or predicting therapeutic success. These elements also provide an assay for detecting chromosomal rearrangements in chromosome 3 in a human cell. The solution of the p23 polymucleotide permits the manipulation of malignant growth in cancer. The present sequence represents a primer used in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide #1 containing 3'-C-amino-5'(S)-C,3'-N-ethanothymidine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Newly isolated nucleic acid molecule (designated p23) encoding a p2
polypeptide – useful for inducing a senescence phenotype in a cell.
Human, senescence factor; p23; cancer; persistent inflammation; proliferative disorder; degenerative disorder; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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bicyclic sugar nucleoside analogue; gene probe; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.8%; Score 14; DB 1; Length 14; 100.0%; Pred. No. 7.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14 BP; 0 A; 0 C; 1 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kubbies M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 18; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA62349 standard; DNA; 14 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-US016343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-00908873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Swisshelm K, Hosier S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NPI; 1999-167454/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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AAF84160 standard; DNA; 14 BP.

RESULT 1223

AAF84160/

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The present sequence is an oligonucleotide containing 3'-C-amino-5'(S)-C'3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in the sequence were incorporated by phosphoramidite chemistry using a DNA synthesiser. Bicyclic sugar nucleosides are conformationally restricted 3',5'-bridged nucleosides which can be used as building blocks for oligonucleotides. Oligonucleotides can be produced that have certain, desired, geometrical shapes and entropy advantages. They may have superior hybridisation to DNA and RNA, and excellent biological as antisense inhibitors of gene expression or as gene probes, and may therefore be used in antisense therapeutics or gene-specific diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New conformationally restricted 3',5'-bridged nucleosides and oligonucleotides useful as antisense therapeutics or as gene-specific
                                                                                                                                                                                                                                                                                                                                                       /*tag= g
/mod_base= OTHER
/note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
                             *tag= a
/mod_base= OTHER
/oce= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
                                                                                                                                                 /mod_base= OTHER
/note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine'
                                                                                                                                                                                                       /mod_base= OTHER
/note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine'
                                                                                                                                                                                                                                                           /mod_base= OTHER
/note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine'
                                                                                                                                                                                                                                                                                                                mod_base= OTHER
'note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine'
                                                                                                           note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;
  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 20; Col 16; 10pp; English.
                                                                                              mod base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-00309742.
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                                                                               *tag=
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                                                                                                                                                                                                                                                                                                      *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ICNC ) ICN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-451496/39.
Key
modified_base
                                                                                                                      modified base
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                                                                  modified base
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                                                                                                                                                                                                                                                                                      modified base
                                                                                                                                                                                                                                                                                                                                           modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                             US6083482-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnostics.
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                                                                                                                           RNA oligonucleotide #1 used in a binding assay.
                                                                             AAC83821 standard; RNA; 14 BP
                       1736 AAAAAAAAAAAA 1749
                                                                                                            (first entry)
                                      14 AAAAAAAAAAAA 1
       14; Conservative
Local Similarity
                                                                                                                                                                         W0200066604-A2
                                                                                                                                                          Inidentified,
                                                                                                            28-FEB-2001
                                                                                             AAC83821;
                                                              RESULT 1224
       Matches
                                                                     AAC83821
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Length 14;

0.8%; Score 14; DB 1; Length 14; 100.0%; Pred. No. 7.1e+02; ative 0; Mismatches 0; Indels

1736 AAAAAAAAAAAA 1749

Conservative

Local Similarity es 14; Conser

Best Loca Matches

Query Match

14 AAAAAAAAAAA 1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to light responsive oligonucleotide, which contain one or more organic groups which can undergo structural stomerisation upon irradiation at a specific wavelength. The melting temperature of a double-strand formed by the light-responsive oligonucleotide, and another oligonucleotide complementary to the light-responsive oligonucleotide, reversibly changes depending on light irradiation. The oligonucleotides are useful in biotechnology, e.g. in controlling DNA elongation, gene expression, amplification and transcription, and for efficient gene diagnosis and gene therapy. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L-ribo-configurated Locked Nucleoside Analogue; L-ribo-LNA analogue; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               and gene expression, have structural isomerization on irradiation, and
reversible change in melting temperature of the formed double or triple
                                                                                                                                                                                                                                                                                                                                                                                                                                           Light-responsive oligonucleotides, useful in controlling DNA synthesis
                                                                                                                       Light responsive oligonucleotide; light irradiation; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence is an oligonucleotide used in the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.8%; Score 14; DB 1; Length 14;
100.0%; Pred. No. 7.1e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                       Yoshida T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Page 20; 43pp; Japanese.
                                                                                                                                                                                                                                                                  20-SEP-2000; 2000WO-JP006415
                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                         Asanuma H,
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-266061/27
                                                                                                                                                                                                                                                                                                                                      (KOMI/) KOMIYAMA M.
                                                                                      Oligonucleotide #2
                                                                                                                                                                                          WO200121637-A1
                                                                                                                                                         Unidentified.
                                                                                                                                                                                                                                                                                                 20-SEP-1999;
                                                   08-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                       Komiyama M,
                                                                                                                                                                                                                               29-MAR-2001
                  AAF84160;
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                                                                                                                                Oligomers comprising L-ribo-Locked Nucleic Acid (LNA) nucleosides, useful for therapeutic purposes e.g. in the construction of oligonucleotides, as substrates for nucleic acids polymerases and in RNA mediated catalytic
                                                                                                                                                                                                The present invention relates to an oligomer comprising L-ribo-configurated Locked Nucleoside Analogues (L-ribo-LNA analogues). The present sequence is an RNA oligomucleotide. Binding studies of the L-ribo-LNA analogues towards the present sequence were carried out, to determine the thermostability of the L-ribo-LNA analogues. The analogs of the present invention have a variety of uses e.g. in the preparation of conjugates of the L-ribo-LNA modified oligomucleotides (oligomers)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Construction of cDNA tags for identifying expressed genes with specific linkers and recognition sequences, applicable in gene expression
                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA tag; identification; gene expression analysis; linker; expressed gene identification; EGI; ss.
                                                                                                                                                                                                                                                                                               0.8%; Score 14; DB 1; Length 14;
100.0%; Pred. No. 7.1e+02;
                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                             Sequence 14 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              3GI cDNA tag related oligonucleotide SEQ ID NO:51
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                                                                                                                                                                                                                                                                                                    100.0%; Prec. ...
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                                                                                                                                                                               Example 11; Page 56; 79pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                    ABQ83278 standard; DNA; 14 BP
                                   04-MAY-1999; 99DK-0000603.
01-SEP-1999; 99DK-00001225.
11-JAN-2000; 2000DK-00000032.
                 34-MAY-2000; 2000WO-DK000225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-MAR-2002; 2002WO-JP002338
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                                                                                                                                                                                                                                                                                                                                                 18-JAN-2003 (first entry)
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                                                                                                                                                                                                                                                                                                       Local Similarity 100.
hes 14; Conservative
                                                                                                               WPI; 2001-060972/07.
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                                                                         (EXIQ-) EXIQON AS
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09-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                             Wengel J;
                                                                                                                                                                                                                                                                                                                                                                                                                        AB083278
                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                             The present invention describes a method for constructing a cDNA tag for identifying an expressed gene. The method comprises: (a) preparation of complementary deoxyribonucleic acid; (b) producing cDNA fragment by cleavage with II type restriction enzyme; (c) obtaining a linker X-CDNA fragment ligated material; (d) amplification of the linker X-CDNA tagines and attrial; and (e) cleaving the amplification product. The method can be used for the construction of cDNA tags for identifying expressed genes, which is applicable in gene expression analysis, disease diagnosis and identifying target for gene therapy, including the clarification of difference in function or morphology of cells under beysiological or pathological conditions. The cDNA or cells for assay can be especifically expressed, with reproducibility and accuracy in the detection of genes. The present sequence represents an expressed gene identification (EGI) cDNA tag related oligonucleotide which is used in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a method for constructing a cDNA tag for identifying an expressed gene. The method comprises: (a) preparation of complementary deoxyribonucleic acid; (b) producing cDNA fragment by cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA fragment ligated meterial; (d) amplification of the linker X-cDNA tag-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Construction of cDNA tags for identifying expressed genes with specific linkers and recognition sequences, applicable in gene expression analysis, disease diagnosis and identifying target for gene therapy.
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analysis, disease diagnosis and identifying target for gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 14; DB 1; Length 14;
Pred. No. 7.1e+02;
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Local Similarity 100.0%; Pred. No. '..
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                                                                        Example 1, Page 24; 59pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hirose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1274/c
ABQ83274 standard; DNA; 14 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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example from the present invention

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linker Y ligated material; and (e) cleaving the amplification product. The method can be used for the construction of cDNA tags for identifying expressed genes, which is applicable in gene expression analysis, disease diagnosis and identifying target for gene therapy, including the clarification of difference in function or morphology of cells under physiological or pathological conditions. The cDNA or cells for assay can be specifically expressed, with reproducibility and accuracy in the detection of genes. The present sequence represents an expressed gene identification (EGI) cDNA tag related oligonucleotide which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Construction of cDNA tags for identifying expressed genes with specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linkers and recognition sequences, applicable in gene expression analysis, disease diagnosis and identifying target for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA tag; identification; gene expression analysis; linker; expressed gene identification; EGI; ss.
                                                                                                                                                                                        Score 14; DB 1; Length 14;
Pred. No. 7.1e+02;
                                                                                                                                                                                                                    0; Indels
                                                                                                                                                             Sequence 14 BP; 0 A; 0 C; 1 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                    EGI cDNA tag related oligonucleotide SEQ ID NO:50.
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                                                                                                                                                                                                 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamamoto M, Yamamoto N, Hirose K,
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                                                                                                                                                                                         0.8%;
                                                                                                                                                                                                                                                                                                                                                ABQ83277 standard; DNA; 14
                                                                                                                                                                         Query Match
Best Local Similarity 100..
Best 14; Conservative
                                                                                                                                                                                                                                                                           14 ACAAAAAAAAAA 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200274951-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
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                                                                                                                                                                                                                                                                                                                        RESULT 1227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detection of genes. The present sequence represents an expressed gene identification (EGI) cDNA tag related oligonucleotide which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a method for constructing a cDNA tag for identifying an expressed gene. The method comprises: (a) preparation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Construction of cDNA tags for identifying expressed genes with specific linkers and recognition sequences, applicable in gene expression analysis, disease diagnosis and identifying target for gene therapy.
                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA tag; identification; gene expression analysis; linker; expressed gene identification; EGI; ss.
                                                                      Query Match 0.8%; Score 14; DB 1; Length 14; Best Local Similarity 100.0%; Pred. No. 7.1e+02; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.8%; Score 14; DB 1; Length 14;
100.0%; Pred. No. 7.1e+02;
tive 0; Mismatches 0; Indels
                                     Sequence 14 BP; 0 A; 0 C; 1 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                  EGI cDNA tag related oligonucleotide SEQ ID NO:42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kasai J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamamoto M, Yamamoto N, Hirose K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 24; 59pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KURE ) KUREHA CHEM IND CO LTD
                                                                                                                                                                                                                                                                                   ABQ83269 standard; DNA; 14 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-MAR-2001; 2001JP-00073959.
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Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (YAMA/) YAMAMOTO M. (YAMA/) YAMAMOTO N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200274951-A1.
                                                                                                                                                                                                                                                                                                                                                              18-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                         ABQ83269;
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1736 AAAAAAAAAAAA 1749

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The present invention describes a method for constructing a cDNA tag for identifying an expressed gene. The method comprises: (a) preparation of complementary decoxyribonucleic acid; (b) producing cDNA fragment by cleavage with II type restriction enzyme; (c) obtaining a linker X-CDNA fragment Ligated material; (d) amplification of the linker X-CDNA taglinker Y ligated material; and (e) cleaving the amplification product. The method can be used for the construction of cDNA tags for identifying expressed genes, which is applicable in gene expression analysis, disease diagnosis and identifying target for gene therapy, including the physiological or pathological conditions. The cDNA or cells for assay can be specifically expressed, with reproducibility and accuracy in the detection of genes. The present sequence represents an expressed gene identification (EGI) cDNA tag related oligonucleotide which is used in an

Example 1; Page 24; 59pp; Japanese

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Detecting single nucleotide polymorphism for expressing sensitivity information of diseases and drugs, comprises using a new oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a method for detecting single nucleotide polymorphisms (SNPs). Also described is an oligonucleotide used in the detection of an SNP, prepared by binding an oligonucleotide having a complementary sequence or those devoid of up to several bases with 1 or more organic group(s) to be tested by light irradiation of a specific wave length to vary a double strand formation property of the oligonucleotide to be tested. The method is used for detecting SNPs. The present sequence represents a light responsive oligonucleotide which is used in an example from the present invention
                                                            Light responsive; detection; single nucleotide polymorphism; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.8%; Score 14; DB 1; Length 14; Best Local Similarity 100.0%; Pred. No. 7.1e+02; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;
Light responsive oligonucleotide (X1) T14.
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                                                                                            irradiation; ss.
                                                                                                                                                                                                               JP2001346579-A.
                                                                                                                                                                                                                                                                            18-DEC-2001.
                                                                                                                                                      Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New DNA fragments having promoter activity, useful in retinoid metabolism, as well as in producing retinoic acid metabolizing cytochrome P450s that are useful as targets for the treatment of certain cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to retinoid (e.g., retinoic acid (RA), vitamin A) metabolising proteins and nucleic acid sequences encoding them. RA metabolising proteins contain a hasme-blinding motif which is characteristic of the group of proteins known as cytochrome P450s. The sequences of the invention are useful in retinoid metabolism and in particularly useful as targets for the treatment of certain cancers such as prostate cancer. The invention also relates to a method of screening drugs for their effect on activity of RA inducible proteins. The present DNA sequence is poly(T) PCR primer which is used for isolating retinoid regulating genes by differential display of mRNAs
                                                                                                                                                                                                                                                                                                                                                                                                                         Retinoid metabolism; retinoic acid; RA; haeme-binding motif; vitamin A; cytochrome P450; prostate cancer; drug screening; PCR primer; retinoid-regulated gene; ss.
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100.0%; Pred. No. 7.1e+02;
rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                      Retinoid-regulated gene isolating poly(T) PCR primer #3
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96US-00724466.
97WO-CA000440.
                                                                                                                                                                                   AAD24489 standard; DNA; 14 BP
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                               1 AAAAAAAAAAA 14
                                                                                                                                                                                                                                                                                                         07-MAR-2002 (first entry)
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01-OCT-1996;
23-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JUN-1997;
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                                                                                                                                                                                                                                               AAD24489;
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AAD24489/ID AAD2
XXX AAD2
XXX AAD2
XXX AAD2
XXX CYCO
XXX UNid
XXX U
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ASANUMA H.

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Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; atheroselerosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
                                                                                                                                                                                                                 Mouse ICAM hammerhead ribozyme target sequence (nt. position 510).
                                                                                      AAT52238 standard; RNA; 15 BP
                                                                                                                                                                             (first entry)
14 AAAAAAAAAAA 1
                                                                                                                                                             (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aus musculus
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Gaps .; 0

1734 ACAAAAAAAAAA 1747

14; Conservative

Best Local Similarity

Matches

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Gaps

us10008789-3.rng

Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; atheroselerosis; myoardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;

Mus musculus. WO9523225-A2

Mouse relA hammerhead ribozyme target sequence (nt. position 129)

(first entry) (revised)

25-MAR-2003 07-APR-1997

AAT54816;

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The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the nucleotide base position indicated in the DE line. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes cleave the ICAM-1 target sequences and thereby inhibit ICAM-1 expression, making them useful for reducing transplant rejection and alleviating symptoms in patients with rheumatoid arthritis, asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                              b DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
Usman N, Wincott FE, Woolf T;
                                                                                                                                                                                                                                                                                                                                                                             Ribozymes having modified bases and methods for producing them - for use in inhibiting disease related genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.8%; Score 14; DB 1; Length 15;
100.0%; Pred. No. 7.5e+02;
rative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 177; 407pp; English.
                                   94US-00201109.
94US-00218334.
94US-00224483.
94US-00227958.
94US-00227958.
94US-0021280.
94US-0029133.
94US-0029133.
94US-0029133.
94US-00311486.
94US-00311486.
94US-00311486.
94US-00311486.
94US-00311486.
94US-00311486.
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94US-00345516.
94US-00357577.
                  95WO-IB000156
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95US-00380734
                                                                                                                                                                                                                                                                                            (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-351090/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                               Stinchcomb DT,
                                                                                                                                                                                                         07-OCT-1994;
11-OCT-1994;
04-NOV-1994;
                                                                        15-APR-1994;
15-APR-1994;
18-MAY-1994;
                                                                                                    06-JUL-1994;
                                                                                                                                                                                                                                    10-NOV-1994;
28-NOV-1994;
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                  23-FEB-1995;
                                                                                                                        16-AUG-1994;
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                                                                                                                                                  02-SEP-1994;
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31-AUG-1995
                                                                 07-APR-1994
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Modak A,
Tracz D,
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The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves relA mRNA at the nucleotide base position indicated in the DE line. The relA gene product is a subunit of the transcriptional regulator NF-kappaB and is implicated specifically in the induction of inflammatory responses. Regions of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thompson JD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grimm S, Karpeisky S, Kisich K, Matuli Laget N, Kudyigen JA;
Modak A, Pavoc P, Beigleman L, Sullivan SM, Sweedler D, Thompse
Tracz D, Usman N, Wincott FE, Woolf T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dudycz LW;
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                                                                                94US-00201109.
94US-00218934.
94US-00222495.
94US-00221958.
94US-0021280.
94US-00211280.
94US-00211280.
94US-00211280.
94US-00211280.
94US-00211280.
94US-00211439.
94US-003114397.
94US-00311486.
94US-00311497.
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94US-00363233.
95US-00380734.
                                            95WO-IB000156
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19-AUG-1994;
02-SEP-1994;
                                            23-FEB-1995;
31-AUG-1995
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07-OCT-1994
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Gaps

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AAT54816 standard; RNA; 15 BP.

AAT54816 ID AAT5

RESULT 1232

257 CCCACGGAGCAGCA 270

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14; Conservative

Matches

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mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes are designed to cleave the target sequences and thereby inhibit rela expression, making them potentially useful for treating rheumatoid arthritis, restenosis and asthma as well as for increasing tolerance to transplanted tissues. The potential immunosuppressive properties of a ribozyme that cleaves relA mRNA means that uses are limited to local delivery, acute indications or ex vivo treatment. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; attoke; restenosis; transplant rejection; rheumatoin attoke; restenosis; transplant rejection; rheumatoin atthitis; psoriasis; myocardial infarction; attoke; testenosis; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ICAM hammerhead ribozyme target sequence (nt. position 2912)
                                                                                                                                                                                                                      Similarity 78.6%; Pred. No. 7.5e+02;
11; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                          Sequence 15 BP; 1 A; 5 C; 5 G; 0 T; 4 U; 0 Other;
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94US-00218934.
94US-00224483.
94US-00224483.
94US-00228041.
94US-0021932.
94US-00291832.
94US-00291832.
94US-00291832.
94US-00391839.
94US-00391839.
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94US-00316771.
94US-00319492.
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(first entry)
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Best Local Similarity 78.6
Matches 11, Conservative
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07-OCT-1994;
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25-MAR-1997
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15-APR-1994;
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02-SEP-1994
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                                                                                                                                                                               Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
Tracz D, Usman N, Wincott FE, Woolf T;
                                                                                                                                                                                                                                                                                                                Ribozymes having modified bases and methods for producing them - for use in inhibiting disease related genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; atheroselerosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoin arthitis; psoriasis; myocardial; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.8%; Score 14; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 7.5e+02; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15 BP; 0 A; 1 C; 0 G; 0 T; 14 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 175; 407pp; English.
94US-00321993.
94US-00334847.
94US-00337608.
94US-00355716.
94US-00353233.
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                                                                                                             95US-00380734
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                                                                                                                                                (RIBO-) RIBOZYME PHARM INC.
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(first entry)
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11-OCT-1994;
04-NOV-1994;
10-NOV-1994;
28-NOV-1994;
16-DEC-1994;
23-DEC-1994;
30-JAN-1995;
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09-MAR-1997
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94US-00201109.
94US-00218934
94US-00224483.
94US-00224481
94US-0022641.
94US-0021932.
94US-0029132.
94US-0029132.
94US-0029132.
94US-00311439.
94US-00311439.
94US-00311439.
94US-00311439.
                                                                                                                                94US-00334847.
94US-00337608.
94US-00345516.
94US-00357577.
           95WO-IB000156
                                                                                                                                                       94US-00363233
                                                                                                                                                            95US-00380734
                                                                                                                                                                       (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                            WPI; 1995-351090/45.
                                                                                                                                                                                  Stinchcomb DT,
                                                                                19-AUG-1994;
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10-NOV-1994;
                                                 15-APR-1994;
                                                      18-MAY-1994;
                                                                     16-AUG-1994;
                                                                            17-AUG-1994;
                                                                                            08-SEP-1994;
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31-AUG-1995
                                           15-APR-1994
                                                                                                                                            28-NOV-1994;
                                                                                                                                                 16-DEC-1994
                                                                                                                                                                                       Grimm S,
Modak A,
Tracz D,
82
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o DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
Karpelsky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
Pavco P, Belgleman L, Sullivan SM, Sweedler D, Thompson JD;
Usman N, Wincott FE, Woolf T;

Ribozymes having modified bases and methods for producing them - for use in inhibiting disease related genes.

Claim 2; Page 172; 407pp; English.

The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease resistance. The ribozymes cleave the ICAM-1 target sequences and thereby inhibit ICAM-1 expression, making them useful for reducing transplant rejection and alleviating symptoms in patients with rheumatoid arthritis, asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to correct PI field.)

Sequence 15 BP; 0 A; 4 C; 7 G; 0 T; 4 U; 0 Other;

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Query Match 0.8%; Score 14; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 7.5e+02; Matches 14; Conservative 0; Mismatches 0; Indels
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Gaps

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RESULT 1235 AAT52134,

AATS2134 standard; RNA; 15 BP AAT52134

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Enzymatic nucleic acid, ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel A; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RS, bcr-abl; oncogene; translocation; chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; inflammation; autoimmune disease; atherosclerosis; myocardial infarction; stroke; restenosis; transplant rejection; rheumatoid arthritis; psoriasis; myocardial; Kawasaki disease; septic shock; HIV; myocardial; Kawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
                                       Human ICAM hammerhead ribozyme target sequence (nt. position 2909).
                                                                                                                                                                                                                                                                                                                                                                                                                           940S-00316771.
940S-00319492.
940S-00331847.
940S-00334847.
940S-00337608.
                                                                                                                                                                                                                                                       94US-00201109.
94US-00218934.
94US-0022795.
94US-00227958.
94US-00227958.
94US-00211280.
94US-00271280.
94US-00292620.
94US-00292620.
94US-002932.
94US-00303039.
94US-00303039.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (RIBO-) RIBOZYME PHARM INC.
                    (first entry)
           (revised)
                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                         17-AUG-1994;
19-AUG-1994;
02-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                     08-SEP-1994;
23-SEP-1994;
23-SEP-1994;
28-SEP-1994;
          25-MAR-2003
25-MAR-1997
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07-OCT-1994;
11-OCT-1994;
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Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
Stinm S, Karpelsky A, Risich K, Matulio-Adamic J, Mcswiggen JA;
Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
Tracz D, Usman N, Wincott FE, Woolf T; Ribozymes having modified bases and methods for producing them - for use in inhibiting disease related genes. WPI; 1995-351090/45. Stinchcomb

The present sequence represents a preferred target sequence for an enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the nucleotide base position indicated in the DE line. Regions of the mRNA that do not form secondary folding structures and that contain potential hammerhead and hairpin ribozyme cleavage sites were identified by computer analysis. Ribozymes directed against these mRNA sequences were

Claim 2; Page 175; 407pp; English.

us10008789-3.rng

(first entry)

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3astric acid production inhibiting oligonucleotide SEQ ID NO: 90.
                                                                                                                                                Gastric acid disturbance, gastric reflux, gastritis, dyspepsia, stomach ulcer, duodenal ulcer, Helicobacter pylori, antisense;
                                    AAF16603 standard; DNA; 15 BP.
                                                                                                                                                                                                                                                                                          24-MAY-2000; 2000WO-AU000498.
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-025093/03.
                                                                                                                                                                             DNA-RNA hybrid; ss
                                                                                                                                                                                                                                                                                                                                                (TACH/) TACHAS G.
                                                                                                                                                                                                                                    WO200071164-A1.
                                                                                                                                                                                                           Homo sapiens.
                                                                                            13-MAR-2001
                                                                                                                                                                                                                                                                                                                     24-MAY-1999;
                                                                                                                                                                                                                                                              30-NOV-2000
                                                                AAF16603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF49042;
                                                                                                                                                                                                                                                                                                                                                                             Tachas G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                       AAF16603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma) K-delta-N3'; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; v = adennine, guanine or cytosine; N = adenine, guanine, cytosine or thymine; gamma = thymine; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene
designed and synthesised with modifications that improve their nuclease resistance. The ribozymes cleave the ICAM-1 target sequences and thereby inhibit ICAM-1 expression, making them useful for reducing transplant rejection and alleviating symptoms in patients with rhumatoid arthritis, asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                       RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
                                                                                                                                                                Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptides having at least two new nucleotides - useful as primers in PCR.
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0
                                                                                                                                  0.8%; Score 14; DB 1; Length 15;
100.0%; Pred. No. 7.5e+02;
vative 0; Mismatches 0; Indels
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                                                                                                       Sequence 15 BP; 1 A; 0 C; 0 G; 0 T; 14 U; 0 Other;
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100.0%; Pred. No. 7.5e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                          RT-PCR primer of the invention SEQ ID 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 10; 19pp; Japanese.
                                                                                                                                                                                                                                                                                           ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97JP-00208312.
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AAX18364 standard; DNA; 15
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                                                                                                                                                               14; Conservative
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                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                11-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JUL-1997;
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                                                                                                                                                                               The present invention provides oligonucleotides, and methods for their use, which are useful in modulating the action of proteins involved in gastric acid production. The target protein is preferably the histamine H2 receptor or one of the proteins which form part of the gastric proton pump. The sequences and methods of the invention are useful in the treatment of gastric rellux, gastritis, dyspepsia, stomach ulcers, duodenal ulcers and other gastric acid disturbances, most of which are caused by Helicobacter pylori
Treating gastric acid disturbance by administering an oligonucleotide which modulates the activity of a polypeptide involved in gastric acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.8%; Score 14; DB 1; Length 15;
100.0%; Pred. No. 7.5e+02;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15 BP; 14 A; 0 C; 0 G; 1 T; 0 U; 0 Other;
                                                                                                                           Example 3; Page 148; 164pp; English.
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                                                                    production or secretion.
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0; Indels

1735 CAAAAAAAAAAA 1748

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Best Local Similarity 100. Matches 14; Conservative

CAAAAAAAAAAA 1

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Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
neovascular condition of the retina; ss.
                                                                                                                   Wraight CJ, Werther GA, Edmondson SR;
                                                                                                 (MURD-) MURDOCH CHILDRENS RES INST.
                                                                  21-JUN-2000; 2000WO-AU000693,
                                                                                  99US-0140345P.
                                                                                                                                  WPI; 2001-041421/05.
                                 WO200078341-A1
                 Homo sapiens.
                                                                                                                                                                           inflammation.
                                                                                  21-JUN-1999;
                                                 28-DEC-2000.
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The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligomucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBB]-2 or IGFBB], which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligomucleotide which can be used to design the antisense oligomucleotide of the present invention (see AAF4151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic brain or skin, growth factor-mediated malignancies, other sclerotic Example 8; Page 60; 201pp; English. vessels or any other hyperplasia

Sequence 15 BP; 1 A; 0 C; 1 G; 13 T; 0 U; 0 Other;

Score 14; DB 1; Le Pred. No. 7.5e+02; Match
Local Similarity 100.0%; Pred. No. /.. 1735 CAAAAAAAAAAA 1748 14 CAAAAAAAAAA 1 Query Match Matches ઠે 셤

RESULT 1239

ABK98169 standard; DNA; 15 BP ABK98169; 

Triple helix forming associated oligonucleotide #39.

(first entry)

07-OCT-2002

Triple-helix formation; purine-rich target sequence; double-helix DNA; gene expression; regulatory sequence; pathogenic double-stranded DNA; pathogenic bacteria; virus; replication; virulence; cancer; concer; oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

Synthetic

US6403302-B1

11-JUN-2002

93US-00168920. 16-DEC-1993;

92US-00946976,

(CALY ) CALIFORNIA INST OF TECHNOLOGY.

Dervan PB, Beal PA;

WPI; 2002-536030/57

A triple-helix comprising a double helical nucleic acid (DHNA) and an olisonuclectide which binds in parallel and antiparallel orientation, respectively, for targetting sequences on alternate strands of DHNA to control gene expression.

Example 6; Fig 20A; 108pp; English

The present invention relates to methods and oligonucleotides for forming a triple-helix comprising a double helical nucleic acid comprising first and second substantially complementary strands, and an oligonucleotide bound to a putine-rich target sequence within the double helical nucleic acid, where the oligonucleotide binds in a parallel and antiparallel or orientation, respectively, to target sequences on alternate strands of the double helical nucleic acid. The method has therapeut. applications, where gene expression is controlled by selective triple-helix formation within expression regulatory sequences of a target gene. The oligonucleotides can be used to form triple-helices, and are useful to detect the presence or absence of specific sequences within genomic DNA for diagnostic and therapeutic purposes. The oligonucleotides can be selected to specific and therapeutic purposes. The oligonucleotides can be selected to specific and therapeutic purposes. The oligonucleotide can be chosen to target a unique sequence of the pathogen which is not found in the genome of pathogenic of triple-helix cupin confidence and be used in cancer treatment by way of triple-helix suppression of specific oncogenes including those of endogenous or viral conjun. Such therapeutic oligonucleotides are capable of forming triple-helices with such sequences in cancer treatment by way of triple-helix conjun. Such therapeutic oligonucleotides are capable of forming triple-helices with such sequences in cancer treatment by way of triple-helix conjuncated the present sequences and concerned and concerned consing concerns an oligonucleotide used in the methods of the present invention

Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

Gaps ö Length 15; 1; Indels Query Match 0.8%; Score 14; DB 1; I Best Local Similarity 93.3%; Pred. No. 7.5e+02; Matches 14; Conservative 0; Mismatches 1;

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Gaps . 0

Length 15; 0; Indels ö

g

ABK98187 standard; DNA; 15 RESULT 1240 ABK98187,

BP

ABK98187;

(first entry) 07-0CT-2002

Triple helix forming associated oligonucleotide #51.

Triple-helix formation; purine-rich target sequence; double-helix DNA; gene expression; requilatory sequence; pathogenic double-stranded DNA; pathogenic bacteria; virus; replication; virulence; cancer; cancer oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss. BXBXBXBXBXGXGX

Synthetic.

JS6403302-B1

11-JUN-2002.

Triple-helix formation; purine-rich target sequence; double-helix DNA; gene expression; regulatory sequence; pathogenic double-stranded DNA; pathogenic bacteria; virus; replication; virulence; cancer; oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss. Triple helix forming associated oligonucleotide #38. ABK98168 standard; DNA; 15 BP 1736 AAAAAAAAAAAAA 1750 07-OCT-2002 (first entry) AAAAAANAAAAAA 14; Conservative Local Similarity US6403302-B1 Dervan PB, Synthetic. ABK98168; Query Match ઠે 셤

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The present invention relates to methods and oligonucleotides for forming a triple-helix comprising a double helical nucleic acid comprising first and second substantially complementary strands, and an oligonucleotide bound to a purine-rich target sequence within the double helical nucleic acid, where the oligonucleotide binds in a parallel and antiparallel corientation, respectively, to target sequences on alternate strands of the double helical nucleic acid. The method has therapeutic applications, where gene expression is controlled by selective triple-helix formation within expression regulatory sequences of a target gene. The oligonucleotides can be used to form triple-helices, and are useful to detect the presence or absence of specific sequences within genomic DNA coligonucleotides can be used to form triple-helicetides can be elected to specific and therapeutic purposes. The oligonucleotides can be become to target sense can be selected to specific and therapeutic purposes. The oligonucleotides can be chosen to target to viruses for the oligonucleotides can be chosen to target a unique sequence of the coligonucleotides can be chosen to target a unique sequence of the coligonucleotides can be chosen to target a unique sequence of pathogen which is not found in the genome of pathogen's host. The pathogen which is not found in the genome of pathogen's host. The coligonucleotides and be chosen to target the anique sequence of endogenous or viral coligonucleotides are capable of forming triple-coligon. Such therapeutic oligonucleotides are capable of forming triple-coligonucleotides with such sequences in cancer treatment by way of triple-helix coligonucleotides are capable of containing the activated concogene, so preferentially killing or repressing the cancer causing call. The present sequence represents an oligonucleotide are capable of the present invention
The present invention relates to methods and oligonucleotides for forming a triple-helix comprising a double helical nucleic acid comprising first and second substantially complementary strands, and an oligonucleotide bound to a purine-rich target sequence within the double helical nucleic acid, where the oligonucleotide binds in a parallel and antiparallel confentation, respectively, to target sequences on alternate strands of the double helical nucleic acid, The method has therapeutic applications, where gene expression is controlled by selective triple-helix formation within expression is controlled by selective triple-helix formation of the presence or absence of specific sequences within genomic DNA coligonucleotides can be used to form triple-helices, and are useful to detect the presence or absence of specific sequences within genomic DNA coligonucleotides can be be used to form triple-helices, and are useful to selected to apecifically bind to patchogenic double-stranded DNA including specific sequences required by pathogenic bacteria or viruses for replication or virulence, reducing their pathogen; shost: The present sort found in the genome of pathogen's host: The coligonucleotides can be used in cancer treatment by way of triple-helix suppression of specific oncogenes including those of endogenous or viral origin. Such therapeutic oligonucleotides are capable of forming triple-balless with such sequences in cancer treatment by was of triple-helix oncogenes with such sequences in cancer causing cell. The present sequence represents an oligonucleotide used in the
                                                                                                                                                                                                                                                                                                                                                                                                       A triple-helix comprising a double helical nucleic acid (DHNA) and an oligomuclectide which binds in parallel and antiparallel orientation, respectively, for targetting sequences on alternate strands of DHNA to control gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell. The present sequence represents an oligonucleotide used in the methods of the present invention
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                                                                                                                                                                                (CALY ) CALIFORNIA INST OF TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 7; Fig 24A; 108pp; English.
                                   93US-00168920.
                                                                                                         92US-00946976
                                                                                                                                                                                                                                                          Beal PA;
                                                                                                                                                                                                                                                                                                                                 WPI; 2002-536030/57.
                                                                                                             17-SEP-1992;
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oligonucleotide which binds in parallel and antiparallel orientation, respectively, for targetting sequences on alternate strands of DHNA to

Example 6; Fig 20A; 108pp; English.

control gene expression.

A triple-helix comprising a double helical nucleic acid (DHNA) and an

WPI; 2002-536030/57.

(CALY ) CALIFORNIA INST OF TECHNOLOGY.

9305-00168920 92US-00946976

16-DEC-1993; 17-SEP-1992;

11-JUN-2002

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                                                                                                                                                                                                                                                                                                                 Triple-helix formation; purine-rich target sequence; double-helix DNA; gene expression; regulatory sequence; pathogenic double-stranded DNA; pathogenic bacteria; virus; replication; virulence; cancer; oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
                                                          Gaps
                                                          ö
                            0.8%; Score 14; DB 1; Length 15;
33.3%; Pred. No. 7.5e+02;
lve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                      Triple helix forming associated oligonucleotide #37.
Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;
                                                                                         1736 AAAAAAAAAAAA 1750
                                                                                                                                                                                               ABK98167 standard; DNA; 15 BP
                                          93.3%;
                                                                                                                    15 AAAAAANAAAAAA 1
                                                                                                                                                                                                                                                          (first entry)
                                                          14; Conservative
                                          Local Similarity
                                                                                                                                                                                                                                                          07-OCT-2002
                                                                                                                                                                                                                             ABK98167;
                               Query Match
                                                                                                                                                                   RESULT 1242
                                                           Matches
                                                                                                                                                                                 ABK98167
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Gaps

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i, Indels

0; Mismatches

US6403302-B1

Synthetic.

93US-00168920 92US-00946976.

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Gaps ö

0; Mismatches

14, Conservative

Matches

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1736 AAAAAAAAAAAA 1750 AAAAAAAAAAAAA 1

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Triple helix forming associated oligonucleotide #50. ABK98186 standard; DNA; 15 07-OCT-2002 (first entry) ABK98186; RESULT 1243 

Triple-helix formation; purine-rich target sequence; double-helix DNA; gene expression; regulatory sequence; pathogenic double-stranded DNA; pathogenic bacteria; virus; replication; virulence; cancer; cancer; oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

Synthetic

artiple-helix computation tenance to mertions and objects to the comprising a double helical nucleic and second substantially complementary strands, and an oligonucleotide bound to a purine-rich target sequence within the double helical nucleic acid, where the oligonucleotide binds in a parallel and antiparallel or crientation, respectively, to target sequences on alternate strands of the double helical nucleic acid. The method has therapeutic applications, where gene expression is controlled by selective triple-helix formation within expression regulatory sequences of a target gene. The oligonucleotides can be used to form triple-helices, and are useful to detect the presence or absence of specific sequences within genomic DNA for diagnostic and therapeutic purposes. The oligonucleotides can be selected to specifically bind to pathogenic double-stranded DNA including selected to specifically bind to pathogenic double-stranded DNA including selected to specific sequence required by pathogenic bacteria or viruses for replication or virulence, reducing their pathogenicity. Alternatively, the oligonucleotide can be chosen to target a unique sequence of the pathogen which is not found in the genome of pathogen's host. The presence can be used in cancer treatment by way of triple-helices with such sequences including those of endogenous or viral origin. Such therapeutic oligonucleotides are capable of forming triple-helices with such sequences in cancer causing the cancer causing one of a preferentially killing or repressing the cancer causing calls. The presents equence represents an oligonucleotide used in the The present invention relates to methods and oligonucleotides for forming A triple-helix comprising a double helical nucleic acid (DHNA) and an olisonuclectide which binds in parallel and antiparallel orientation, respectively, for targetting sequences on alternate strands of DHNA to control gene expression. (CALY ) CALIFORNIA INST OF TECHNOLOGY. Example 7; Fig 24A; 108pp; English. methods of the present invention Dervan PB, Beal PA; WPI; 2002-536030/57. US6403302-B1 16-DEC-1993; 17-SEP-1992; 11-JUN-2002 The present invention relates to methods and oligomucleotides for forming a triple-helix comprising a double helical nucleic acid comprising first and second substantially complementary strands, and an oligomucleotide bound to a purine-rich target sequence within the double helical nucleic acid, where the oligomucleotide binds in a parallel and antiparallel or orientation, respectively, to target sequences on alternate strands of the double helical nucleic acid. The method has therapeutic applications, where gene expression is controlled by selective triple-helix formation within expression regulatory sequences of a target gene. The oligomucleotides can be used to form triple-helices; and are useful to detect the presence or absence of specific sequences within genomic DNA for diagnostic and therapeutic purposes. The oligomucleotides can be constituted by pathogenic double-stranded DNA including selected to specifically bind to pathogenic double-stranded DNA including specific sequences required by pathogenic bacteria or viruses for replication or virulence, reducing their pathogenicity. Alternatively, the oligomucleotides can be chosen to target a unique sequence of the pathogen which is not found in the genome of pathogen of forming triple-helix suppression of specific oncogenes including those of endogenous or viral corigin. Such therapeutic oligomucleotides are capable of forming triple-helix suppression of specific oncogenes including those of endogenous or viral corigin such herapeutic oligomucleotides are capable of forming triple-helix coligomucleotides can be ensed in cancer capable of forming triple-helix coligomucleotides each septement and pathogenic calls in the cancer causing colliginally willing or repressing the cancer causing the ensemble triple pathogen in the colligomucleotide can be the colligomucleotide are oligomucleotide in the cancer causing colliginal triple colliginal triple colliginal triple cancer is not of specific oncogenes. A triple-helix comprising a double helical nucleic acid (DHNA) and an oligonucleotide which binds in parallel and antiparallel orientation, respectively, for targetting sequences on alternate strands of DHNA to control gene expression. Score 14; DB 1; Length 15; Pred. No. 7.5e+02; 0; Mismatches 1; Indels Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other; (CALY ) CALIFORNIA INST OF TECHNOLOGY. Example 6; Fig 20A; 108pp; English. methods of the present invention 0.8%; 93US-00168920 92US-00946976 Beal PA; WPI; 2002-536030/57. Query Match Best Local Similarity 16-DEC-1993; 17-SEP-1992; 11-JUN-2002. Dervan PB,

Gaps ö 0.8%; Score 14; DB 1; Length 15; 13.3%; Pred. No. 7.5e+02; ve 0; Mismatches 1; Indels Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other; EST polymorphic DNA repeat polynucleotide #158. ABX79833 standard; cDNA; 15 BP 1736 AAAAAAAAAAAAA 1750 93.3%; 15 AAAAAANAAAAAA 1 17-APR-2003 (first entry) Query Match 0.8 Best Local Similarity 93.3 Matches 14; Conservative ABX79833; RESULT 1244 ABX79833 셤 ò

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EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat; polymorphic marker prediction of ubiquitous simple sequences; POMPOI Rep-X; human; genetic disease; drug-treatment; Machado-Joseph; Haw River syndrome; Huntington's disease; fragile-X syndrome; Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia; spinal atrophy; bulbar atrophy; spinocerebellar ataxis.

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repeat within a coding sequence (expressed sequence tag, PST), which comprises detecting tandem repeats in a target coding sequence, scoring the repeats for polymorphic probability and generating a dataset correlating the repeats with polymorphic probability to identify a candidate polymorphic repeat. The computational methods (polymorphic marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are useful for identifying and detecting candidate polymorphic repeats in human genes, which can be used to understand, treat or eliminate genetic diseases, predispositions or adverse drug-treatment reactions. Examples of diseases linked to nucleotide repeats are Machado-Joseph, Haw River syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis, myotomic dystrophy, hyperandrogensemia, spinal and bulbar atrophy and expinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are the polymorphic repeats identified for a search of human ESTS
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                                                                                                                                                                                                                                                                                                                                                                                       The invention discloses a method for identifying a candidate polymorphic
                                                                                                                                                                                                                                                                                         tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RT-PCR primer; DNA sequence determination; gene sequence analysis; ss
                                                                                                                                                                                                                                                                    Identifying a candidate polymorphic repeat within a coding sequence, understanding or treating genetic disease, comprises detecting tandem repeats in a target coding sequence and scoring the repeats for polymorphic probability.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.8%; Score 14; DB 1; Length 15; 93.3%; Pred. No. 7.5e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;
                                                                                                                                                                                                            Fondon JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RT-PCR primer of the invention SEQ ID 3.
                                                                                                                                                                                                                                                                                                                                                      Example; Col 747; 588pp; English.
                                                                                                                                                                                                            Minna JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1736 AAAAAAAAAAAAA 1750
                                                                                                           99US-00475947.
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AAX18362 standard, DNA, 16
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                                                                                                                                                                           (TEXA ) UNIV TEXAS SYSTEM
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hes 14, Conservative
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                                                                                                                                                                                                           Sarner HR, Wren JD,
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                Homo sapiens
                                             US6472154-B1
                                                                                                             31-DEC-1999;
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                                                                             29-OCT-2002
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Matches
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                                                                                                                 RT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.8%; Score 14; DB 1; Length 16;
100.0%; Pred. No. 7.88+02;
:ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16 BP; 1 A; 1 C; 0 G; 14 T; 0 U; 0 Other;
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                                                                                                                                                                                                  Disclosure; Page 10; 19pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Page 10; 19pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX18369 standard; DNA; 16 BP
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(TAKI ) TAKARA SHUZO CO LID.
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                                                        WPI; 1999-183822/16
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useful as primers for RT-PCR and determination of base sequences. The r
sequences allow for reproductive and highly efficient analysis of gene
                                                                         Sequence 16 BP; 1 A; 1 C; 0 G; 14 T; 0 U; 0 Other;
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Matches 14; Conservative
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0.8%; Score 14; DB 1; Length 16; 100.0%; Pred. No. 7.8e+02; cive 0; Mismatches 0; Indels

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BP.
AAZ40730 standard; DNA; 16
                          AAZ40730;
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21-FEB-2000 (first entry)

VHalphaTAG; anti-tumour associated sialylated glycoprotein antigen; TAG-72; variable region; heavy chain; carcinoma; detect; tumour; ss; mouse-human chimeric antibody; therapeutic agent; intraoperative therapy; Primer for sequencing the heavy chain of antibody CC83. primer.

US5993813-A. Synthetic. Mus sp. RESULT 11

AAZ40730

AAZ40

88US-00259943. 88US-00261942. 89US-00424362. 93US-00040687. 97US-00822028, 19-0CT-1988; 24-0CT-1988; 19-0CT-1989; 31-MAR-1993; 24-MAR-1997; 30-NOV-1999

Anderson WHK; Kaplan DA, Schlom J, Gourlie BB, Mezes PS, Rixon MW;

(DOWC ) DOW CHEM CO.

WPI; 2000-038240/03.

mouse-human chimeric antibody, useful for in vivo diagnosis of cancer

Example; Col 37; 120pp; English

variable region exons and heavy chain variable region exons of antibodies coty and coss. The Cantibodies are directed against TAG-72, and are produced from the rearrangement of WhalpharRG (AAZ4701). The antibodies are used in the invention which relates to a new anti-tumour associated sialylated glycoprotein antigen (TAG)-72 mouse-human chimeric antibody. The variable region of the antibody has a heavy chain (VH) where VH is choosed by a DNA sequence homologous to the VHalpharAG germline gene. The invention includes a method for in vivo carcinoma targeting through the administration to an animal of an anti-TAG-72 mouse-human chimeric antibody produced by specific cell lines. The antibody or a fragment are conjugated to an imaging marker or therapeutic agent, in a pharmaceutically acceptable, nontoxic, sterile carrier. The chimeric antibody binds to TAG-72 which is found on certain human tumour cells. The tissue regions containing the tumours can be detected via the markers and/or can be treated via the therapeutic agents. The method is useful for in vivo diagnosis and treatment of cancer by administering to an AAZ40722-Z40734 are primers used in the sequencing of the light chain

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                                                                                                                                                                                                                                                                                     VHalphaTAG; anti-tumour associated sialylated glycoprotein antigen;
TAG-72; variable region; heavy chain; carcinoma; detect; tumour; ss;
mouse-human chimeric antibody; therapeutic agent; intraoperative therapy;
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animal an effective amount of a composition for the in situ detection carcinoma lesions. The method is useful for intraoperative therapy, consisting of locating the position of a tumour through the administration of the antibody, followed by excising the tumour
                                                                                                   Gaps
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                                                                           0.8%; Score 14; DB 1; Length 16;
100.0%; Pred. No. 7.8e+02;
.ive 0; Mismatches 0; Indels
                                                      Sequence 16 BP; 4 A; 2 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                  Primer for sequencing antibody CC83 heavy chain.
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88US-00261942.
89US-00424362.
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                                                                                                                                   3 GAGGAGACTGTGAG 16
                                                                                                                                                                                                                                             (first entry)
                                                                                                 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gourlie BB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DOWC ) DOW CHEM CO.
                                                                            Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                      24-MAR-1997;
                                                                                                                                                                                                                                            21-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                            US5993813-A.
                                                                                                                                                                                                                                                                                                                                                                                                 30-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                            19-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-OCT-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-0CT-1989
                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mezes PS,
Rixon MW;
                                                                                                                                                                                                                        AAZ40717;
                                                                                                                                                                                                                                                                                                                        primer.
                                                                                                                                                                            RESULT 1248
                                                                                                                                                                                                                                                                                                                                                         Mus sp
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                                                                                                                                                                                                             CCCCCCCCCCCCCCX8X44X8X111X4X8X84X8X8X8X8X8X8X8X8X8X
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monoclonal antibodies directed against TAG-72, designated colon cancer (CC) antibodies. The CC antibodies are produced from the rearrangement of VHalphaTAG (AAZ40701). The antibodies are used in the invention which relates to a new anti-tumour associated sialylated glycoprotein antigen (TAG)-72 mouse-human chimeric antibody. The variable region of the antibody has a heavy chain (YM) where VM is encoded by a DNA sequence homologous to the VHalphaTAG germline gene. The invention includes a method for in vivo carcinoma targeting through the administration to an animal an of anti-TAG-72 mouse-human chimeric antibody produced by specific cell lines. The antibody or a fragment are conjugated to an imaging marker or therapeutic agent, in a pharmaceutically acceptable, nontoxic, sterile carrier. The chimeric antibody binds to TAG-72 which is found on certain human tumour cells. The tissue regions containing the tumours can be detected via the markers and/or can be treated via the therapeutic agents. The method is useful for in vivo diagnosis and AAZ40715-Z40718 are primers used to sequence the heavy chains of

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New mouse-human chimeric antibody, useful for in vivo diagnosis

WPI; 2000-038240/03.

Example, Col 34; 120pp; English.

us10008789-3.rng

1409

1396 GAGGAGACTGTGAG

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treatment of cancer by administering to an animal an effective amount of a composition for the in situ detection of carcinoma lesions. The method is useful for intraoperative therapy, consisting of locating the position of a tumour through the administration of the antibody, followed by excising the tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric antibody, WhalphaTAG; TAG-72; human; mouse; diagnosis; tumour-associated sialylated glycoprotein antigen; cytostatic; carcinoma; cancer; detection; therapy; primer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes an antibody (I) produced by one of the following cell lines: CH44-1 (ATCC HB98B4); CH44-2 (ATCC HB98B07); CH88-1 (ATCC HB98B1); CH88-3 (ATCC HB98B7); CH88-4 (ATCC HB98B3); CH88-3 (ATCC HB9B76); CH88-4 (ATCC HB9B79); CH84-4 (ATCC HB9B75); CH89-2 (ATCC HB9B79); CH84-3 (ATCC HB9B75); CH84-4 (ATCC HB9B75); CH94-2 (ATCC HB9B79); CH84-3 (ATCC HB9B75); CH84-2 (ATCC HB9B79); CH84-3 (ATCC HB9B75); Capable of binding to tumour-associated sialylated glycoprotein (TAG)-72 with an affinity at least 25% greater than B72.3. (I) can be used for treating and diagnosing cancer, and for the istu detection of carcinoma lesions and for in vivo therapy. AAA29682 to AAA2944, and AAY90714 to AAY90723, represent sequences used in the exemplification of the present invention
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel family of chimeric antibodies for treating cancer with high affinities to a high molecular weight tumor-associated sialylated glycoprotein antigen of human origin.
                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS:
                                                                                                                                                  0.8%; Score 14; DB 1; Length 16;
100.0%; Pred. No. 7.8e+02;
/ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mezes
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC83 heavy chain oligonucleotide primer SEQ ID NO:39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gourlie BB,
                                                                                                                   Sequence 16 BP; 4 A; 2 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 16 BP; 4 A; 2 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schlom J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3xample; Col 37; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88US-00259943.
88US-00261942.
89US-00424362.
                                                                                                                                                                                                                                                                                                                                                    AAA29709 standard; DNA; 16 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93US-00040687.
                                                                                                                                                                                                                           1396 GAGGAGACTGTGAG 1409
                                                                                                                                                                                                                                                            3 caccacacrercae 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anderson WHK, Kaplan DA,
                                                                                                                                                                                        Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-349294/30.
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                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-OCT-1988;
19-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .9-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US6051225-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                         AAA29709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rixon MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus sp.
                                                                                                                                                                                                                                                                                                                RESULT 1249
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                                                                                                                                    Chimeric antibody, VHalphaTAG; TAG-72; human; mouse; diagnosis; tumour-associated sialylated glycoprotein antigen; cytostatic; carcinoma; cancer; detection; therapy; primer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel family of chimeric antibodies for treating cancer with high affinities to a high molecular weight tumor-associated sialylated glycoprotein antigen of human origin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mezes PS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.8%; Score 14; DB 1; Length 16;
100.0%; Pred. No. 7.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                       CC83 heavy chain oligonucleotide primer SEQ ID NO:23.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gourlie BB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16 BP; 4 A; 2 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                     Schlom J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example; Col 34; 122pp; English.
                                                                                                                                                                                                                                                                                                                                       88US-00259943.
88US-00261942.
89US-00424362.
            AAA29696 standard; DNA; 16 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS03546 standard; DNA; 16 BP
                                                                                                                                                                                                                                                                                                            93US-00040687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1396 GAGGAGACTGTGAG 1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16
                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Anderson WHK, Kaplan DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-349294/30.
                                                                                                                                                                                                                                                                                                                                                                                                      DOWC ) DOW CHEM CO
                                                                      14-AUG-2000
                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                            31-MAR-1993;
                                                                                                                                                                                                                                                                                                                                         19-OCT-1988;
24-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                         19-OCT-1989;
                                                                                                                                                                                                                                                JS6051225-A.
                                                                                                                                                                                                                                                                               18-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rixon MW;
                                           AAA29696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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AAA29696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS03546
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Gaps

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0.8%; Score 14; DB 1; Length 16; 100.0%; Pred. No. 7.8e+02; ative 0; Mismatches 0; Indels

14; Conservative

Matches

Best Local Similarity

Query Match

(first entry)

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Sequence 16 BP; 4 A; 2 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                     Example, Col 34; 120pp; English.
                                                                                                                                                                                                                                                                                                            1396 GAGGAGACTGTGAG 1409
                                                                                                                                                                                                                                                                                                                                                     AAD44145 standard; DNA; 16
                                                                                                                                                                                                                                                                                                                         GAGGACACTGTGAG 16
                                                                                                                                                                                                                                                                                                                                                                            13-DEC-2002 (first entry)
                                                                                                                                                                                                                                                                                                  14; Conservative
                                                                                                                                   Gourlie BB,
                                                                                                                                                   WPI; 2001-298946/31.
                                                                                                                       (DOWC ) DOW CHEM CO
                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                24-OCT-1988;
19-OCT-1989;
31-MAR-1993;
     29-AUG-2001
                                                                                                                                       Anderson WHK
                                                        US6207815-B1
                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
                                                                               07-JUN-1995;
                                                                                          19-OCT-1988;
                                                                   27-MAR-2001.
                                                                                                                                  Mezes PS,
                                                                                                                                                                                                                                                                                                                                                                AAD44145;
                                                                                                                                                                                                                                                                                       Query Match
                                             Mus sp.
                                                                                                                                                                                                                                                                                                  Matches
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AAD44145/C
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AC AAD4.
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DE 01:90
XX
KW Seque
KW Seque
KW Grim
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BP,

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amplification for sorting a mixture of DNAB into 2 or more subsets or distinguishing gene expression patterns in 2 samples. The methods, kits and oligonucleotides are useful for sorting a mixture of DNAB into 2 or more subsets or distinguishing gene expression patterns in 2 samples e.g. for disease diagnosis and gene analysis. The present sequence is oligo dT PCR primer used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method of sequential consensus region-directed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequential consensus region-directed amplification for sorting mixture of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequential consensus region-directed amplification; gene expression; disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR; primer; 88.
                                                                                                                                                                                                                                                                                                                                               Sequential consensus region-directed amplification for sorting mixture DNAs into 2 or more subsets or distinguishing gene expression patterns 2 samples, useful for disease diagnosis and gene analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligo-dT PCR primer #7 used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.8%; Score 14; DB 1; Length 16; Best Local Similarity 100.0%; Pred. No. 7.8e+02; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 16 BP; 0 A; 1 C; 0 G; 14 T; 0 U; 1 Other;
                                                                                                                                                                                                                  VIRGINIA COMMONWEALTH INTELLECTUAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VIRGINIA COMMONWEALTH INTELLECTUAL.
                                                                                                                                                                                                                                                           Gillies G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gillies G;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Example, Fig 1C; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD44147 standard; DNA; 16 BP
                                                                                                        98US-00163485.
                                                                                                                                                   97US-00943162
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97US-0108152P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Broaddus W,
                                                                                                                                                                                                                                                                                                      WPI; 2002-412824/44.
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                                                                                                                                                                                                                  VINU (-IVYU)
                    US6277571-B1
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                                                                                                        30-SEP-1998;
                                                                                                                                                                       03-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US6277571-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-OCT-1997;
03-OCT-1997;
                                                                                                                                                                                                                                                           Fillmore H,
                                                                                                                                                     03-OCT-1997;
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                                                             21-AUG-2001
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AAD44147/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence is a sequencing primer for nucleic acids encoding Mouse antibody heavy chains CC83VH, which can form chimaeric antibody molecules of the invention. The invention concerns chimaeric antibody heavy chains or their chimaeric antigen-binding fragment which have the ability to combine with anti-TAG-72 antibody light chain to form a binding site having an affinity for TAG-72 which is at least 25% greater than that of B72.3 (an antibody known to the prior art). TAG-72 is a human tumour antigen thought to be a mucin glycoprotein. DNA sequences encoding the chimaeric heavy chains are useful for producing antibodies that are useful for ancer treatment, such as in vivo diagnostic assays, in vivo therapy and radioimmunoguided surgery. The antibodies produce significantly fewer side-effects when administered to human patients
                                                                                                 Mouse; antibody; CC83VH; TAG-72; mucin; chimaeric heavy chain; B72.3; tumour; cancer; radioimmunoguided surgery; sequencing primer; ss; JH2(-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel DNA sequence encoding chimeric antibody heavy chain or its chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequential consensus region-directed amplification; gene expression; disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antigen-binding fragment, useful for cancer treatment, such as in vivo diagnostic assays, in vivo therapy and radioimmunoguided surgery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligo-dT PCR primer #5 used to illustrate the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                          Mouse immunoglobulin heavy chain sequencing primer JH2(-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.8%; Score 14; DB 1; Length 16;
100.0%; Pred. No. 7.8e+02;
tive 0; Mismatches 0; Indels
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88US-00259943. 88US-00261942. 89US-00424362. 93US-00040687.

95US-00479285

Gaps

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Indels

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Mismatches

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14; Conservative

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Matches
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                                                        The invention relates to a method of sequential consensus region-directed amplification for sorting a mixture of DNAs into 2 or more subsets or distinguishing gene expression patterns in 2 samples. The methods, kits and oligonucleotides are useful for sorting a mixture of DNAs into 2 or more subsets or distinguishing gene expression patterns in 2 samples e.g. for disease diagnosis and gene expression patterns in 2 samples e.g. For primer used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method of sequential consensus region-directed amplification for sotting a mixture of DNAs into 2 or more subsets or distinguishing gene expression patterns in 2 samples. The methods, kits and oligonucleotides are useful for sorting a mixture of DNAs into 2 or more subsets or distinguishing gene expression patterns in 2 samples e.g. for disease disgnosis and gene expression patterns in 2 samples e.g. For primer used to illustrate the method of the invention
DNAs into 2 or more subsets or distinguishing gene expression patterns in 2 samples, useful for disease diagnosis and gene analysis.
                                                                                                                                                                                                                                                                                                                                                                                                               Sequential consensus region-directed amplification; gene expression; disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
                                                                                                                                                                                                                                                                                                                                                                                          Oligo-dT PCR primer #9 used to illustrate the method of the invention.
                                                                                                                                                                                                        Gaps
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                                                                                                                                                                               0.8%; Score 14; DB 1; Length 16;
100.0%; Pred. No. 7.8e+02;
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                                                                                                                                                        Seguence 16 BP; 0 A; 0 C; 1 G; 14 T; 0 U; 1 Other;
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                                   Example; Fig 1C; 19pp; English
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97US-0108152P.
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                                                                                                                                                                                                         Conservative
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Best Local Similarity
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Best Local Similarity
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03-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          primer; 88.
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vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage; tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease; fms-like tyrosine kinase 1; kinase insert domain containing receptor; foetal liver kinase 1; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient.
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                                                                                                                                                                                                                                                                                                                                                                             Human flt1 VEGF receptor hammerhead ribozyme substrate #1093
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                                                                                                                                                                                                      AAX69798 standard; RNA; 17 BP.
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1736 AAAAAAAAAAAA 1749
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                                                      16 AAAAAAAAAAAA 3
                                                                                                                                                                                                                                                                                                                       (first entry)
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Les 14; Conservative
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Matches
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ID AAX6
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AAX69798,
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related macular degeneration; inflammation; neovascular glaucoma;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient.
                                                                                                 Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1; KDSF, hammerhead ribozyme; cleavage; tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease; fms-like tyrosine kinase 1; kinase insert domain containing receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention describes nucleic acid molecules which modulate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; aryl hydrocarbon nuclear transport; ARNT; TIB-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytostatic; antidabetic; ophthalmologic; antidinflammatory; antiarthritic; antipsoriatic; ARND; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
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                                                                   Human flt1 VEGF receptor hammerhead ribozyme substrate #1098.
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00.0%; Pred. No. 8.1e+02;
ve 0; Mismatches 0; Indels
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                                 (first entry)
                                                                                                                                                                     foetal liver kinase 1; ss.
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11-JAN-1996;
                                 28-JUL-1999
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 AAX69803
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The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl cleaving activity, which specifically cleave RNA encoded by an aryl cleaving activity, which specifically cleave RNA encoded by an aryl colleaving activity, which specifically cleave RNA encoded by an aryl gene, an integrin subunit beta 3 certain AAA17167 and AAA17681 to AAA1762 to AAA17650 and AAA17681 to AAA17684 represent their corresponding target sequences AAA19154 to AAA19155 to AAA19155 to AAA19155 to AAA19155 to AAA191522 represent their corresponding target sequences; cand AAAA19155 to AAA191522 represent their corresponding target sequences; cand AAAA19155 to AAA191501 and AAA17681 to AAA21685 to AAA19155 to AAA191501 and AAA17681 encresponding target sequences; cand AAA21685 to AAA21685 and AAA21685 to AAA21845 to AAA21685 to AAA21685 to AAA21685 to AAA21685 to AAA21685 to AAA21685 to AAA21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors.
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                    myopic degeneration; paoriasis; verruca vulgaris; angiofibroma;
tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Mcswiggen JA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 56; Page 100; 305pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 Jarvis T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .447/c
AAA25447 standard; DNA; 17 BP.
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                                                                                                                                                                                                                                                                                                                                                                 (RIBO-) RIBOZYME PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Roberts E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-591315/50.
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                                                                                                                                                                                                                                                                 24-MAR-1999;
                                                                                                                                                                                                                                                                                                                 27-MAR-1998;
                                                                                                                      Homo sapiens
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vulnerary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis; tumour angiogenesis; diabetic retinopathy; macular degeneration; neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris; angiofibroma of tuberous sclerosis; port-wine stain; wound healing; Sturge Weber syndrome; kippel-Trenaunay-Weber syndrome; leukaemia; 88; Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;

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Human, hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ERG hammerhead ribozyme target sequence, Seq ID No 838
                                                                                                                                                                                                                                                                                                                                                                                                             ABK18191 standard; RNA; 17 BP
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                                                                                                                                                                                                                                                                                                                                                                             AAAAAAAAAAAAA 4
                                                                                                                                                              to treat cancer.
                                                                                                                                          WPI; 2000-013248/01.
                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                             Matulic-Adamic J;
                                                                                                                Thompson JD,
Reynolds M,
                                                                     19-APR-1999;
                                sapiens
                                           W09954459-A2
                                                                                  20-APR-1998;
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                                                       28-OCT-1999
                                                                                                                                                                                                                                                                                                               invention
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ID ABK.
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AC ABK.
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The present invention describes nucleic acids (A) that interact stably with a target sequence and contain at least one phosphoro (di)thioate link, having endonuclease activity. (A), and more generally are catalytic nucleic acid (A') that modulates expression of the oestrogen receptor gene, are used to treat cancer (particularly of breast or endometrium), in vivo or by transforming cells ex vivo and implanting treated cells, or for other conditions associated with levels of oestrogen receptor. Because of the high selectivity for targeted RNA, (A) can also be used to correlate inhibition of gene expression with alterations in phenotype, particularly for identification of therapeutic targets, and as research reagents (for RNA, in the same way that restriction endonucleases are used with DNA). The combination of modifications in (A) improves to sesistance to nucleases, binding affinity and/or activity. AAA23533 to AAA2474 tepresent oestrogen receptor hammerhead ribozyme sequences.

AAA24748 to AAA25392 represent their corresponding target sequences. AAA26107 to AAAA2618 represent their corresponding target sequences. Sequences. AAAA26107 to AAAA26218 represent their corresponding target sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acids that interact, and optionally cleave, target sequences,
Destrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage; hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide; gene expression modification; cancer; phosphorothioate; endonuclease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beigelman L, Mcswiggen JA, Karpeisky A, Zwick M, Jarvis T, Woolf T, Haeberli P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                  anticancer; breast cancer; endometrium cancer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 77; Page 79; 148pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0082404P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US008547.
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Novel polynucleotide which down regulates expression of Ets-related genuseful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.

Claim 4; Page 74; 149pp; English.

Von Carlowitz I, Mcswiggen JA, Mclaughlin F,

16-MAY-2001; 2001WO-US015866. 16-MAY-2000; 2000US-00572021.

WO200188124-A2 22-NOV-2001

amberzyme.

RIBOZYME PHARM INC.

RIBO-) (GLAX )

GLAXO GROUP LTD

WPI; 2002-082995/11.

Jarvis T,

The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for treating conditions selected from cancer, lymphom, Bwing's sarcoms, melanoma, conditions selected from cancer, lymphom, macular degeneration, tumour angiogenesis, diabetic retinopathy, macular degeneration, cumour angiogenesis, diabetic retinopathy, macular degeneration, cumour angiogenesis, diabetic retinopathy, macular degeneration, cumour angiogenesis, diabetic retinopathy, anthritis, psoriasis, verruca vulgaris, angiofibroma of tumborous sclerosis, port-wine stains, Sturge Weber syndrome, leukaemia, osteoporosis and wound healing (I) is useful for treating a patient having a condition associated with he level of ERG, by contacting cells of the patient with (I) under conditions suitable for the treatment. The method comprises the use of one or more theraples under conditions suitable for the treatment. Leukaemia or tumour conjunction with one or more of other theraples such as radiation or conjunction with one or more of other theraples such as radiation or conjunction with one or more of other theraples such as radiation or cell, by contacting (I) is useful for reducing ERG activity in a cell, by contacting (I) with RNA, in the presence of a divalent cation such as Mg2+. (I) is useful for diagnosis of conditions and diseases related to the expression of ERG, and as diagnostic cool to the presence of ERG RNA in a cell. (I) is useful for specifically contacting genes that share homology with ERG spens or ERG fusion genes. ABRI3334-ABRI2719 represent nucleic acide, including antisense and carged procession of the invention catide, including antisense and carged procession catide, including antisense and catated PCR primers of the invention ö Gaps ö 8%; Score 14; DB 1; Length 17; 0.0%; Pred. No. 8.1e+02; 0; Indels

100.0%; Pred. ... 1736 AAAAAAAAAAAA 1749 14; Conservative

ö Gaps ö 0.8%; Score 14; DB 1; Length 17; 92.9%; Pred. No. 8.1e+02; tive 1; Mismatches 0; Indels Sequence 17 BP; 2 A; 12 C; 2 G; 0 T; 1 U; 0 Other; ABV90789 standard; DNA; 17 BP. 272 TCCAGCCCCACCC 285 13; Conservative Similarity ABV90789; Query Match Local RESULT 1260 ABV90789/C ID ABV90789 XX AC ABV90789 Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene; Rho GTPase; signal transduction; gene expression; cancer; vaccine;

gene therapy; transgenic; ss.

Homo sapiens. EP1239051-A2

Human POSHL1 scanning oligonucleotide SEQ ID NO 1506.

(first entry)

23-DEC-2002

ABV90793;

ABV90793 standard; DNA; 17 BP.

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30-JAN-2001; 2001WO-US000663.
30-JAN-2001; 2001WO-US000664.
30-JAN-2001; 2001WO-US000665.
30-JAN-2001; 2001WO-US000666.
30-JAN-2001; 2010WO-US000667.
30-JAN-2001; 2010WO-US000668.
                                   gene therapy; transgenic; ss
                                                                           28-JAN-2002; 2002EP-00001165
                                                                                                                              23-MAY-2001; 2001US-00864761, 10-OCT-2001; 2001US-0328205P.
    23-DEC-2002 (first entry)
                                                                                                                                                                  WPI; 2002-684061/74.
                                                                                                                                              (AEOM-) AEOMICA INC
                                                       EP1239051-A2.
                                             Homo sapiens,
                                                                 11-SEP-2002
                                                                                                                                                        Shannon M;
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The invention relates to an isolated SH3 domain (POSH)-like signalling protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino acide (SI, Masha9399). a sequence having 6\$\$ sequence identity to (S1), (S1), having 9\$\$ deviations, especially conservative substitutions or a fragment of the sequences comprising at least 8 contiguous amino acids. Human POSHL 1 is a proto-oncogene/oncogene product that functions as an adaptor protein that interacts with Rho family small GTPases as well as downstream components of the signal transduction pathway. (I) is useful correction a sequence of the signal transduction pathway. (I) is useful correcting a specific binding partner. (I) and nucleic acids (II) caused by altered expression of human POSHL1 including disease and treating cancer, they useful in the development of vaccines and (II) is useful in gene therapy. (II) is useful for constructing microarrays which are useful for measuring and for surveying gene expression and creating transgenic non-human animals capable of producing the proteins. The present sequence is that of a scanning oligonucleotide useful in examples continued specification. But is based on sequence information supplied to printed specification, but is based on sequence information supplied to Derwent by the European Patent Office

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Gaps
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                                            0.8%; Score 14; DB 1; Length 17;
100.0%; Pred. No. 8.1e+02;
tive 0; Mismatches 0; Indels
Sequence 17 BP; 2 A; 4 C; 9 G; 2 T; 0 U; 0 Other;
                                                 Query Match
Best Local Similarity 100.0
Matches 14; Conservative
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898 CCCCTGAGCCAGCC 911
              17 CCCTGAGCCAGCC 4
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8 셤 RESULT 1261 ABV90793/c

셤 8

Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL -1, useful for treating disorders associated with decreased expression or activity of human POSHL1. Human, POSHL 1; SH3 domain, POSH-like signalling protein 1; oncogene; Rho GTPase; signal transduction; gene expression; cancer; vaccine; Example 2; SEQ ID NO 1502; 60pp + Sequence Listing; English. Human POSHL1 scanning oligonucleotide SEQ ID NO 1502.

30-JAN-2001; 2001WO-US006665. 30-JAN-2001; 2001WO-US006665. 30-JAN-2001; 2001WO-US006666. 30-JAN-2001; 2001WO-US00666. 30-JAN-2001; 2001WO-US006668. 30-JAN-2001; 2001WO-US006668.

23-MAY-2001; 2001US-00864761. 10-OCT-2001; 2001US-0328205P.

(AEOM-) AEOMICA INC.

WPI; 2002-684061/74.

Shannon M;

28-JAN-2002; 2002EP-00001165

11-SEP-2002

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The invention relates to an isolated SH3 domain (POSH)-like signalling protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino acids (St, ABBR3999), a sequence having 65% sequence of 6511, (S1), having 95% deviations, especially conservative substitutions or a fragment of the sequences comprising at least 8 contiguous amino acids. Human POSHL 1 is a proto-oncogene/oncogene product that functions as an adaptor protein that interacts with Rho family small GTPsases as well as downstream components of the signal transduction pathway. (I) is useful as concoling (I) are useful for diagnosing, monitoring disease and treating cansed by altered expression of human POSHL1 including diagnosing and conserv, they useful in the development of vaccines and (II) is useful in gene therapy. (II) is useful for constructing microarrays which are useful for measuring and for surveying gene expression and creating care useful for measuring and for surveying gene expression and creating created sequence is that of a scanning oligonucleotide useful in examples of the invention. Note: The present sequence information supplied to printed specification, but is pased on sequence information supplied to
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Example 2; SEQ ID NO 1506; 60pp + Sequence Listing; English.
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14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 1 A; 5 C; 8 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              897 GCCCCTGAGCCAGC 910
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Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL-1, useful for treating disorders associated with decreased expression or activity of human POSHL1.

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Cytostatic; immunostimulant; gene therapy; vaccine; human; zinc finger protein; MDZ3; MDZ4; MDZ12; chromosome 7q22.1; chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
                                                                                                                                                                                                                                                                                                          New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7 or MDZ12, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17 BP; 2 A; 0 C; 2 G; 13 T; 0 U; 0 Other;
                                                              Human MDZ7 scanning oligonucleotide SEQ ID 5261.
                                                                                                                                                                                                                                                                                                                                                                 3xample 8; SEQ ID NO 5261; 103pp; English.
ADB04275 standard; DNA; 17 BP
                                                                                                                                                                                                    30-JUL-2002; 2002EP-00016874.
                                                                                                                                                                                                                         32-AUG-2001; 2001US-00922181
                                                                                                                                                                                                                                                                   Gu Y, Nguyen C;
                                                                                                                developmental disorder; ss.
                                       (first entry)
                                                                                                                                                                                                                                                                                       WPI; 2003-423107/40.
                                                                                                                                                                                                                                              (AEOM-) AEOMICA INC
                                                                                                                                       Homo sapiens.
                                                                                                                                                           EP1281758-A2
                                         20-NOV-2003
                                                                                                                                                                                05-FEB-2003
                                                                                                                                                                                                                                                                   Shannon M,
                   ADB04275
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The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MDZ3, MDZ4, MDZ12, MDZ12 is concoded at chromosome 7422.1, MDZ4 is encoded at chromosome 7422.1, MDZ4 is encoded at chromosome 6521.3-22.2, MDZ7 is encoded at chromosome 6521.3-22.2, MDZ7 is encoded at chromosome 1621.2 and MDZ12 is encoded at chromosome second in the and in manufacturing a medicament for treating or preventing a disorder or increased expression or activity of MDZ3, MDZ4, MDZ1, or MDZ12, e.g. cancer or developmental disorders. The nucleic acids and proteins are also useful for disgnosing or monitoring a disease acids can also be used as probes to detect and characterize gross alterations in MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic acids can also be used as probes to detect and characterize gross alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are useful in constructing microarrays for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as proteins are useful as therapeutic agents for gene therapy or as

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Length 17;
0.8%; Score 14; DB 1; Length 17;
100.0%; Pred. No. 8.1e+02;
vative 0; Mismatches 0; Indels
                                                                            1735 CAAAAAAAAAAA 1748
              Best Local Similarity 100.
Matches 14; Conservative
Query Match
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Gaps .. 0

> ACC68542 standard; DNA; 17 BP 14 CAAAAAAAAAAA 1 RESULT 1263
> ACC68542/c
> ID ACC6854;
> XX
> AC ACC6854;
> XX
> DT 01-JUL-;

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01-JUL-2003 (first entry)

ACC68542

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ACC68806), which are associated with tumour suppression, tumour reversion, apoptosis and virus resistance. The oligonucleotides are quantifying and/or amplifying nectecting, identifying of a gene chip, in vitro as (anti)sense reagents; and (2) for production of a gene chip, in vitro as (anti)sense reagents; and (2) for production of a recombinant polypeptides. The oligonucleotides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.
                                              Cytostatic, virucide, neuroprotective, nootropic, neuroleptic, murine, tumour suppression, tumour reversion, apoptosis, virus resistance, viral disease, tumour; cell degeneration, cancer, Alzheimer's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine; tumour suppression; tumour reversion; apoptosis; virus resistance; viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
            Murine oligonucleotide associated with tumour supression, SEQ ID 5789.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine oligonucleotide associated with tumour supression, SEQ ID 2303.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention relates to murine oligonucleotides (ACC62754-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specifically cancer but also Alzheimer's disease and schizophrenia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17 BP; 6 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 707; 738pp; French.
                                                                                                                                                                                                                                                                                                                                                     Tuijnder M;
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ACC65056 standard; DNA; 17 BP.
                                                                                                                                                                                                                                                                                                                  (MOLE-) MOLECULAR ENGINES LAB
                                                                                                                                                                                                                                            17-SEP-2002; 2002WO-IB004210.
                                                                                                                                                                                                                                                                               17-SEP-2001; 2001FR-00011979
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                                                                                                                                                                                                                                                                                                                                                     Telerman A, Amson R,
                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-333167/31.
                                                                                                     schizophrenia; ss.
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                                                                                                                                                                        WO2003025176-A2.
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ACC6886), which are associated with tumour suppression, tumour reversion, apoptosis and virus resistance. The oligonucleotides are useful as (1) as probes and primers for detecting, identifying quantifying and/or amplifying nucleic acid, e.g. as one component of a gene chip; in viro as (anti) sense reagents; and (2) for production of recombinant polypeptides. The oligonucleotides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration.
                                                                                                                                                                    New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murine oligonucleotide associated with tumour supression, SEQ ID 5854
                                                                                                                                                                                                                                                                          present invention relates to murine oligonucleotides (ACC62754-
                                                                                                                                                                                                                                                                                                                                                                                                                             specifically cancer but also Alzheimer's disease and schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.8%; Score 14; DB 1; Length 17;
100.0%; Pred. No. 8.1e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 1 A; 7 C; 4 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                         Disclosure; Page 300; 738pp; French
                                                                                                      Tuijnder M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tuijnder M;
                                                                 (MOLE-) MOLECULAR ENGINES LAB
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 17-SEP-2002; 2002WO-IB004210
                                 17-SEP-2001; 2001FR-00011979.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-SEP-2002; 2002WO-IB004210.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  336 GGGACCGGAGGATC 349
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                                                                                                    Telerman A, Amson R,
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                                                                                                                                    WPI; 2003-333167/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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ACC68607/
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The present invention relates to murine oligonucleotides (ACC62754-ACC68806), which are associated with tumour suppression, tumour reversion, apoptosis and virus resistence. The oligonucleotides are useful as (1) as probes and primers for detecting, identifying, quantifying and/or amplifying nucleic acid, e.g. as one component of a gene chip, in virto as (anti) sense reagents; and (2) for production of recombinant polypeptides. The oligonucleotides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic, antiviral, neuroprotective, nootropic, neuroleptic, ss;
primer; probe; tumour suppression; tumour reversion; apoptosis;
virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to the isolation of 6327 nucleotide sequences, fragments of at least 15 consecutive nucleotides of these nucleotides, a sequence having at least 80% identity, after optimal alignment, with the nucleotides, a sequence that hybridizes under stringent conditions with the nucleotides, or the complement, or corresponding RNA, of the nucleotides are used as probes or primers for detecting, identifying, quantifying and/or amplifying nucleic acids, as in vitro sense and antisense sequences, of nucleotides involved in tumour recombinant polypeptides, and to prepare transgenic animals, as experimental models. The nucleotides (also vectors containing them and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related polypeptide and antibodies.
                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                0.8%; Score 14; DB 1; Length 17;
100.0%; Pred. No. 8.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumour suppression/reversion associated nucleotide #3226.
                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                             Sequence 17 BP; 5 A; 3 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                          100.0%; Prec. ...
Disclosure; Page 715; 738pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 409; 771pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tuijnder M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB42903 standard; DNA; 17 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-SEP-2002; 2002WO-IB004219.
                                                                                                                                                                                                                                                                                                                                                         1286 CCTTCACAGTGGAT 1299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-441574/41.
                                                                                                                                                                                                                                                                                                  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ното варіеля
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis.
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                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1266
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The invention relates to the isolation of 6327 nucleotide sequences, fragments of at least 15 consecutive nucleotides of these nucleotides, a sequence having at least 80% identity, after optimal alignment, with the nucleotides, a sequence that hybridizes under stringent conditions with the nucleotides, or the complement, or corresponding RNA, of the nucleotides. The nucleotides are used as probes or primers for detecting, consense and antisense sequences, of nucleotides involved in tumour sense and antisense sequences, of nucleotides involved in tumour suppression or reversion, apoptosis and or viral resistance, to produce recombinant polypeptides, and to prepare transgenic animals, as experimental models. The nucleotides (also vectors containing them and calls containing the vectors), the encoded polypeptides and antibodies (Ab) against the polypeptide are useful for prevention and/or treatment of viral infections or diseases characterized by development of tumours or cell degeneration (e.g. Alzheimer's disease or schizophrenia). cytostatic, antiviral, neuroprotective, nootropic, neuroleptic, ss; primer; probe; tumour suppression; tumour reversion; apoptosis; virus resistance; transgenic animals; Alzheimer's disease; schizophrenia; cells containing the vectors), the encoded polypeptides and antibodies (Ab) against the polypeptide are useful for prevention and/or treatment of viral infections or diseases characterized by development of tumours or cell degeneration (e.g. Alzheimer's disease or schizophrenia). Analysis of the expression of the nucleotides can be used for diagnosis and/or prognosis of these diseases. The nucleotides and polypeptides can also be used to screen for their specific interactive molecules, potentially useful for treating diseases associated with abnormal New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related polypeptide and antibodies. Gaps ö 0.8%; Score 14; DB 1; Length 17; 00.0%; Pred. No. 8.1e+02; Tumour suppression/reversion associated nucleotide #5791. 0; Indels Sequence 17 BP; 4 A; 6 C; 2 G; 5 T; 0 U; 0 Other; Mismatches Disclosure; Page 709; 771pp; French Ξ .; 0 Tuijnder expression of the nucleotides. ADB45468 standard; DNA; 17 BP. (MOLE-) MOLECULAR ENGINES LAB 100.04; 17-SEP-2002; 2002WO-IB004219. 17-SEP-2001; 2001FR-00011981. 620 CAGCCTCTTACACT 633 4 cagccrcrracacr 17 18-DEC-2003 (first entry) Best Local Similarity 100. Matches 14; Conservative Telerman A, Amson R, WPI; 2003-441574/41. WO2003040369-A2. Homo sapiens. 15-MAY-2003 diagnosis. ADB45468; Query Match RESULT 1267 88888888888888 셤

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The invention describes an isolated or recombinant polypeptide (I)

comprising a sequence: (a) comprising 1 of 30 sequences (S1), as given in

the specification, or a conservative variant; (b) encoded by 1 of 30,

sequences (S2), as given in the specification, or a conservative variant;

(c) encoded by a sequence that hybridises under stringent conditions to

S2; and (d) encoded by a sequence 70 % identical to S2. The expression or

activity of (I) is modulated to modulate a plant growth trait in a

flowering plant, of the family Brassicaceae, preferably in a plant that

is Arabidopsis, Brassica, Zea, Oryza, Triticum, Hordeum, Lolium, Sorghum,

Glycine, Medicago, Helianthus, Lactuca, Beta, Vitis, Solamum,

Lycoperation, Capsicum, Gossypium, Hevea, Linum, Prunus, Citrus, Populus,

Lycoperation, Capsicum, Gossypium, Hevea, Linum, Prunus, Citrus, Populus,

Cycoperation, Capsicum, Gossypium, Hevea, Linum, Prunus, Citrus, Populus,

Cycoperation, This sequence represents a polynucleotide isolated from the

Cycowth trait. This sequence represents a polynucleotide isolated from the

Cycomer prometry associated genes of the invention that can be used a a

primer, probe or genetic marker.
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Analysis of the expression of the nucleotides can be used for diagnosis and/or prognosis of these diseases. The nucleotides and polypeptides can also be used to screen for their specific interactive molecules, potentially useful for treating diseases associated with abnormal expression of the nucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated or recombinant polypeptide for use in modulating a plant growth trait in a flowering plant e.g. in Arabidopsis, Brassica, Zea, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plant growth; plant growth trait modulation; Brassicaceae; Arabidopsis; Brassica; Zea; Oryza; Triticum; Hordeum; Lolium; Sorghum; Glycine; Medicago; Helianthus; Lactuca; Beta; Vitis; Solanum; Lycopersicon; Capsicum; Gossypium; Hevea; Linum; Prunus; Citrus; Populus; Pinus;
                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                     Score 14; DB 1; Length 17; Pred. No. 8.1e+02;
                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plant growth associated polynucleotide seq id 196
                                                                                                                                Sequence 17 BP; 4 A; 7 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 8.1
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                                                                                                                                                                                                                                                                                                                                                                                                              ADE25221 Btandard; DNA; 17 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37-JAN-2003; 2003US-00338777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39-JAN-2002; 2002US-0347288P.
                                                                                                                                                                                                                                                              1574 TCACCACTGACTGC 1587
                                                                                                                                                                                                                                                                                      TCACCACTGACTGC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-803305/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JS2003188343-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADE25221;
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Sequence 17 BP; 14 A; 1 C; 1 G; 1 T; 0 U; 0 Other;

polymorphism; SNP; single nucleotide primer extension;

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SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenesis imperfecta; autoimune disease; acute intermittent porphyria; rheumatod arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; PCR primer; ss.
                          SNP specific lower PCR primer SEQ ID 1726.
  14-AUG-2001 (first entry)
                                                Single nucleotide
                                                                                                                                                         WO200129262-A2
                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The specification describes a method for determining a nucleotide sequence signature. The method comprises obtaining optical measurements with values indicating each nucleotide in a group of nucleotide positions, adjusting the values until the ratio of highest value in the set to next highest values in the set is at least a predetermined factor, and generating a base call for a position in the group based on results after the adjustment of values. The method is used for determining a signature of a nucleotide sequence, and for determining a nucleotide sequence of a polynucleotide from a series of optical measurements. The present sequence represents an adaptor, which is used in the course of
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Determining nucleotide sequence signature, by obtaining optical values for each nucleotide position in a group, adjusting them to get ratio of final highest values near predetermined factor, generating base call.
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Score 14; DB 1; Length 17;
Pred. No. 8.1e+02;
0; Mismatches 0; Indels
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Pred. No. 8.4e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                              Nucleotide sequence signature; nucleotide sequencing; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 19; 73pp; English
       100.0%; Pre
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                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                      (LYNX-) LYNX THERAPEUTICS INC.
                                                1735 CAAAAAAAAAAA 1748
                                                                                                                                                                                                                                                                                                                           15-FEB-2001; 2001WO-US005032
                                                                                                                                                                                                                                                                                                                                                   15-FEB-2000; 2000US-0182454P.
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                                                                                                                                                                                                        DNA sequence of cap adaptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.88;
                                                                                                                                AAH74930 standard; DNA; 18
                                                                       4 CAAAAAAAAAAAA 17
                                                                                                                                                                              (first entry)
                        14; Conservative
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Query Match
Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                            Corcoran KC,
                                                                                                                                                                               29-OCT-2001
                                                                                                                                                                                                                                                                                                     23-AUG-2001.
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                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                        AAH74930;
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Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide polymorphisms SNPs. The present invention false of single nucleotide polymorphisms SNPs. The present invention includes kits for determining the presence or absence of a SNP, using the includes kits for determining the presence or absence of a SNP, using the oligonucleotides of the invention. The PCR primers are used to amplify a SNP for the SNPs primer is used as a genotyping primer. The oligonucleotides are useful for genotyping a nucleic acid sample by performing a single-nucleotide primer extension reaction. The coligonucleotides are useful for genotyping nucleic acid samples, for e.g. to clasmity of a SNP and for genotyping nucleic acid samples, for e.g. to assess by association analysis the genotype of an individual or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits include diseases e.g. capammaglobulinaemia, diabeter inspidus, Lesch-Nyhan syndrome, muscular dystrophy, familial hypercholesterolaemia, polycystic kidney disease. Creategenesis imperfected and acute intermittent porphyria. Phenotypic traits also include symptoms of or susceptibility to multifactorial cisease of which a component is or may be genetic such as autoimmune createses, including, rheumatoid arthritis, multiple sclerosis, ciflammation, cancer, nervous system diseases and infection by pathogenic microorganism. The method is also useful in forensic investigations and content and partains and partainty analysis. The present sequence represents a PCR primer specific
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polynucleotide polymorphism in a nucleic
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Pred. No. 8.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for a human SNP containing DNA sequence
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tive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 58; 83pp; English
                                                                                                                                                                                                                      ORCH-) ORCHID BIOSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    )037/C
AAL49037 standard; DNA; 18 BP.
                                                                          13-OCT-2000; 2000WO-US028436.
                                                                                                                                                99US-0160096P.
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                                                                                                                                                                                                                                                                                                 Picoult-Newburg L, Pohl M;
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es 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-290930/30.
                                                                                                                                                15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acid sample.
26-APR-2001.
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ID AAL
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AC AAL4
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AAL49037

ВЪ.

930/c AAH38930 standard; DNA; 18

RESULT 1270

AAH38930,

AAH38930/ ID AAH3 XX AC AAH3

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JP2001321190-A.
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ADC64943/c
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a method of determining polynucleotide expression, which comprises hybridising digested cDNA to a capture probe coupled to a solid particle under stringent conditions, where the capture probe is specific for the target polynucleotide and the particle identifies the capture probe. The method is useful for expression profiling, where the presence and/or the amount of a target polynucleotide is simultaneously determined, for diagnosing a disease, condition, disorder, or predisposition associated with a change in expression patterns, in determining the developmental or physiological state of a cell or tissue, for detecting SNPs, which may be used to screen individuals for a genetic predisposition to a disease, condition, or disorder, and in marker assisted selection. The present sequence is a hybridisation tag described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Determining polynucleotide expression, useful for expressing profiling or detecting single nucleotide polymorphisms, comprises hybridizing digested cDNA to a capture probe coupled to a solid particle under stringent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
                                                                                       Nucleic acid analysis, microarray, single nucleotide polymorphism, SNP, multiplex; expression analysis; hybridisation tag; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                     Drosophila ubx gene SNP analysis universal hybridisation tag #11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.8%; Score 14; DB 1; Length 18; 100.0%; Pred. No. 8.4e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human chromosome 1p36-35 PCR primer SEQ ID NO:375.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18 BP; 3 A; 9 C; 1 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                  (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 28; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        Kimmerly WJ, Yang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABL43331 standard; DNA; 18 BP.
                                                                                                                                                                                                                                                                                          29-JAN-2001; 2001US-0264972P.
02-FEB-2001; 2001US-0266186P.
04-JUN-2001; 2001US-0295986P.
                                                                                                                                                                                                                                                          28-JAN-2002; 2002WO-EP000868.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-APR-2002 (first entry)
                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-636566/68
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                                                                                                                                                                                  WO200261121-A2.
                  29-OCT-2002
                                                                                                                                                                                                                      38-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conditions.
                                                                                                                                                                                                                                                                                                                                                                                                        Hinkel CA,
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Homo sapiens

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The present invention describes a method of arraying genome clones. The method comprises: (a) clones of the genomic libraries contained in method comprises: (a) clones of the genomic libraries contained in multiwell plates independent of activities of the marker is dedected from the resultant sequence is added to the mixture to carry out an amplification reaction; (c) a signal corresponding to the marker is detected from the resultant plates containing the clones having said marker sequence; (d) the order of the markers is changed so that the same discrimination Nos. succeed to the maximum in the specified discrimination Nos. to array the multiwell plates; (e) the clones in the multiwell plates of the specified discrimination Nos. are mixed respectively in each wells of longitudinal candinate cultures are amplified by using the above primer; (g) signals resultant cultures are amplified products; (h) the clones in the multiwell candinate of the amplified products; (h) the clones in the multiwell candinate of the maxed the maximum in the specified products; (h) the clones in the multiwell plates of the specified resultant cultures are amplified products; (h) the clones in the multiwell candinate of the maxed the multiwell plates of the plates of the maxed th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 are detected from the amplified products; (h) the clones in the multiwe plates are specified from the detected result; and (i) the clones are reconstituted as the positions on the chromosome and arrayed. The microarray is useful for gene analysis. ABL42957 to ABL45322 represent PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634 represent PCR primers for human chromosome 21q22.1, which are specifically claimed for use in the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.8%; Score 14; DB 1; Length 18;
100.0%; Pred. No. 8.4e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18 BP; 5 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 12; 528pp; Japanese.
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                                                                                                                                                                        10-MAR-2000; 2000JP-00066716.
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                                                                             .2-MAR-2001; 2001JP-00068285.
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                                                                                                                                                                                                                                                     (RIKA ) RIKAGAKU KENKYUSHO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arraying genome clones.
                                                                                                                                                                                                                                                                                                                                                                                         PI; 2002-144136/19
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Camellia sinensis.
20-NOV-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e.g. c-myb,
                                                                                                                                                                                                                                  The present invention describes the cloning of a new gene sequence expressed and inhibited during hibernation of the top plumelet of a Camellia sinensis L.(O.) Kuntze tea tree. Also described is the identification, cloning and analysis of a primer terminal in the gene sequence expressed and inhibited during hibernation of the top plumelet of the tea tree. The present sequence represents a PCR primer which is used in an example from the present invention.
                                                                                       Cloning of a new gene sequence expressed and inhibited during winter dormancy of a tea tree top plumelet, comprises identification, cloning and analysis of a new primer in the gene sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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smooth muscle cell; hyperproliferation; restenosis; cancer; c-myb;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.8%; Score 14; DB 1; Length 18;
100.0%; Pred. No. 8.4e+02;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treating restenosis or cancer.
                                                                                                                                                                                         Example 3; Page 32; 66pp; Chinese.
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(SCIN-) SCI & IND RES COMMISSION
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95US-00373124.
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                                           WPI; 2003-230959/23
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by modification to prevent degradation by nucleases. The ribozymes cleave the c-myb sequence and can be used to prevent smooth muscle cell hyperproliferation in restenosis, especially after coronary angioplasty,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid molecule modulating VBGF receptor(s) gene expression or mRNA stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (VEGF). A patient (preferably human) having a condition associated with the level of the fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient. AAX67275 to AAX75752 represent specific examples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vascular endothelial growth factor receptor; VBGF receptor; flt-1; flk-1; MSR; hammerhead ribozyme; hairpin ribozyme; cleavage; tumeur angiogenesis; psoriasis; rheumatoid arthritis; ocular disease; fms-like tyrosine kinase 1; kinase insert domain conteaining receptor;
                                                                                                                                                                                                                                                                                                             Gaps
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88.2%; Pred. No. 8.6e+02;
tive 0; Mismatches 2; Indels
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                                                                                                                                                                      Sequence 17 BP; 0 A; 9 C; 0 G; 0 T; 8 U; 0 Other;
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96US-00584040.
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11-JAN-1996;
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RESULT 1276

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The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (WEGF). A patient (preferably human) having a condition associated with the level of the fims-like tyrosine kinase 1 (fil-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase 1 (filk-1) (e.g. tumour angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient. AAX67275 to AAX75752 represent specific examples of nucleic acid molecules from the present invention
                                                                              Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid molecule modulating VEGF receptor(s) gene expression or stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient.
                                                                                                 KDR; hammerhead ribozyme; hairpin ribozyme; cleavage; tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease; fms-like tyrosine kinase 1; kinase insert domain containing receptor;
                                         Human flt1 VEGF receptor hammerhead ribozyme substrate #1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.8%; Score 13.8; DB 1; Length 17; 38.2%; Pred. No. 8.6e+02; ved. No. 8.10e+02; Indels 1ve 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 2 A; 2 C; 0 G; 0 T; 13 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stinchcomb D, Escobedo
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(first entry)
                                                                                                                                                                 foetal liver kinase 1; ss
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                    25-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                             26-OCT-1995;
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                                                                                                                                                                                                            Homo sapiens
  28-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (VEGF). A patient (preferably human) having a condition associated with the level of the fms-like tyrosine kinase 1 (fll-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour anglogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient. AAX67275 to AAX75752 represent specific examples of nucleic acid molecules from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient.
                                                                                                                                                                                                                                                                                                                endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
                                                                                                                                                                                                                                                                                                                                    KDR; hammerhead ribozyme; hairpin ribozyme; cleavage; tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease; fms-like tyrosine kinase 1; kinase insert domain containing receptor;
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88.2%; Pred. No. 8.6e+02;
Aative 0; Mismatches 2; Indels
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AAAAAAAAAAAAAA 1752
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(CHIR ) CHIRON CORP
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Best Local Simi
Matches 15;
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11-JAN-1996;
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   Gaps
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foetal liver kinase 1; ss
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AAX69804 standard; RNA; 17

RESULT 1277

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AAX69804/c ID AAX698 XX AC AAX698 XX

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The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vaccular endothelial growth factor (VEGF). A patient (preferably human) having a condition associated with the level of the fims-like tyrosine kinase 1 (fLL-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour anglogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient. AAX67275 to AAX75752 represent specific examples of nucleic acid molecules from the present invention
                                                                                                                                        Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
                                                                                                                                                              stability – useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.8%; Score 13.8; DB 1; Length 17;
88.2%; Pred. No. 8.6e+02;
ve 0; Mismatches 2; Indels
                                               Escobedo J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17 BP; 0 A; 0 C; 2 G; 0 T; 15 U; 0 Other;
                                               Stinchcomb D,
                                                                                                                                                                                                                                   Claim 4; Page 173; 218pp; English.
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96US-00584040.
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Best Local Similarity 88.2
Matches 15, Conservative
                                               Mcswiggen J,
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  (CHIR ) CHIRON CORP.
                                                                                           WPI; 1997-259017/23.
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                                               Pavco P,
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                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient.
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88.2%; Pred. No. 8.6e+02;
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96US-00584040.
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11-JAN-1996;
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Gaps

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Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage; thumur anglogenesis; psoriasis; theumatoid arthritis; ocular disease; fms-1ike tyrosine kinase i; kinase insert domain containing receptor; foetal liver kinase 1; ss.
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Human flt1 VEGF receptor hammerhead ribozyme substrate #675.
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              The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (VEGF). A patient (preferably human) having a condition associated with the level of the fims-like tyrosine kinase 1 (flt-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient. AAX67275 to AAX75752 represent specific examples of nucleic acid molecules from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1; MSR; hammerhead ribozyme; hairpin ribozyme; cleavage; tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease; fms-like tyrosine kinase 1; kinase insert domain containing receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse flt-1 VEGF receptor hammerhead ribozyme substrate #599.
                                                                                                                                                                                                                                                                    0.8%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 8.6e+02;
                                                                                                                                                                                                                                                                                                          2; Indels
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foetal liver kinase 1; ss
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(CHIR ) CHIRON CORP
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11-JAN-1996;
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                                                                                                                                                                                                                                                                                                                                    Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or mRNA
                                                                                                                                                                                                                                                                                                                                                   KDR, hammerhead ribozyme; hairpin ribozyme; cleavage; tumour angiogeneais; psoriaais; rheumatoid arthritis; ocular disease; fms-like tyrosine kinase 1; kinase insert domain containing receptor; foetal liver kinase 1; se
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                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid molecule modulating VEGF receptor(s) gene expression or stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient.
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18.2%; Pred. No. 8.6e+02;
ve 0; Mismatches 2; Indels
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Seguence 17 BP; 0 A; 0 C; 3 G; 0 T; 14 U; 0 Other;
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                          Score 13.8; DB 1;
Pred. No. 8.6e+02;
0; Mismatches 2;
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                                                                                                                            17 ACAAAACAAAAAACAAA
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                                              Local Similarity 88.2
les 15; Conservative
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integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; anglogenic factor; cytostatic; antidiabetic; ophthalmologic, antimilammatory; antiarthritic; antipaciatic; ARMD; dermatchlogical; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; vernora vulgaris; anglofibroma; tuberous sclerosis; pot wine stain; Sturge Weber syndrome; ss. Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

Homo sapiens WO9950403-A2 24-MAR-1999;

07-0CT-1999

Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;

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The present invention describes an enzymatic nucleic acid molecule (I) with RNA cleaving activity, which modulates the expression of a plant gene. Also described is a gene comprising a cDNA sequence encoding maize Delta-9 desaturase. (I) can be used to modulate expression of a gene, preferably Delta-9 desaturase or a granule bound starch synthase (GBSS) gene, in a plant (preferably a maize or canola plant). (I) can be used to modulate caffeine synthesis in a coffee plant, nicotine production in a tobacco plant, fruit ripening processes in an apple, tomato, pear, plum or peach plant, flower pigmentation in a rose, petunia, chrysanthemum or marigold plant or lignin production in a tobacco, aspen, poplar or pine plant.
                                                                                                                                                                                                                                                                                                                                                                  Maize; corn; Zea mays; delta-9 desaturase; GBSS; target; substrate; granule bound starch synthase; hammerhead ribozyme; hairpin ribozyme; modulation; gene expression; transgenic plant; cleavage; canola plant; caffeine synthesis; coffee plant; nicotine production; tobacco; fruit ripening; flower pigmentation; lignin production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mcswiggen JA, Merlo PAO, Guo L, Skokut TA;
Merlo DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ribozyme which modulates plant gene expression - preferably modulates expression of DELTA-9 desaturase or granule bound starch synthase in
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                                                                                                                                                                                                                                                                                                  Delta-9 desaturase hamerhead ribozyme target SEQ ID NO:881.
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Pred. No. 8.6e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 38; Page 87; 155pp; English.
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                                                                               AAX63006 standard; RNA; 17 BP.
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Young SA, Folkerts O,
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RESULT 1283
AAX63006/C
AXC AAX6300
XX AAX6300
XX AX6300
XX Delta-9
XX Maize;
XW Granule
XX Calmay
CC Gene,
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The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl cleaving activity, which specifically cleave RNA encoded by an aryl cleaving activity, which specifically cleave RNA encoded by an aryl control of AAA17161 to AAA1762 represent ribozyme sequences for ARNT, and AAA1761 to AAA1762 to AAA1768 to AAA1768 to AAA19675 to AAA19675 to AAA19675 to AAA19675 to AAA19675 to AAA1967 to AAA2168 to AAA2168 to AAA2169 to AAA2168 to AAA2169 to AAA2168 to AAA216
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4.7%; Pred. No. 8.6e+02;
ve 4; Mismatches 2; Indels
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Best Local Similarity
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AAA20382 standard; RNA; 17

RESULT 1284

Integrin alpha 6 subunit substrate sequence SEQ ID NO:3608.

19-JUN-2000 (first entry)

AAA20382;

AAA20382 ID AAA2 XX AC AAA2 XX DT 19-J XX

07-OCT-1999. 

AAA20383;

19-JUN-2000 (first entry)

Integrin alpha 6 subunit substrate sequence SEQ ID NO:3609.

Human; aryl hydrocarbon nuclear transport, ARNT, TIE-2; angiogenesis, integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; andiogenic factor; cytostatic; antidiabetic; ophthalmologic; antidiamatory; antiarthritic; antipsoriatic; ARNU; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; veruca vulgaris; angiofibroma; tuberous solerosis; pot-wine stain; Sturge Weber syndrome; ss.

Homo sapiens

WO9950403-A2

27-MAR-1998; 98US-0079678P.

(RIBO-) RIBOZYME PHARM INC

Mcswiggen JA; Coeshott C, Jarvis T, Pavco PA, Roberts E,

WPI; 1999-591315/50.

Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors.

Claim 55; Page 142; 305pp; English.

The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl cleaving activity, which specifically cleave RNA encoded by an aryl cleaving activity, which specifically cleave RNA encoded by an aryl cleaving activity, which specifically cleave RNA encoded by an aryl clear an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to AAA17165 and AAA17165 to AAA17165 and AAA1768 to AAA19185 to AAA19185 to AAA19185 to AAA19185 to AAA19185 and AAA19087 to AAA19185 to AAA19185 to AAA19185 to AAA19185 to AAA19185 to AAA19186 to AAA19186 to AAA19180 to AAA11895 represent their corresponding target sequences; AAA11689 to AAA2168 represent their corresponding target sequences; AAA21689 to AAA21681 represent their corresponding target sequences; AAA21689 to AAA21689 represent their corresponding target sequences; AAA21689 to AAA21681 and AAA21635 to AAA23142 to AAA23143 to Corresponding target sequences; AAA21689 to AAA21689 represent their corresponding target sequences; AAA21689 to AAA21681 and AAA22265 to AAA23142 to AAA23143 to Corresponding target sequences; AAA21689 to AAA21689 represent their corresponding target sequences; AAA21689 to AAA21689 to AAA23142 represent their corresponding target sequences; correspon integrin subunit alpha-6, or integrin subunit beta-3

Sequence 17 BP; 1 A; 6 C; 4 G; 0 T; 6 U; 0 Other;

Gaps ö 0.8%; Score 13.8; DB 1; Length 17; 58.8%; Pred. No. 8.6e+02; artive 5; Mismatches 2; Indels Conservative Similarity Ma. Local S... 10; Query Match Best Loca Matches

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1286 AAA18807

AAA18807 standard; RNA; 17 BP

AAA18807;

(first entry) 19-JUN-2000

Human TIE-2 substrate sequence SEQ ID NO:2033.

Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytostatic; antidabetic; ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; veruca vulgaris; angiofibroma; tuberous solerosis; pot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

Homo sapiens

409950403-A2

17-0CT-1999.

99WO-US006507. 24-MAR-1999;

27-MAR-1998;

(RIBO-) RIBOZYME PHARM INC.

Coeshott C, Mcswiggen JA; Pavco PA, Roberts E, Jarvis T,

WPI; 1999-591315/50.

Novel ribozymes for modulating the synthesis, expression and/or stability of an mkN $\lambda$  encoding an angiogenic factors.

Claim 56; Page 118; 305pp; English

The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl cleaving activity, which specifically cleave RNA encoded by an aryl cleaving activity, which specifically cleave RNA encoded by an aryl concarbon nuclear transporter (RNAT) gene, an integrin subunit beta 3 cene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to AAA1761 to AAA1762 represent ribozyme sequences for AAA1915 to AAA1915 and AAA1915 to AAA1915 to AAA1915 to AAA1915 to AAA1915 to AAA1915 and AAA1915 to AAA1915 and AAA1915 and AAA1915 to AAA1915 to AAA1915 and AAA1915 to AAA1915 and AAA1915 to AAA1915 and AAA2160 to AAA2160 and AAA1915 to AAA2160 and AAA2160 to AAA216 integrin subunit alpha-6, or integrin subunit beta-3

Sequence 17 BP; 3 A; 0 C; 10 G; 0 T; 4 U; 0 Other;

Gapa ö 0.8%; Score 13.8; DB 1; Length 17; 54.7%; Pred. No. 8.6e+02; ive 4; Mismatches 2; Indels 64.7%; 11; Conservative Best Local Similarity Query Match Matches

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A method has been developed for detecting the presence or absence of a single nucleotide polymorphism (SNP) allele in a genomic sample. The method comprises preparing a reduced complexity genome (RGG) from the genomic sample and analysing the RGG for the presence or absence of a SNP genomic pattern for an individual genome or to generate a genomic capattern for an individual genome or to generate a genomic classification code for a genome. The method can be used to assess whether a subject is at risk for developing a disease or to identify a set of SNP alleles associated with a disease. The method can also be used to perform linkage analysis. AAAA35944 to AAA35947 represent sequences used in the exemplification of the present invention. AAA35948 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detection of single nucleotide polymorphisms in genomes by preparation and analysis of reduced complexity genomes, useful for genotyping, fingerprinting and determining allele frequency of SNPs.
                                                                                                                                                                                                                                             Human; single nucleotide polymorphism; SNP; genotyping; DNA analysis; allele specific oligonucleotide; ASO; reduced complexity genome; RCG; genomic classification; identification; DNA fingerprinting; tumour characterisation; hybridisation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                            Human genomic SNP allele specific oligonucleotide SEQ ID NO:414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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88.2%; Pred. No. 8.68+02;
ative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA36632 represent nucleotide sequences containing SNPs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17 BP; 3 A; 4 C; 4 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Charest A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MASI ) MASSACHUSETTS INST TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Housman DE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 66; 111pp; English
1012 GATGTGGTTGGGGATGG 1028
                 ВЪ.
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                                                                                                               AAA36380 standard; DNA; 17
                                                                                                                                                                             26-JUL-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-293181/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                WO200018960-A2
                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                  24-SEP-1999;
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                                                                                                                                              AAA36380;
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ID AAA3
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AC AAA3
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A method has been developed for detecting the presence or absence of a single nucleotide polymorphism (SNP) allele in a genomic sample. The method comprises preparing a reduced complexity genome (RCG) from the genomic sample and analysing the RCG for the presence or absence of a SNP allele. The method can be used to characterise a tumour, to generate a genomic pattern for an individual genome or to generate a genomic classification code for a genome. The method can be used to assess whether a subject is at risk for developing a disease or to identify a set of SNP alleles associated with a disease. The method can also be used to perform linkage analysis. AAA35944 to AAA35947 represent sequences used in the exemplification of the present invention. AAA35948 to AAA36532 represent nucleotide sequences containing SNPs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detection of single nucleotide polymorphisms in genomes by preparation and analysis of reduced complexity genomes, useful for genotyping, fingerprinting and determining allele frequency of SNPs.
                                                                          Human; single nucleotide polymorphism; SNP; genotyping; DNA analysis;
allels specific oligonucleotide; ASO; reduced complexity genome; RCG;
genomic classification; identification; DNA fingerprinting;
tumour characterisation; hybridisation; 8s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insertion sequence; IS element; yoghurt; secondary metabolite; beta-spalatcosidase; cell wall protease; catabolite control protein A; lactate dehydrogenase; glycosyltransferase; lysogenic prophage; lac operon permease; ISL6; ISL7; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                       Human genomic SNP allele specific oligonucleotide SEQ ID NO:416.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.8%; Score 13.8; DB 1; Length 17;
18.2%; Pred. No. 8.6e+02;
ve 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                  Housman DE, Charest A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      720 AGCCTCTCAGGCTTCTG 736
                                                                                                                                                                                                                                                                                      99WO-US022283.
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26-JUL-2000 (first entry)
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Best Local Similarity 88.2
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                  Jordan B,
                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-293181/25.
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                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                  Landers JE,
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EP965643-A1

AAA36382 standard; DNA; 17 BP.

AAA36382;

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99WO-US008547.

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17-JUN-1998;
       17-JUN-1998;
                                                                                                           Homo sapiens
                                                                                                              WO9954459-A2
                                                                                                                 28-OCT-1999
              Mollet B,
                                                                                         AAA25445;
                                                                    Query Match
                                                                                  RESULT 1290
                                                                       Matches
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19-APR-1999;
This invention describes a novel use of insertion sequences (IS) elements (I) as tools for genetically modifying the genome of Lactobacillus Actobacillus helvericus (III). (II) are used as tools for genetically modifying the genome of (III). (II) and (III). This has applications in screening experiments to identify relevant genetic functionalities, for integration experiments or for gene expression onto the bacterial genome of (II) or (III). (II) and (III) are used for the preparation of a fermented product, secondary metabolites, betagalactosidase, cell wall protease, catabolite control protein A, lactate galactosidase, cell wall protease, a restriction system, a lysogenic prophage or the permease of the lac operon, where the gene is inactivated by insertion of at least 1 IS element. (I) are also useful for gene capting, gene inactivation and integration and/or gene expression on a plasmid and/or genomic level. Prior art IS elements were not used for modifying Lactobacilli, as this species, used for yoghurt production, were difficult to modify. (I) provide new genetic tools for Lactobacillus species which can be used for many processes such as gene tagging, unlike prior art lactobacilli IS elements, which are very limited. The modified becreatal strains are useful for producing a yoghurt in which post-aciditication and bitter taste which occurs during storage, is admiticantly reduced. This sequence represents a PCR primer used in the asguisticantly reduced. This sequence elements ISL6 and ISL7.
                                                                                                                                                                                                                                                                                                                           Use of insertion sequence elements for modifying the genomes of Lactobacillus bacteria, useful for screening and integration experiments.
                                                                                                                                                                                                                         Germond JE, Lapierre L;
                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 11; 19pp; English.
                                                                       98EP-00202028
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                                             Match 0.8%; Score 13.8; DB 1; Length 17; Local Similarity 88.2%; Pred. No. 8.6e+02; les 15; Conservative 0; Mismatches 2; Indels
Seguence 17 BP; 3 A; 4 C; 4 G; 6 T; 0 U; 0 Other;
                                                                                                                                                1672 GACTITGICACCAAATG 1688
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17 GACATTGTCACCAAAGG 1

.445/c AAA25445 standard; DNA; 17 19-JUL-2000 (first entry)

Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1943

Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage; hammerhead ribozyme; hairpin ribozyme; antisense Oligonucleotide; gene expression modification; cancer; phosphorothioate; endonuclease; anticancer; breast cancer; endometrium cancer; ss

The present invention describes nucleic acids (A) that interact stably with a target sequence and contain at least one phosphoro(di)thioate with a target sequence and contain at least one phosphoro(di)thioate link, having endonuclases activity. (A), and more generally any catalytic nucleic acid (A') that modulates expression of the oestrogen receptor cancer (particularly of breast or endometrium), converse transforming cells ex vivo and implanting treated cells, or for other conditions associated with levels of oestrogen receptor.

Because of the high selectivity for targeted RNA, (A) can also be used to correlate inhibition of gene expression with alterations in phenotype, particularly for identification of therapeutic targets, and as research reagents (for RNA, in the same way that restriction endonucleases are used with DNA). The combination of modifications in (A) improves resistance to nucleases, binding affinity and/or activity. AAA23503 to AAA24747 represent oestrogen receptor hammerhead ribozyme sequences.

AAA24742 represent oestrogen receptor hammerhead ribozyme sequences.

AAA2593 to AAA2502 represent their corresponding target sequences.

Sequences. AAA26107 to AAA26271 represent their corresponding target sequences. New nucleic acids that interact, and optionally cleave, target sequences, used to treat cancer. sequences. AAA26219 to AAA26271 represent other ribozyme sequences and antisense oligonucleotides used in the exemplification of the present Gaps Bellon L; .. 0 0.8%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 8.6e+02; 2; Indels Mcswiggen JA, Karpeisky A, is T, Woolf T, Haeberli P; Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other; 0; Mismatches Claim 77; Page 79; 148pp; English. Thompson JD, Beigelman L, Mcswig Reynolds M, Zwick M, Jarvis T, 1736 AAAAAAAAAAAAAA 1752 98US-0082404P. 98US-00103636. (RIBO-) RIBOZYME PHARM INC Matches 15; Conservative WPI; 2000-013248/01. Best Local Similarity Matulic-Adamic J; 20-APR-1998; 23-JUN-1998; Query Match ò

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17 AAAAAAAAAAACTAAA 1

AAA25182 standard; DNA; 17 BP AAA25182; RESULT 12 AAA25182/

19-JUL-2000 (first entry)

Destrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1680

Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage; hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide; gene expression modification; cancer; phosphorothioate; endonuclease; anticancer; breast cancer; endometrium cancer; ss.

Homo sapiens

409954459-A2

8-OCT-1999 

99WO-US008547. 19-APR-1999;

98US-0082404P

20-APR-1998;

Karpeisky A, Haeberli P;

Mcswiggen JA, is T, Woolf T,

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The present invention describes nucleic acids (A) that interact stably with a target sequence and contain at least one phosphoro(di)thioate with a target sequence and contain at least one phosphoro(di)thioate link, having endoauclease activity. (A), and more generally any catalytic nucleic acid (A') that modulates expression of the oestrogen receptor. Gene, are used to treat cancer (particularly of breast or endometrium), and vice or by transforming cells ex vivo and implanting treated cells, or for other conditions associated with levels of cestrogen receptor. Because of the high selectivity for targeted RNA, (A) can also be used to correlate inhibition of gene expression with alterations in phenotype, correlate inhibition of gene expression with alterations in phenotype, correlate inhibition of therapeutic targets, and as research cestents (for RNA, in the same way that restriction endoaucleases are used with DNA). The combination of therapeutic targets, and as research castrogen receptor hammerhead ribozyme sequences. AAA24747 represent cestrogen receptor harrpin ribozyme sequences. CC AAA24748 to AAA25010 represent their corresponding target sequences. AAA25017 represent cestrogen receptor harrpin ribozyme sequences and sequences and antisense oligonucleotides used in the exemplification of the present
                                                                                                                                                                                                                                       New nucleic acids that interact, and optionally cleave, target sequences, used to treat cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage; hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide; gene expression modification; cancer; phosphorothioate; endonuclease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 0.8%; Score 13.8; DB 1; Length 17; Local Similarity 88.2%; Pred. No. 8.68+02; nes 15; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17 BP; 1 A; 0 C; 2 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anticancer; breast cancer; endometrium cancer; ss
                                                                                                        Beigelman L, Mcswig
Zwick M, Jarvis T,
                                                                                                                                                                                                                                                                                                   Claim 77; Page 71; 148pp; English
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                        98US-00103636
                                                                (RIBO-) RIBOZYME PHARM INC.
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                                                                                                        Thompson JD,
Reynolds M,
                        23-JUN-1998;
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PF 19-2

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PF 20-2

PR 23-2
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99WO-US008547 98US-0082404P. 98US-00103636.

19-APR-1999; 20-APR-1998; 23-JUN-1998;

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with a target sequence and contain at least one phosphoro(di)thioate link, having endonuclease activity. (A), and more generally any catalytic nucleic acid (A') that modulates expression of the oestrogen receptor gene, are used to treat cancer (particularly of breast or endometrium), in vivo or by transforming cells ex vivo and implanting treated cells, or for other conditions associated with levels of oestrogen receptor. Because of the high selectivity for targeted RNA, (A) can also be used to correlate inhibition of gene expression with alterations in phenotype, particularly for identification of therapeutic targets, and as research reagents (for RNA, in the same way that restriction endonucleases are used with DNA). The combination of modifications in (A) improves
                                                                                                                                                                       nucleic acids that interact, and optionally cleave, target sequences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  resistance to nucleases, binding affinity and/or activity. AAA23503 to AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and AAA44748 to AAA25992 represent their corresponding target sequences. AAA25992 represent their corresponding target sequences. Sequences, and AAA26105 represent receptor hairpin ribozyme sequences, and AAA26107 to AAAA26128 represent their corresponding target sequences. AAA26219 to AAA26217 represent other ribozyme sequences and antisense oligonucleotides used in the exemplification of the present
                                                                                                                                                                                                                                                                      The present invention describes nucleic acids (A) that interact stably
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 0.8%; Score 13.8; DB 1; Length 17; Local Similarity 88.2%; Pred. No. 8.6e+02; es 15; Conservative 0; Mismatches 2; Indels
                                                        Karpeisky A,
Haeberli P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
                                                        n L, Mcswiggen JA,
Jarvis T, Woolf T,
                                                                                                                                                                                                                                Claim 77; Page 71; 148pp; English.
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                  (RIBO-) RIBOZYME PHARM INC.
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                                                      Thompson JD, Beigelman L,
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                                                                        Zwick M,
                                                                                                                                                                                             used to treat cancer.
                                                                                                                                   WPI; 2000-013248/01
                                                                                            Matulic-Adamic J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                          Reynolds M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA25446;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1293
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                                                                                              Bellon L;
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WPI; 2000-013248/01.
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hes 15; Conserv
                                                                                     Matulic-Adamic J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09954459-A2
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Matches
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Thompson JD,

20-APR-1998; 23-JUN-1998;

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with a target sequence and contain at least one phosphoro(dilthioate link, having endomuclease activity. (A), and more generally any catalytic nucleic acid (A), that modulates expression of the oestrogen receptor gene, are used to treat cancer (particularly of breast or endometrium), in vivo or by transforming cells at vivo and implanting treated cells, or for other conditions associated with levels of oestrogen receptor. Because of the high selectivity for targeted RNA, (A) can also be used to correlate inhibition of gene expression with alterations in phenotype, particularly for identification of therapeutic targets, and as research research for RNA, in the same way that contains and as research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reagents (for RNA, in the same way that restriction endonucleases are used with DNA). The combination of modifications in (A) improves resistance to mucleases, binding affinity and/or activity. Analysis to AAA24177 represent cestrogen receptor hammerhead riboxyme sequences, and AAA24778 to AAA25992 represent their corresponding target sequences, and AAA25992 to AAA26105 represent their receptor hairpin riboxyme sequences, and AAA26107 to AAA36218 represent their corresponding target sequences sequences.
                                                                                                                               nucleic acids that interact, and optionally cleave, target sequences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequences. AAA26219 to AAA26271 represent their corresponding target and antisense oligonucleotides used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein,
                                                                                                                                                                                                                                                                    The present invention describes nucleic acids (A) that interact stably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ribozyme; erythropoietin; granulocyte colony stimulating factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 0.8%; Score 13.8; DB 1; Length 17; 1 Similarity 88.2%; Pred. No. 8.6e+02; 15; Conservative 0; Mismatches 2; Indels
Haeberli P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17 BP; 1 A; 0 C; 2 G; 14 T; 0 U; 0 Other;
Jarvis T, Woolf T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mcswiggen J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hammerhead ribozyme substrate #844.
                                                                                                                                                                                                               Claim 77; Page 71; 148pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF02549 standard; DNA; 17 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-APR-2000; 2000WO-US009721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-FEB-2001 (first entry)
Zwick M,
                                                                                                                                                           used to treat cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interferon alpha; ss.
                                                                             WPI; 2000-013248/01.
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Best Local Similarity
                           Matulic-Adamic J;
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link, having endonuclease activity. (A), and more generally any catalytic

nucleic acid (A') that modulates expression of the oestrogen receptor

gene, are used to treat cancer (particularly of breast or endometrium),

in vivo or by transforming cells ex vivo and implanting treated cells, or

for other conditions associated with levels of oestrogen receptor.

Because of the high selectivity for targeted RNA, (A) can also be used to

correlate inhibition of gene expression with alterations in phenotype,

particularly for identification of therapeutic targets, and as research

c reagents (for RNA, in the same way that restriction endonucleases are

used with DNA). The combination of modifications in (A) improves

c AAA24747 represent cestrogen receptor hammerhad ribozyme sequences, and

AAA2593 to AAA2592 represent their corresponding target sequences.
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                                                                                                                                                                                    nucleic acids that interact, and optionally cleave, target sequences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences, and AAA26107 to AAA26218 represent their corresponding target sequences. AAA26219 to AAA26271 represent other ribozyme sequences and antisense oligonucleotides used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                      present invention describes nucleic acids (A) that interact stably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage; hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide; gene expression modification; cancer; phosphorothioate; endonuclease; anticancer; breast cancer; endometrium cancer; ss.
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                           Bellon
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88.2%; Pred. No. 8.6e+02;
iive 0; Mismatches 2; Indels
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                        Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Reynolds M, Zwick M, Jarvis T, Woolf T, Haeberli P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                               Claim 77; Page 79; 148pp; English
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98US-00103636.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUL-2000 (first entry)
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Gaps

interferon alpha and erythropoietin.

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Gaps

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The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of errythropoletin, granulocyte colony stimulating factor protein and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  erythropoletin, granulocyte colony stimulating factor protein and interferon alpha
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88.2%; Pred. No. 8.6e+02;
Live 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17 BP; 1 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
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88.2%; Pred. No. 8.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                 Claim 37; Page 75; 164pp; English.
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Best Local Similarity 88.2%
Matches 15; Conservative
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The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, ER3/COUP-TF-1, the GATA transcription factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoletin, granulocyte colony stimulating factor protein and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                         Ribozyme; erythropoietin; granulocyte colony stimulating factor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 13.8; DB 1; Length 17;
Pred. No. 8.6e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                  Zwick M, Pavco P, Mcswiggen J;
                                                                                                                                                                              Hammerhead ribozyme substrate #3178.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 42; Page 128; 164pp; English.
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1733 TACAAAAAAAAAAA 1749
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                                                                                              AAF06381 standard; DNA; 17 BP
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                                                                                                                                                                                                                         interferon alpha; ss
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                                                                                                                          AAF06381;
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                                                                                                                                                                                                                        The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription factor gene, IRF-2 and/or the CAATI Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoletin, granulocyte colony stimulating factor protein and interferon alpha
                                                                                                                                                                 Ensymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                 Score 13.8; DB 1; Length 17;
Pred. No. 8.6e+02;
0; Mismatches 2; Indels
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                                                                                                                            Mcswiggen J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hammerhead ribozyme substrate #1677.
                                                                                                                                                                                                      Claim 37; Page 93; 164pp; English
                                                                                                                                                                                                                                                                                                                                                                          1731 TTTACAAAAAAAAA 1747
                                                                                                                                                                                                                                                                                                                                     0.8%;
                                                                  11-APR-2000; 2000WO-US009721.
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                                                                                    99US-0129390P
                                                                                                                            Zwick M, Pavco P,
                                                                                                                                                                                                                                                                                                                                                                                             17 TTCACAAAGAAAAAA 1
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                                                                                                        (RIBO-) RIBOZYME PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF03382 standard; DNA; 17
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                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interferon alpha; ss
                                                                                                                                             WPI; 2000-647423/62.
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                            WO200061729-A2
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           Homo sapiens.
                                                                                    12-APR-1999;
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                                               19-OCT-2000
                                                                                                                           Blatt L,
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                                                                                                                                         The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoietin, granulocyte colony stimulating factor protein and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
useful for producing e.\,g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
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Pred. No. 8.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17 BP; 2 A; 3 C; 1 G; 11 T; 0 U; 0 Other;
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                                                                                      Claim 37; Page 94; 164pp; English.
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                                                                                                                                                                                                                                                                                                                                                       interferon alpha
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Alzheimer's disease; mtDNA; PCR primer;
                                                                                                               (MITO-) MITOKOR.
                                   WO200063441-A2
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                  Homo sapiens.
                                                                                     20-APR-1999;
22-OCT-1999;
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                                                    26-OCT-2000.
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                                                                                                                                                                                                                                                                                                                 Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
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 Gaps
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                                                                                                                                                 Ribozyme, erythropoietin, granulocyte colony stimulating factor; interferon alpha; ss.
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Indels
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Mismatches
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                                                                                                                               Hammerhead ribozyme substrate #500.
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                 1731 TTTACAAAAAAAAAA 1747
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                                                                            AAF02205 standard; DNA; 17
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                                 17 TTTACAAAAATGAAAA
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15; Conservative
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                                                                                                                                                                                                                                                                                 Zwick M,
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Human; 88; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; notropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgith's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; lymphocytic leukaemia; huma; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of or diagnosing Alzheimer's disease using single nucleotide polymorphisms (SNPs) present in an individual's mitochondrial DNA (mtDNA). In additon, the SNPs identified can be used to identifie agents suitable for use in treating Alzheimer's disease. Sequences AAC67301-C67610 are PCR primers used to demonstrate the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a novel method for determining the risk
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88.2%; Pred. No. 8.6e+02;
tive 0; Mismatches 2; Indels
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.9-APR-2000; 2000WO-US010906
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                                                                                                                                                                                                                                                                                             Herrnstadt C, Davis RE;
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Best Local Similarity
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The invention relates to a nucleic acid molecule which down regulates expression of a current growth inhibitor good.

Tegulates expression of a neurite growth inhibitor good.

Tegulates expression of a neurite growth inhibitor good.

Tegulates expression of a neurite growth inhibitor good.

The incleic acids may be enzymatic nucleic acid cleaving a nr RNA molecule possessing an NCH motifi), a G-cleaver (cleaving RNA with an NCH with an NCH motifi) proposessing an NCH motifi) a G-cleaver (cleaving RNA with an NCH with an NCH with an NCH with an NCH cD20-targetting nucleic acid is used to cleave RNA of coll of the presence of a divalent eation that is preferably MG<sup>2+</sup>.

Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targetting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-flowkaemia, HIV (human immunodeficiency virus) associated NHL, suphoma, leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, immunocytoma (IMC), small B-cell lymphocytic lymphoma, immunocytoma (IMC), small B-cell lymphocytic lymphoma, implanmancy arthropathy. The NOGO gene in the presence of a divalent cation that is preferably MG<sup>2+</sup>. Furthermore, the concated may be contacted with a cell co cleave RNA of the NOGO gene in the cell and treat a patient having a condition associated with the level of NOGO. The treatment may further comprise the use of one or more coll and treat a patient having a condition associated with the level of theraptes. In particular, the NOGO injury and cereborovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), parkinson's disease, ataxia, Huntington's disease, creates which response to the coll and to the model and patention of the invention
                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      central nervous system injury.
                                                                    11-FEB-2000; 2000US-0181797P.
28-FEB-2000; 2000US-0185516P.
06-MAR-2000; 2000US-0187128P.
                         09-FEB-2001; 2001WO-US004273
                                                                                                                                                                        RIBOZYME PHARM INC
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MCSWIGGEN J.
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                                                                                                                                                                        (RIBO-)
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(MCSW/)
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Sequence 17 BP; 6 A; 2 C; 4 G; 0 T; 5 U; 0 Other;

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Gaps
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0.8%; Score 13.8; DB 1; Length 17;
88.2%; Pred. No. 8.6e+02;
tive 0; Mismatches 2; Indels
                 Best Local Similarity 88.2
Matches 15; Conservative
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ABK02358 standard; RNA; 17 RESULT 1304 ABK02358
ID ABK0
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AC ABK0
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DT 12-M

12-MAR-2002 (first entry)

ABK02358;

Human NOGO Amberzyme #30

cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS; Parkinson's disease; ataxia; Huntington's disease; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease. Human, 88; antisense therapy; cytostatic; antiinflammatory; haemostatic;

Homo sapiens

Synthetic.

40200159103-A2

16-AUG-2001.

09-FEB-2001; 2001WO-US004273

11-FEB-2000; 2000US-0181797P. 28-FEB-2000; 2000US-0185516P. 06-MAR-2000; 2000US-0187128P.

RIBOZYME PHARM INC. RIBO-) 

CHOWRIRA B M. BLATT L. MCSWIGGEN J. MCSM/) CHOM/) BLAT/)

Chowrira BM, Blatt L, Mcswiggen J,

WPI; 2001-607195/69.

Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury.

Claim 88; Page 131; 200pp; English.

contraction relates to a nucleic acid molecule which down requiates expression of a neurite growth inhibitor gene (NGGO). The nucleic acide may be enzymatic nucleic acid molecule which down requiates expression of a neurite growth inhibitor gene (NGGO). The nucleic acide acide may be enzymatic nucleic acid cleaving an RNA molecule DNBzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA with a NYN motif) proposessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif). The CD20-targeting nucleic acid is used to cleave RNA with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg^2+. Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more charges. In particular, the CD20 targeting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphomy, low-grade or follicular non-thoughting lymphoma, leukaemia, B-cell lymphomy, Inwedge or follicular non-thoughting nucleic acid is used to cleave RNA of the NOGO-tre immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-tre cargetting nucleic acid may be contacted with a cell to reduce NOGO activity of the presence of a divalent cation that is preferably Mg^2+. Furthermore, the coll and treat a patient having a condition associated with the leval of NOGO. The treatment may further comprise the use of one or more therapies. In particular, the NOGO-targetting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (ALS), chemotherapy-induced neuropathy, annyliple sclerosis (ALS), chemotherapy-induced neuropathy, annyliple sclerosis (ALS), chemotherapy-induced neuropathy, annyliple accented for the acid and patient having disease, dementia, multiple sclerosis (ALS), chemotherapy-induced neuropathy. The invention relates to a nucleic acid molecule which down regulates

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NOGO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNAzyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr
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           states which respond to the modulation of NOGO expression. The present sequence is an amberzyme molecule of the invention
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muscular dystrophy, and/or other neurodegenerative disease
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                                                Sequence 17 BP; 8 A; 0 C; 9 G; 0 T; 0 U; 0 Other;
                                                                       Score 13.8; DB 1;
Pred. No. 8.6e+02;
0; Mismatches 2;
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28-FEB-2000; 2000US-0185516P.
06-MAR-2000; 2000US-0187128P.
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                                                                                                                                                                                                              ABK02357 standard; RNA; 17
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(BLAT/) BLATT L.
                                                                                                                                                                                                                                                                 12-MAR-2002 (first entry)
                                                                        Query Match
Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                          Human NOGO Amberzyme #29.
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an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA cc f CD20 in the presence of a divalent carion that is preferably Mg<sup>2</sup> +.

Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-bodgkin's lymphoma (NHL), bulky low-grade or follicular non-leukaemia, HV (human immunodeficiency virus) associated NHL, lymphocytic lymphocytic lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, immunodeficiency virus) associated NHL, mantle-cell cymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, immunodeficiency acid is used to cleave RNGO activity of the presence of a divalent cation that is preferably MG<sup>2</sup> +. Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the presence of a divalent having a condition associated with the level of NOGO. The treatment may further comprise the use of one or more therapies. In particular, the NOGO-targetting nucleic acid may be used to creat central nervous system (CNS) injury and cerebrovascular accident (CVM, stroke), Alzheimer's disease, dementia, multiple sclerosis (ALS), chemotherapy induced neuropathy, amyotrophic lateral sclerosis (ALS), chemotherapy induced neuropathy, amyotrophic lateral sclerosis (ALS), chemotherapy induced neuropathy, amyotrophic lateral sclerosis (ALS), barkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease, states which respond to the modulation of NOGO expression. The present cost and amberzyme molecule of the invention
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88.2%; Pred. No. 8.6e+02;
tive 0; Mismatches 2; Indels
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regulates expression of a neurite growth inhibitor gene (NOGO). The inversion and a coldence acids melecule which down regulates expression of a neurite growth inhibitor gene (NOGO). The nucleic acids may be enzymatic nucleic acids miss an RNA molecule possessing an Inozyme (an endolytic nucleic acid miss an RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NNY motif) proposessing an NCH motif), a G-cleaver (cleaving RNA with a NNY motif) proposessing an NCH motif). The CD20-targetting nucleic acid is used to cleave RNA with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA clear a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more the cell and treat a patient having a condition associated with the level of the creat lymphoma, leukaemia, B-cell lymphoma, loukaemia, helds way grade or follicular NHL, lymphocytic treat lymphoma, leukaemia, bulky low-grade or follicular NHL, lymphoma, loukaemia, HIV (human immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-targetting nucleic acid may be contacted with a condition associated with the level of nucleic acid may be contacted with a condition associated with the level of nucleic acid may be contacted with a condition associated with the level of the reatment may further comprise the use of one or more therapies. In particular, the NOGO-targetting nucleic acid may be contacted with a condition associated with the level of therapies. In particular, hunding a condition associated with the level of therapies. In particular, and of the neurodegenerative disease the entered a patient having a condition associated with the level of themperapy induced neuropathy, and/or other neurodegenerative disease the ambarrance is an ambarrance of the entered of the invarience of succession. The present of the analystyne of the invarience o
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                                                                                                                                                                                                                   Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury.
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                                                                                                                        Chowrira BM,
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RIBOZYME PHARM INC.
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MCSWIGGEN J.
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les 15; Conservative
                                                                                                                        Blatt L, Mcswiggen J,
                                                                            CHOWRIRA B M.
                                                                                                                                                                     WPI; 2001-607195/69
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(RIBO-) (BLAT/) (MCSW/)
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The invention relates to a nucleic acid molecule which down regulates expression of a neurite growth inhibitor good. The regulates expression of a neurite growth inhibitor good. The nucleic acids (e.g. a riboxyme or a nucleic acids may be enzymatic nucleic acid cleaving RNA with an NCH with an NCH with a NCH motif), a G-cleaver (cleaving RNA with an NCH with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA of CD20 in the presence of a divalent cation that is preferably MG'2 +... Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targetting nucleic acid may be used to treat lymphoma, leukemia, HIV (human immunodeficiency virus) associated WHL, mantle-cell lymphoma (MCL), immunocytona (INC), small B-cell lymphocytic lymphoma, inwinocytona (INC), small B-cell lymphocytic lymphoma, inwinocytona (INC), small B-cell lymphocytic lymphoma, invited a divalent cation that is preferably Mg'2 +. Furthermore, the presence of a divalent cation that is preferably Mg'2 +. Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO gene in the presence of the ratement may further comprise the use of one or more cell and treat a patient having a condition associated with the level of NOGO. The treatment may further comprise the use of one or more treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzhaimer's disease, dementia, multiple sclerosis (ALS), chemocherapy-induced neuropathy, amyorrophic lateral sclerosis (ALS), parkinson's disease, muscular B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerobrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; cerobrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; Parkinson's disease; ataxia; Huntington's disease; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease. Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury. Chowrira BM; Claim 88; Page 131; 200pp; English. 11-FEB-2000; 2000US-0181797P. 28-FEB-2000; 2000US-0185516P. 06-MAR-2000; 2000US-0187128P. 09-FEB-2001; 2001WO-US004273 RIBOZYME PHARM INC. Blatt L, Mcswiggen J, CHOWRIRA B M. BLATT L. MCSWIGGEN J. WPI; 2001-607195/69. 40200159103-A2 Homo sapiens. 16-AUG-2001. Synthetic. (BLAT/) (MCSW/) (RIBO-) (CHOM/) ö Gaps ö

0.8%; Score 13.8; DB 1; Length 17;

Query Match

sequence is an amberzyme molecule of the invention Sequence 17 BP; 7 A; 1 C; 9 G; 0 T; 0 U; 0 Other;

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ABL46643;
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leukaemia; cytostatic; ss.
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88.2%; Pred. No. 8.6e+02;
iive 0; Mismatches 2; Indels
Pred. No. 8.6e+02;
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                  88.2%;
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                                                                             861 AGGAAGAGGAAGAGGAG
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                  Best Local Similarity
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The present invention relates to oligonucleotides that downregulate the expression of human Grb2-related with Insert Domain (GRID) gene. GRID is a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful for modulating the expression of GRID, to treat conditions such as tissue/graft rejection and leukaemia. The oligonucleotides can also be administered in conjunction with other therapies such as radiation, chemotherapy and cyclosporin treatment. The present oligonucleotide was used to illustrate the invention
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                                                  Human, Grb2-related with Insert Domain; GRID; T-cell;
co-stimulatory adaptor protein; tissue rejection; graft rejection;
leukaemia; cytostatic; ss.
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Pred. No. 8.6e+02;
0; Mismatches 2; Indels
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Human GRID NCH ribozyme substrate oligonucleotide #194.
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15; Conservative
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Ellis JH;

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The present invention relates to oligonucleotides that downregulate the expression of human Grb2-related with Insert Domain (GRID) gene. GRID is a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful for modulating the expression of GRID, to treat conditions such as tissue/graft rejection and leukaemia. The oligonucleotides can also be administered in conjunction with other therapies such as radiation, chemotherapy and cyclosporin treatment. The present oligonucleotide was used to illustrate the invention
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                                                                                                               New nucleic acid(s) for regulating the Grb2-related with Insert [GRID) gene comprises using antisense and enzymatic nucleic acid molecules such as hammerhead ribozymes.
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                                                  Mcswiggen JA, Hamblin PA,
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                                                Von Carlowitz I,
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(RIBO-) RIBOZYME PHARM INC. (GLAX ) GLAXO GROUP LTD.
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                                                  Jarvis T,
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Ellis JH

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for modulating the expression of GRID, to treat conditions such as tissue/graft rejection and leukaemia. The oligomucleotides can also be administered in conjunction with other therapies such as radiation, chemotherapy and cyclosporin treatment. The present oligonucleotide was used to illustrate the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                Human, Grb2-related with Insert Domain, GRID, T-cell;
costimilatory adaptor protein; tissue rejection; graft rejection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid(s) for regulating the Grb2-related with Insert [GRID) gene comprises using antisense and enzymatic nucleic acid molecules such as hammerhead ribozymes.
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                                                                                                                              Length 17;
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                                                                                                                              Score 13.8; DB 1; Length 1
Pred. No. 8.6e+02;
0; Mismatches 2; Indels
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88.2%; Pred. No. 8.6e+02;
tive 0; Mismatches 2;
                                                                                                  Sequence 17 BP; 3 A; 7 C; 6 G; 0 T; 1 U; 0 Other;
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                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                              203 CCAGAGCCCCTCAGGGG 219
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                                                                                                                                                                                                                                                                                                        ABL46888 standard; RNA; 17 BP
                                                                                                                                 0.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (RIBO-) RIBOZYME PHARM INC. (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    leukaemia; cytostatic; ss.
                                                                                                                                                                15; Conservative
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                       ABL46888
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Gaps

25-MAY-2001; 2001WO-US016981

WO200192524-A2. Homo sapiens.

06-DEC-2001

2000US-0236359P

30-JAN-2001; 2001WO-US000662.

04-OCT-2000; 30-JAN-2001;

2001WO-US000665 2001WO-US000666. 2001WO-US000667.

2001WO-US000664

30-JAN-2001; 2001WO-US000669.

30-JAN-2001;

30-JAN-2001;

30-JAN-2001;

30-JAN-2001;

30-JAN-2001; 2001WO-US000670 05-FEB-2001; 2001US-0266860P

(AEOM-) AEOMICA INC.

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The present invention relates to a hairpin oligonucleotide primer for extension by a DNA polymerase, comprising a stem formed by complementary 3, and 5, arm sequences and a single-stranded loop sequence separating the arm sequences, where the 3 arm sequence and the loop sequence are both complementary to a selected priming region of a target nucleic acid strand. The invention is useful for nucleic acid amplification by a polymerase chain reaction (FOR), a strand displacement reaction (SDA), a nucleic acid sequence-based amplification (NASBA), transcription-mediated process includes real-time detection of intended amplification products utilizing separate detection probes having interactive labels, at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel primers for nucleic acid amplification, comprise a hairpin
structure in which a single-stranded loop separates complementary 3' and
5' arms and the loop and the 3' arm are complementary to target nucleic
                                                                                                                                                                  Hairpin oligonucleotide; amplification; prímer; ss.
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                               AAC89333 standard; DNA; 17 BP
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                                                                                                07-MAR-2001 (first entry)
                                                                                                                                 First conventional primer.
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                                                               AAC89333;
RESULT 1313
AAC89333/c
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ö Gaps ö Query Match 0.8%; Score 13.8; DB 1; Length 17; Best Local Similarity 88.2%; Pred. No. 8.6e+02; Matches 15; Conservative 0; Mismatches 2; Indels

242 CGGGGCCACCACGGCC 258 17 CGCGGCGACCACCGGCC 1 쉽

Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss. Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10504. ABN10512 standard; DNA; 17 BP 29-MAY-2002 (first entry) ABN10512; ABN1051 ID ABI XX XX AC ABI XX XX XX XX YW HUW KW MUW KW WW

RESULT 1314

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1 GAGAGAGCCAGGGACGG 17

RESULT 1315 ABN07887

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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 mucleic acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to hGDMLP-1 provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunosens to raise antibodies that specifically recognise hGDMLP-1 proteins, as specifically recognise hGDMLP-1 proteins, as specifically of hGDMLP proteins, as specific blomolecule and/or amount specifically of hGDMLP proteins, as specific blomolecule and/or amount specifically of hGDMLP proteins, as specific blomolecule conduction, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production and in vaccines or for replacement therapy. The collapse disorders specific disorders, hGDMLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence of the patent din out form part of the printed processification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
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18.2%; Pred. No. 8.6e+02;
ve 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rank DR,
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Best Local Similarity 88.2<sup>3</sup>
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gu Y, Ji Y, Penn SG,
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Human, genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
skeletal muscle disorder; amplicon; screening; ss.
                                    Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7879.
                                                                                                                                    2000US-0234687P.
2000US-0236359P.
2000GB-00024263.
2001WO-US000661.
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2001WO-US000663.
2001WO-US000664.
2001WO-US000665.
2001WO-US000666.
                                                                                                                 25-MAY-2001; 2001WO-US016981
                                                                                                                                                                                              2001WO-US000667
ABN07887 standard; DNA; 17
                         (first entry)
                                                                                       WO200192524-A2.
                                                                                                                                                                         30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
                                                                           Homo sapiens
                                                                                                                              26-MAY-2000;
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27-SEP-2000;
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                         29-MAY-2002
                                                                                                     06-DEC-2001
            ABN07887
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Shannon ME; Chen W, Hanzel DK, Rank DR, Gu Y, Ji Y, Penn SG, (AEOM-) AEOMICA INC. WPI; 2002-179446/23.

2001WO-US000668. 2001WO-US000670

30-JAN-2001; 30-JAN-2001; 30-JAN-2001;

05-FEB-2001; 2001US-0266860P

New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.

Disclosure; SEQ ID NO 7879; 214pp; English.

The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids in samples, as amplification substrates, to nucleic acids in samples, as amplification substrates, to hGDMLP-1 nucleic acids in samples, as amplification substrates, to hGDMLP-1 nucleic acids in samples, as amplification substrates, to hGDMLP-1 provided initial substrates for the recombinant engineering of hGDMLP-1 proteins variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polyreptides may be used as immunospens to raise antibodies that specifically recognise hGDMLP-1 proteins, as specifically recognise hGDMLP-1 proteins, as specific biomolecule and/or amount specifically proteins, as specific biomolecule and/or amount specifically proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production and in vaccines or for replacement therapy. The production and skeletal muscle disorders. hGDMLP-1 may be used for diagnosing a disorder associated with the exemplification of the present sequence represents an oligomer used in the screening of the hGDMLP-1. Sequence data for this patent aid not form part of the printed specification, but was obtained in electronic format directly from WIPO capture acides and sequence and electronic format directly from WIPO captures.

Sequence 17 BP; 2 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                         Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.
                                      Gaps
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                                                                                                                                                                                                                                                                                                          Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:896.
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         Length 17;
                                        IndelB
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Query Match 0.8%; Score 13.8; DB 1;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches, 15; Conservative 0; Mismatches 2;
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30-JAN-2001; 2001WO-US000661.
30-JAN-2001; 2001WO-US000662.
30-JAN-2001; 2001WO-US000664.
30-JAN-2001; 2001WO-US000665.
30-JAN-2001; 2001WO-US000666.
30-JAN-2001; 2001WO-US000666.
30-JAN-2001; 2001WO-US000668.
30-JAN-2001; 2001WO-US000669.
                                                                           835 GAAGCTGCTGGGGTCTC 851
                                                                                                          1 GGAGCTGCTGGGGTCAC 17
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2000US-0234687P.
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27-SEP-2000;
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polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the screening of the present sequence in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
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Pred. No. 8.6e+02;
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30-JAN-2001; 2001WO-US000667.
30-JAN-2001; 2001WO-US000668.
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2001WO-US000663.
2001WO-US000664.
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2001WO-US000661
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Local Similarity 88.2%;
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nucleic acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunospens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production and in vaccines or for replacement therapy. The production as sequences encoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders, hGDMLP-1 is localised to chromosome 22.

The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence in the exemplification of the present invention. N.B.

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fig. at ftp.wipo.int/pub/published_pct_sequence
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Matches ð 유 The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynuclectide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 calds can be used as probes to detect, characterise and quantify can be used in samples, as amplification substrates, to hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser describin ionisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The polymucleotide sequences encoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22. New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1. The present sequence represents an oligomer used in the screening of the hGDWLP-1 sequence in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequence Human, genome-derived myosin-like protein 1, GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss. Gaps Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10022. ö 0.8%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 8.6e+02; ative 0; Mismatches 2; Indels Seguence 17 BP; 4 A; 3 C; 10 G; 0 T; 0 U; 0 Other; Disclosure, SEQ ID NO 10506; 214pp; English 809 GAGAGCCAGGCCAGGG 825 ABN10030 standard; DNA; 17 BP 1 GAGAGCCAGGGACGGGG 17 2000US-0207456P. 2000US-0234687P. 2000GB-00024263 2001WO-US000661 25-MAY-2001; 2001WO-US016981 2000US-0236359P 29-MAY-2002 (first entry) Best Local Similarity 88.2 Matches 15; Conservative WPI; 2002-179446/23.

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expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The and skeletal muscle disorders hGDMLP-1 is now be used for disgnosing a disorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1
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30-JAN-2001; 2001WO-US000668.
30-JAN-2001; 2001WO-US000669.
30-JAN-2001; 2001WO-US000670.
35-PEB-2001; 2001US-0266860P.
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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to hGDMLP-1 nucleic acids in samples, as amplification substrates, to hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunospens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption indisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The concentration and skeletal muscle disorders. hGDMLP-1 mpaticular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence data for this patent did not form part of the printed per printed in the capture of the printed per printed in the capture of the printed per printed per printed in electronic format directly from MIPO and the present directly                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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nes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ji Y, Penn SG,
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Matches
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The invention relates to the use of phytanic acid or its derivatives for relates to a method for treating or preventing non-insulin dependent diabetes mellitus on an method for treating or preventing non-insulin dependent diabetes mellitus (NIDDM) or other conditions associated with impaired glucose tolerance such as obesity using phytanic acid or its derivatives. The phytanic acid, their derivatives or their precursors are useful as pharmaceutical compounds or supplements to foods or feeds for the treatment or prevention of type II or NIDDM, hyperlipidaemia, hyperrisulinaemia, syndrome x, hypertension, hyperrigilyceridaemia, impaired glucose tolerance and related obesity. They are also useful in insulin therapy in combination with known active compounds. The present sequence is low-density lipoprotein receptor (LDLR) cDNA amplifying reverse transcription PCR (RT-PCR) primer used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                           New composition comprising phytanic acid or its derivatives, useful for treating or preventing non-insulin dependent diabetes mellitus, impaired glucose tolerance and related obesity.
                               glucose tolerance, food supplement; feed supplement; hyperinsulinaemia; hyperlipidaemia; hypertension; insulin therapy; hypercholesterolaemia; hypertriqlyceridaemia; primer; RT-PCR; LDLR; reverse transcription PCR; low-density lipoprotein receptor; ss.
              obesity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, UDP-GalNAc.polypeptide N-acetylgalactosaminyltransferase 10;
pp-GaNTase 10; EC 2.4.1.41; chromosome 7q11.2; gene therapy; scanning;
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              Phytanic acid; non-insulin dependent diabetes mellitus; NIDDM;
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Pred. No. 8.6e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                         Hunziker W, Weber P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Page 9; 29pp; English.
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Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                    (HOFF ) ROCHE VITAMINS
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                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-270864/32.
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Synthetic.
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EP1243660-A2

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cetylgalactosaminyltransferase 10 protein is useful to diagnose, prevent and treat disorders associated with reduced or over expression of the
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pp-GaNTase 10; EC 2.4.1.41; chromosome 7q11.2; gene therapy; scanning;
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88.2%; Pred. No. 8.6e+02;
tive 0; Mismatches 2; Indels
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                                                                                                30-JAN-2001; 2001WO-US0006667.
30-JAN-2001; 2010WO-US000667.
30-JAN-2001; 2001WO-US000668.
30-JAN-2001; 2001WO-US000669.
30-JAN-2001; 2001WO-US000670.
33-MAY-2001; 2001US-008064761.
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25-JAN-2002; 2002EP-00001161
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Best Local Similarity
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                                                             30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes an isolated nucleic acid (I) encoding a human UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 10 (pp-GaNTase 10, EC 2.4.1.41) protein. Human pp-GaNTase 10 is located to chromosome 7q11.2. (I) can be used in gene therapy. Molecules of the present invention can be used in therapy, particularly to prevent or treat a disorder associated with decreased expression or activity of pp-GaNTase. The sequences given in ABV8501 to ABV8668 and ABP53502 to ABP53504 are given in the exemplification of the present invention. N.B. The sequence data for this parent is not represented in the printed specification but is based on sequence information supplied by the
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pp-GaNTase 10; EC 2.4.1.41; chromosome 7q11.2; gene therapy; scanning;
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88.2%; Pred. No. 8.6e+02;
rative 0; Mismatches 2; Indels
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2001MO-US000665.
2001MO-US000666.
2001MO-US000667.
2001MO-US000669.
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23-MAY-2001; 2001US-00864761.
30-AUG-2001; 2001US-0315984P.
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ABV85235 standard; DNA; 17
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ses 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoded protein.
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30-JAN-2001; 2
30-JAN-2001; 2
30-JAN-2001; 2
30-JAN-2001; 2
30-JAN-2001; 2
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RESULT 1323

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2001WO-US000667
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     30-JAN-2001;
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                                                                                                    Zhang J,
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Matches
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pp-GaNTase 10; EC 2.4.1.41; chromosome 7q11.2; gene therapy; scanning;
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88.2%; Pred. No. 8.6e+02;
7ative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  1023 GGATGGGGCTGGGGTTG 1039
30-JAN-2001; 2001WO-US000664.
30-JAN-2001; 2001WO-US000665.
30-JAN-2001; 2001WO-US000666.
30-JAN-2001; 2001WO-US000667.
30-JAN-2001; 2001WO-US000669.
30-JAN-2001; 2001WO-US000669.
30-JAN-2001; 2001WO-US0006770.
23-MAY-2001; 2001US-00864761.
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30-JAN-2001; 2001WO-US000665.
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                                                                                                                                Gu Y, Nguyen C;
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nes 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding human UDP-GalNAc:polypeptide N-cetylgalactosaminyltransferase 10 protein is useful to diagnose, prevent and treat disorders associated with reduced or over expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes an isolated nucleic acid (I) encoding a human UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 10 (pp-GaNTase 10, EC 2.4.1.41) protein. Human pp-GaNTase 10 is located to chromosome 7q11.2. (I) can be used in gene therapy. Molecules of the present invention can be used in therapy, particularly to prevent or treat a disorder associated with decreased expression or activity of pp-GaNTase. The sequences given in ABV85011 to ABV86689 and ABP51502 to ABP51504 are given in the exemplification of the present invention. N.B. The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied by the
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human testis expressed Patched like protein; testis; adrenal; liver;
male germ cell development; bone marrow; brain; kidney; lung; placenta;
prostate; skeletal muscle; colon; male infertility; cancer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17 BP; 2 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
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30-JAN-2001; 2001WO-US000664.
30-JAN-2001; 2001WO-US000665.
30-JAN-2001; 2001WO-US000667.
30-JAN-2001; 2001WO-US000668.
30-JAN-2001; 2001WO-US000669.
23-MAY-2001; 2001WS-US000669.
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30-JAN-2001; 2001WO-US000668.
30-JAN-2001; 2001WO-US000669.
30-JAN-2001; 2001US-US00670.
323-MAY-2001; 2001US-0864761.
30-AUG-2001; 2001US-0315984P.
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1es 15; Conservative
                                                                                                                                                                                                                                                                                                            Gu Y, Nguyen
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30-JAN-2001; 2001WO-US000669.
23-MAY-2001; 2001US-00864761.
09-OCT-2001; 2001US-0327898P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                     Zhan J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1328
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                                                                                                             Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1; human testis expressed Patched like protain; testis; adrenal; liver; human testis expressed Patched like protain; kiediey; adrenal; liver; prostate gene cell development; bone marrow; brain; kidney; lung; placenta; prostate; skeletal muscle; colon; male infertility; cancer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human HTPL scanning oligonucleotide SEQ ID 384.
                                                                                                                                                                       Example 2; Page 148; 718pp; English
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2001WO-US000664.
2001WO-US000665.
2001WO-US000667.
2001WO-US000668.
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 09-OCT-2001; 2001US-0327898P.
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                                                                                    WPI; 2002-676582/73.
                            (AEOM-) AEOMICA INC
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30-JAN-2001; 2
30-JAN-2001; 2
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                                                         Shan J;
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The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV8762 and ABB98519 to ABB98520). HTPL has two isoforms, with a few single base pair differences between the two. One of the single base pair changes introduces a premature stop codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL cahares an overall structure organisation with the Patched protein. The shared structural features strongly imply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL is important in regulating male germ cell development, and the HTPL gene was mapped to human chromosome 10pl2.1 HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of such disorder associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal, adult and foetal liver, bone marrow, brain, kidney, lung, placenta, prostate, cakeletal muscle or colon function. HTPL proteins and nucleic acids are calinically useful diagnostic markers and potential therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an
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88.2%; Pred. No. 8.6e+02;
ve 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Page 114; 718pp; English
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nes 15; Conservative
                                                                                                                                                                                    WPI; 2002-676582/73.
(AEOM-) AEOMICA INC
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The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for treating conditions selected from cancer, lymphoma, Ewing's saccoma, metanoma, tumour angiogenesis, diabetic retinopathy, macular degeneration, tumour angiogenesis, diabetic retinopathy, macular degeneration, vulgaris, angiofibroma of tuberous sclerosis, port-whose stains, Sturge (Weber syndrome, Rippel-Trenaunay-Weber syndrome, Osler-Weber-rendu (Syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for creating a pattent having a condition associated with the level of ERG, by contacting cells of the patient with (I) under conditions suitable for the treatment. The method comprises the use of one or more theraples (C) by contacting suitable for the treatment. Leukaemia or tumour angiogenesis is treated by administering (I) to the patient in a conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or chemotherapy treatment. (I) is useful for reducing ERG activity in a cell, by contacting the cell with (I). (I) is useful for cleaving RNA of ERG gene, by contacting the cell with (I). (I) is useful for cleaving RNA of cation such as Mg2+. (I) is useful for specific tool to examine genetic drift and mutations within diseased cells or to detect (C) examine genetic drift and mutations within diseased cells or to detect (C) the presence of ERG RNA in a cell. (I) is useful for specifically chargeting genes that share homology with ERG gene or ERG fusion genes. ABK17354-ABK2719 represent nucleic acide, including antisense and ensymment of the invention which regulate expression of ERG, and ensymment concleanse of ensymments of the invention such as high invention of the invention o
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                                                                                                                                                                                                                                                                                 Novel polynucleotide which down regulates expression of Ets-related gen useful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
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Pred. No. 8.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 83; 149pp; English
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                                                     16-MAY-2000; 2000US-00572021
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                                                                                                    (RIBO-) RIBOZYME PHARM INC.
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The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for treating conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma, tumour angiogenesis, diabetic retinopathy, macular degeneration, cundaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge Weber syndrome, Rippel-Trenaunay-Weber syndrome, Osteoporosis and wound healing. (I) is useful for syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for treating a patient having a condition associated with the level of ERG, by contacting cells of the patient with (I) under conditions suitable for the treatment. The method comprises the use of one or more theraples the treatment. The method comprises the use of one or more theraples conjunction with one or more of other therapies such as radiation or angiogenesis is treated by administering (I) to the patient in angiogenesis is treated by administering (I) to the patient in a cell, by contacting the cell with (I). (I) is useful for cleaving RNA of ERG gene, by contacting the cell with (I). (I) is useful for cleaving the cell, with RNA, in the presence of adivalent examine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically transence of ERG RNA in a cell. (I) is useful for specifically casted, and as diagnostic tool to examine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically casted, and as diagnostic tool to examine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically casted, and as diagnostic tool to examine genetic drift and mutations within the ERG gene or ERG fusion genes. ARX1354-ABK22719 represent nucleic acids, including antisense and enzymetic nucleic acid molecules which regulate expression of ERG, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
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ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                 Mclaughlin F, Randi AM;
                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polynucleotide which down regulates expression of Ets-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 13.8; DB 1; Length 17; Pred. No. 8.6e+02; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 8 A; 1 C; 8 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                   Von Carlowitz I, Mcswiggen JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   related PCR primers of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 94; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                              16-MAY-2001; 2001WO-US015866.
                                                                                                                                                                                                               16-MAY-2000; 2000US-00572021.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.8%;
88.2%;
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                                                                                                                                                                                                                                                            (RIBO-) RIBOZYME PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK18192 standard; RNA; 17
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es 15; Conservative
                                                                                                                                                                                                                                                                                    (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-082995/11.
                                                                     WO200188124-A2.
                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-APR-2002
                                                                                                                    22-NOV-2001
                                                                                                                                                                                                                                                                                                                                 Jarvis T,
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us10008789-3.rng

PAPP-E; human; pregnancy associated plasma protein E; abortive; contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;

dysgenetic pregnancy; primer; ss.

JS2002102252-A1. Homo sapiens.

01-AUG-2002.

Human PAPP-Ea associated 17-mer SEQ ID 484.

(first entry)

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vulnerary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis; tumour angiogenesis; diabetic retinopathy; macular degeneration; neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris; angiofibroma of tuberous sclerosis; port-wine stain; wound healing; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss; Ogler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;
                                                                                                                                                                                                                                                                                       Novel polynucleotide which down regulates expression of Ets-related gen useful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
                                                                                                                                                                                                                                          Mcswiggen JA, Mclaughlin F,
                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 74; 149pp; English.
                                                                                                                                                              16-MAY-2001; 2001WO-US015866.
                                                                                                                                                                                    16-MAY-2000; 2000US-00572021.
                                                                                                                                                                                                                                           Jarvis T, Von Carlowitz I,
                                                                                                                                                                                                        (RIBO-) RIBOZYME PHARM INC. (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                WPI; 2002-082995/11.
                                                                                                                  W0200188124-A2.
                                                                                            Homo sapiens.
                                                                                                                                       22-NOV-2001
                                                                    amberzyme.
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Randi AM;

Expression of an Ets-related gene (ERG). (I) is useful for treating expression of an Ets-related gene (ERG). (I) is useful for treating conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma, conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma, cumpour angiogenesis, diabetic retinopathy, macular degeneration, cumpour angiogenesis, diabetic retinopathy, macular degeneration, cumpour angiogenesis, verruca vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge Weber syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for treating a patient having a condition associated with the level of ERG, by contacting cells of the patient with (I) under conditions suitable for the treatment. The method comprises the use of one or more therapies under conditions suitable for the treatment. Leukaemia or tumour conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or cell, by contacting (I) is useful for reducing ERG activity in a cell, by contacting (I) with RNA, in the presence of a divolent cation such as Mg2+. (I) is useful for diagnosis of conditions and diseases related to the expression of ERG, and as diagnosit coll to examine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically cargeting genes that share homology with ERG gene or ERG fusion genes. ABK17354-ABK22719 represent nucleic acids, including antisense and enzymmatic nucleic acid molecules which regulate expression of ERG, and cargumatic nucleic acid molecules which regulate expression of ERG, and cargumatic nucleic acid molecules acids, including antisense and

Gaps ö 0.8%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 8.6e+02; ative 0; Mismatches 2; Indels Sequence 17 BP; 2 A; 12 C; 3 G; 0 T; 0 U; 0 Other; 15; Conservative Query Match Best Local Similarity

273 CCAGCCCCACCCCAGGG 289 ccasccccacccccd 17

g ò

Human, POSHL 1, SH3 domain, POSH-like signalling protein 1, oncogene, Rho GTPase; signal transduction, gene expression, cancer; vaccine;

gene therapy; transgenic; ss.

Homo sapiens EP1239051-A2

Human POSHL1 scanning oligonucleotide SEQ ID NO 1507.

(first entry)

23-DEC-2002

ABV90794;

ö

ABV90794 standard; DNA; 17 BP

RESULT 1332

ABS74958 standard; DNA; 17 BP ABS74958 RESULT 1331 ABS74958 ID ABS7 XX AC ABS7

ö This invention describes a novel isolated nucleic acid that encodes one of three new isoforms of human pregnancy associated plasma protein E, hepapper. The products of the invention have abortive and contraceptive activity and can be used for gene therapy or in a vaccine. The nucleic acid, polypeptide encoded by it, or antibody to the polypeptide can be used in pharmaceutical compositions or vaccines for preventing or aborting pregnancy. PAPP-E is used in the antenatal diagnosis of dysgenetic pregnancies. The nucleic acids are used as probes to assess the level of PAPP-E isoform mRNA in chorionic villus samples, and the antibodies can be used to assess the expression levels of PAPP-E isoform antibodies can be used to assess the expression levels of PAPP-E isoform proteins in chorionic villus samples, to diagnose dysgenetic pregnancies antenatally. This sequence reperseents an oligomer used in scanning the human PAPP-E genes described in the disclosure of the invention Gaps New isolated nucleic acid encoding an isoform of human pregnancy associated plasma protein E, for preventing or aborting pregnancy ö 0.8%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 8.6e+02; tive 0; Mismatches 2; Indels Sequence 17 BP; 15 A; 0 C; 2 G; 0 T; 0 U; 0 Other; Example 2; Page 138; 353pp; English. 37 AAAAAAAAAGCCAGAAA 53 1 AAAAAAAAAAAAAAA 17 26-MAY-2000; 2000US-0207456P. 06-APR-2001; 2001US-00827998 Query Match Best Local Similarity 88.2⁵ ----hes 15; Conservative (GUYY/) GU Y. (SHAN/) SHANNON M E. WPI; 2002-697817/75. 3u Y; Shannon ME; ð 용

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The invention relates to an isolated SH3 domain (POSH)-like signalling protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino acids (SI, ABB8399), a sequence having 6fs sequence identity to (SI), (SI), and the sequence comprising at least 8 contiguous amino acids. (Isolations) by deviations, especially conservative substitutions or a fragment of the sequences comprising at least 8 contiguous amino acids. Human POSHL is a proto-oncogene/oncogene product that functions as an adaptor protein that interacts with Rho family small GTPases as well as commistream components of the signal transduction pathway. (I) is useful for identifying a specific binding partner. (I) and nucleic acids (II) encoding (I) are useful for diagnosing, monitoring disease and treating caused by altered expression of human POSHL1 including diagnosing and treating caused by altered expression of human POSHL1 including diagnosing and treating caused by measuring and for surveying gene expression and creating are useful for measuring and for surveying gene expression and creating transgenic non-human animals capable of producing the proteins. The present sequence is that of a scanning oligonucleotide useful in examples of the invention. Note: The present sequence did not form mattof the present sequence information supplied to between by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL -1, useful for treating disorders associated with decreased expression or activity of human POSHL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; SEQ ID NO 1507; 60pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.8%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 8.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17 BP; 1 A; 5 C; 7 G; 4 T; 0 U; 0 Other;
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0; Mismatches
                                                                                                    30-JAN-2001; 2001WO-US000663.
30-JAN-2001; 2001WO-US000664.
30-JAN-2001; 2001WO-US000665.
30-JAN-2001; 2001WO-US000666.
30-JAN-2001; 2001WO-US000666.
                                                                                                                                                                                                                                        30-JAN-2001; 2001WO-US000669.
                                                                                                                                                                                                                                                                                      2001US-00864761
                                                               28-JAN-2002; 2002EP-00001165
                                                                                                                                                                                                                                                                                                        10-OCT-2001; 2001US-0328205P
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nes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                    (AEOM-) AEOMICA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-684061/74
                                                                                                                                                                                                                                                                                      23-MAY-2001;
                    11-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                 Shannon M;
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Matches
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a transcriptional unit(s) in a cell, which comprises simultaneously or sequentially subjecting the population of transcripts including nascent.

RNA molecules comprising one or more labeled ribonucleotides to detection, and optionally to amplification to measure the appearance of a detection, and optionally to amplification to measure the appearance of a cetectable product. The method can be used for determining the activity of a transcriptional unit(s) in a cukaryotic cell or cell lineage and monitoring the transcriptional activity of genes in a cell, particularly determining at a quantitative, semi-quantitative or qualitative level the transcriptional activity of selected genetic elements in a cell. The method may also be used to determine the level of expression of the same gene under different conditions and to provide a fingerprint of genetic espenses and an a cell. The method may also be used to conditions and to provide a fingerprint of genetic expression and to provide a fingerprint of genetic espense and may also be used to be transcriptional activity in a cell. The method feature is an and to provide a fingerprint of genetic espense and to provide a fingerprint of the invariance.

oligonuclectide used to demonstrate the method of the invention

Determining the activity of a transcriptional unit(s) in a cell comprises simultaneously or sequentially detecting and amplifying the transcripts including nascent RNA molecules to measure the presence of a detectable

(BENI-) BENITEC AUSTRALIA LTD.

Rice RN, Harrison BT; WPI; 2003-393249/37.

30-AUG-2002; 2002WO-AU001182. 31-AUG-2001; 2001US-0316308P.

WO2003018832-A1

06-MAR-2003.

The present invention relates to a method of determining the activity of

Example 23; Page 78; 114pp; English

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Human; interleukin 4 receptor; IL4R; type 1; diabetes; allele; insulin dependent diabetes mellitus; IDDM; myasthenia gravis; PCR; single nucleotide polymorphism; SNP; autoimmune disease; amplify; T helper type 1 mediated disease; rheumatoid arthritis; primer; multiple sclerosis; inflammatory bowel disease; systemic sclerosis; systemic lupus erythematosus; psoriasis; scleroderma; Grave's disease; Guillain-Barre syndrome; Hashimoto's thyroiditis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Variant primer DBM0195B amplifies IL4R amplicon of 413 bp for SNP #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
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88.2%; Pred. No. 8.6e+02;
ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17 BP; 3 A; 10 C; 2 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1357 TCAGTGTGCGGTGGGGC 1373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABQ80178 standard; DNA; 17 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 TCAGTGTGGGGAGGGGC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.8
Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABQ80178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1334
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0
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893 AGGTGCCCTGAGCCAG 909

ઠે 셤

17 AGACGCCCTGAGCCAG

ACC59531 standard, DNA; 17

WO2003010335-A2

Genetic expression detection; transcriptional activity; run-on transcription; PCR; primer; probe; ss.

Homo sapiens

Human HER-2 gene PCR primer #3.

08-SEP-2003 (first entry)

ACC59531;

06-FEB-2003.

ö

Gaps

relerman A, Query Match Matches The sequences given in ABQ80170-78 represent primers which were used to identify wild type and variant loci in the human interleukin 4 receptor (ILAR). These primer sequences were used in the method of the invention for determining an individual's risk for type I diabetes. The method comprises detecting the presence of an insulin dependent diabetes mellitus (IDDM) -associated interleukin 4 receptor allele in a nucleic caid sample of the individual, where the presence of the allele in a nucleic compressing (SNP) within the ILAR gene listed in the specification. The method and the SNP's are useful for determining an individual's risk for type I diabetes. The ILAR SNP's are also useful for determining an individual's risk for type I diabetes. The ILAR SNP's are also useful for determining an individual's risk for any autoimmune disease or condition cany T helper type I mediated disease, e.g. rheumatoid arthritis, multiple sclerosis, inflammatory bowed disease, systemic lupus crythematosus, psoriasis, scleroderma, Grave's disease, systemic Determining an individual's risk for type 1 diabetes, comprises detecting the presence of an insulin dependent diabetes mellitus-associated interleukin 4 receptor allele in a nucleic acid sample of the individual. sclerosis, myasthenia gravis, Guillain-Barre syndrome, or Hashimoto's thyroiditis Valdez AM; Sequence 17 BP; 2 A; 3 C; 9 G; 3 T; 0 U; 0 Other; Bugawan TL, Noble JA, (HOFF ) ROCHE DIAGNOSTICS GMBH. (HOFF ) HOFFMANN LA ROCHE & CO AG F. Example 5; Page 39; 79pp; English. 20-JUL-2001; 2001US-0306912P. 17-JUL-2002; 2002WO-EP007956. Local Similarity 88.2 hes 15; Conservative Mirel DB, Erlich HA, WPI; 2003-248086/24.

03-JUN-2003 ACA08326; RESULT 1336 ACA08326/ ઠ 셤 ö Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip; antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease; edizophrenia; protein chip; gene therapy; tumour suppression; human fukutin; ds. Gaps ö Tumour suppression related human fukutin oligo SEQ ID No 2478. 0.8%; Score 13.8; DB 1; Length 17; 88.2%; Pred. No. 8.6e+02; ative 0; Mismatches 2; Indels 898 CCCCTGAGCCAGCCTCC 914 ABT36841 standard; DNA; 17 BP 17 CCCTGAGCCAGTCACC 1 12-JUN-2003 (first entry)

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The invention relates to a novel isolated 17 mer nucleic acid sequence,

given in the specification, a sequence containing at least 15 consecutive
nucleotides from the 17 mer sequence, a sequence with, after optimal
alignment, at least 80 % identity to the 17 mer sequence, a sequence that

bybridizes to them under highly stringent conditions, or the complement

cof any of them, or the corresponding RNA. The novel isolated nucleic

acids of the invention are useful as probes and primers for detecting,

component of agence chip, in vitro as (anti) sense reagents, and for

production of recombinant polypeptides. Any of the nucleic acids,

production of recombinant polypeptides. Any of the nucleic acids,

component of agence this in vitro as (anti) sense reagents, and for

production of recombinant polypeptides. Any of the nucleic acids,

component of agence this in vitro as (anti) sense reagents and for

production of recombinant polypeptides. Any of the nucleic acids,

component of pharmaceuticals for prevention and/or treatment of viral

consequence of the invention of pharmaceuticals for prevention and/or treatment of viral
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    degeneration, specifically cancer but also Alzheimer's disease and schizophrenia. Analysis of the expression of the 17 mer nucleic acids in partient samples is useful for disgnosis and/or prognosis of these diseases. The polypeptides can also be used to generate antibodies, and both the polypeptide and antibodies are useful as components of protein chips. The nucleic acid sequences of the invention can be used in generated therapy. This polynucleotide sequence represents a tumour suppression related human fukutin oligonucleotide of the invention
                                                                                                                                                                                          New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guarder, muterayme, cancer; REL-A activity; breast cancer; lung cancer prostate cancer; lung cancer; broader cancer; lung cancer; broader cancer; lung cancer; broader cancer; lung cancer; becomed cancer; becomed cancer; becomed cancer; becomed cancer; ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Snzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;
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88.2%; Pred. No. 8.6e+02;
tive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 322; 720pp; French.
Tuijnder M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               279
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es 15; Conservative
                                                                                                                                                                                                                                                                                             and transfected cells.
                                                                                             WPI; 2003-313353/30.
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Homo sapiens.

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                                                                                                                                                                                                                                     Novel enzymatic nucleic acid molecules which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B useful for treating cancer, inflammatory disorders and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytostatic; immunostimulant; gene therapy; vaccine; human; zinc finger protein; MDZ3; MDZ4; MDZ1; MDZ1; chromosome 7g22.1; chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15g26.1; cancer; developmental disorder; s.
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88.2%; Pred. No. 8.6e+02;
tive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human MDZ3 scanning oligonucleotide SEQ ID 1079.
                                                                                                                                                                                 Stinchcomb DT, Mcswiggen J, Draper KG;
                                                                                                                                                                                                                                                                                               Claim 3; Page 48; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1634 TCCTTTGATTGATCACT 1650
                                                    92US-00987132.
94US-00245466.
94US-00291932.
96US-00777916.
                           23-MAY-2001; 2001US-00864785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 TGCTTTGATTGTTCACT 1
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ses 15; Conservative
                                                                                                                         (STIN/) STINCHCOMB D T. (MCSW/) MCSWIGGEN J.
                                                                                                                                                                                                           WPI; 2003-340953/32.
                                                                                                                                                      DRAPER K G.
                                                                    18-MAY-1994;
                                                                                  15-AUG-1994;
23-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-NOV-2003
                                                      07-DEC-1992;
28-NOV-2002
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                                                                                                                                                      (DRAP/)
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Matches
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The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is concoded at chromesome FQ22.1, MD24 is encoded at chromesome [6p21.3-22.2, MD27  MD27 is encoded at chromesome [6p21.3-22.2, MD27, MD27, or MD22.3, MD23 is encoded at chromesome and encoded at growing and second at growing and second and second at growing and second at genetic locus. The probes are useful an constructing microarrays for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as concernes. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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88.2%; Pred. No. 8.6e+02;
ve 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 8; SEQ ID NO 1079; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MDZ4, MDZ7 or MDZ12, e.g. cancer.
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                                                                                                                                                                30-JUL-2002; 2002EP-00016874.
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                                                                                                                                                                                                                                                   02-AUG-2001; 2001US-00922181
                                                                                                                                                                                                                                                                                                                                                                                                                    Shannon M, Gu Y, Nguyen C;
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-423107/40.
                                                                                                                                                                                                                                                                                                                                 (AEOM-) AEOMICA INC
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EP1281758-A2.
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                                                                                  05-FEB-2003
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05-DEC-2002
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                                                                                                                                                                                                                             Query Match
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ABZ61374/c
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                                                                                                                                                                                     acid molecule or an enzymatic nucleic acid molecule, that modulates expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras, human immunodeficiency virus (HIV) or a component of HIV. The nucleic acid molecule of the invention has cytostatic, anti-HIV, and anti-rheumatic activity. The nucleic acid molecules are useful for reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are also useful for treating breast, ovarian, colorectal, lung, prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences shown in ABZ59889 - ABZ65216, ABZ64544 - ABZ65531, ABZ65520 - ABZ6524, ABZ66530 - ABZ65585 represent substrate/target sequences for the human ribozymes of the invention
                                                                                                                                                                                 The invention relates to a novel short interfering RNA (siRNA) nucleic
                                                                                                            Novel short interfering RNA and enzymatic nucleic acid useful for treating cancer, modulates the expression of a nucleic acid encoding HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, ribozyme, short interfering RNA, siRNA; HER2; K-Ras;
enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
anti-rheumatic; cancer; AIDS; ss.
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                                                                                                                                                                                                                                                                                                                                Sequence 17 BP; 1 A; 8 C; 8 G; 0 T; 0 U; 0 Other;
                                                                                                                                                           Claim 4; Page 133; 185pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                    232 CGCGGCACCCCGGGGCC 248
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29-MAY-2001; 2001US-0294140P.
06-JUN-2001; 2001US-0296249P.
10-SEP-2001; 2001US-0318471P.
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06-JUN-2001; 2001US-0296249P.
10-SEP-2001; 2001US-0318471P.
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                                            (RIBO-) RIBOZYME PHARM INC.
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                                                                   Mcswiggen J;
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acid molecule or an enzymatic nucleic acid molecule, that modulates expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras, human immundeficiency virus (HIV) or a component of HIV. The nucleic acid molecule of the invention has cytostatic, anti-HIV, and anti-rheumatic activity. The nucleic acid molecules are useful for reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are also useful for reating breast, ovarian, colorectal, lung, prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences shown in ABZ69889 - ABZ62216, ABZ65531, ABZ65521, ABZ65530 - ABZ65585 represent substrate/target sequences for the human
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                                                                                                                                                                                                              invention relates to a novel short interfering RNA (siRNA) nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
treating cancer, modulates the expression of a nucleic acid encoding HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
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enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
anti-rheumatic; cancer; AIDS; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                               Claim 58; Page 115; 185pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human H-Ras DNAzyme target #165.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-140484/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mcswiggen J;
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Gaps

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Indels

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Mismatches

3,

12, Conservative

Matches

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also useful for treating breast, ovarian, colorectal, lung, prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences shown in ABZ59899 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ6524, ABZ66530 - ABZ66530 - ABZ66530 - ABZ66530 - ABZ66530 - ABZ66534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acid molecule or an enzymatic nucleic acid molecule, that modulates expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras, human immunodeficiency virus (HIV) or a component of HIV. The nucleic acid molecule of the invention has cytostatic, anti-HIV, and anti-rheumatic activity. The nucleic acid molecules are useful for reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are also useful for treating breast, ovarian, colorectal, lung, prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences shown in ABZ65585 represent substrate/target sequences for the human ABZ65530 - ABZ65585 represent substrate/target sequences for the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequences
- ABZ66524,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention relates to a novel short interfering RNA (siRNA) nucleic
HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treating cancer, modulates the expression of a nucleic acid encoding HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel short interfering RNA and enzymatic nucleic acid useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
anti-rheumatic; cancer; AIDS; ss.
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                                                                                                                                                             Score 13.8; DB 1; Length 17;
Pred. No. 8.6e+02;
0; Mismatches 2; Indels
                                                                                                                           Sequence 17 BP; 0 A; 6 C; 11 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17 BP; 1 A; 8 C; 4 G; 0 T; 4 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 148; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human HER2 DNAzyme substrate #826.
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                                                                                                                                                            0.8%;
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06-JUN-2001; 2001US-0296249P.
10-SEP-2001; 2001US-0318471P.
                                                                                                                                                                                                                                        736 GGCCCCTCCCGGGCCC
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                                                                                                                                                                                                                                                                                                                                                                 ABZ65369 standard; RNA; 17
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                                                                                         ribozymes of the invention
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                                                                                                                                                                                                  15; Conservative
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                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                      ABZ65369;
                                                                                                                                                               Query Match
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Score 13.8; DB 1; Length 17; Pred. No. 8.6e+02;

0.8%;

Query Match Best Local Similarity

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The present invention relates to nucleic acid molecules which modulate the synthesis, expression and/or stability of Hepatitis C virus (HVV) or Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes, inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed transcriptise and/or HBV reverse transcriptises primer sequences, as well as oligonucleotides that specifically bind the Enhancer I region of HBV genes and MBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds that modulate the expression of HBV compounds and/or replication of HCV. The compounds and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel compound useful for treating cirrhosis, liver failure, hepatocellular carcinoma, or condition associated with hepatitis C virus
                                                                                                                                                                                                                                   Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV; RNA stability; RNA expression; RNA synthesis; antisense; enzymatic nucleic acid, hammerhead ribozyme; DNAzyme; inozyme; amberzyme; G-cleaver ribozyme; decoy molecule; aptemer; HBV reverse transcriptase; Enhancer I region; viral replication; degenerative; disease etate; HBV infection; HCV infection; cirrhosis; liver failure; hepatocellular carcinoma; hepatotropic; cytostatic; virucide; antiinflammatory; substrate; ss.
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                                                                                                                                                                                                      HCV minus strand DNAzyme substrate sequence #340.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mcswiggen J,
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1167
                                                                                                           BP.
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08-JUN-2001; 2001US-00877478.
08-JUN-2001; 2001US-0296876P.
24-OCT-2001; 2001US-0335059P.
05-DEC-2001; 2001US-0337055P.
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1151 GCTACGTGGCCACCCTG
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                                                                                                           ACD62029 standard; RNA; 17
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                                                                                                                                                                         (first entry)
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Roberts E;
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MACEJAK D.
MCSWIGGEN J.
MORRISSEY D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-229207/22.
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DRAPER K.
ROBERTS E.
                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                  WO200281494-A1
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Draper K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infection.
                                                                                                                                           ACD62029;
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(MACE/)
(MCSW/)
(MORR/)
(PAVC/)
(LEEP/)
(DRAP/)
(ROBE/)
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17-0CT-2002
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(MACE/)
(MCSW/)
(MORR/)
(PAVC/)
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(ROBE/)
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methods of the invention are useful for the treatment of degenerative and disease states related to HBV and HCV infection, replication and gene expression such as cirrhosis, liver failure, and hepatocollular carcinoma. The present sequence represents a substrate for one of the HCV DNAzyme or minus strand DNAzyme sequences disclosed in the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or condition associated with hepatitis C virus
                                                                                                                                                                                                                                                                                  RNA stability; RNA expression; RNA synthesis; antisense;
enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to nucleic acid molecules which modulate
                                                                                                                                                                                                                                                                         Nucleic acid molecule, Hepatitis C virus, HCV; Hepatitis B virus, HBV;
                                                                                                                                                                                                                                                                                                   amberzyme; G-cleaver ribozyme; decoy molecule; aptamer; HBV reverse transcriptase; Enhancer I region; viral replication; degenerative; disease state; HBV infection; HCV infection; cirrhosis; liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
                                                                                                          Gaps
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                                                                                    0.8%; Score 13.8; DB 1; Length 17; 64.7%; Pred. No. 8.6e+02; ative 4; Mismatches 2; Indels
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                                                                    Seguence 17 BP; 2 A; 2 C; 9 G; 0 T; 4 U; 0 Other;
                                                                                                                                                                                                                                                     HCV minus strand DNAzyme substrate sequence #823.
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                                                                                                                                                                                                                                                                                                                                          virucide, antiinflammatory; substrate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 289; 387pp; English
                                                                                                                            1005 CGGAGAAGATGTGGTTG 1021
                                                                                                                                      1 CGGAGCGGAUGUGGUUG 17
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ACD62960 standard; RNA; 17 BP.
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2001US-0296876P
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05-DEC-2001; 2001US-0337055P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel compound useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hepatocellular carcinoma,
                                                                                               Local Similarity 64.7
nes 11; Conservative
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MORRISSEY D.
PAVCO P.
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Roberts I
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MACEJAK D.
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DRAPER K.
ROBERTS E.
                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus
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Draper K,
                                                 invention
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                                                                                       Query Match
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(LEEP/)
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(ROBE/)
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the synthesis, expression and/or stability of Hepatitis C virus (HCV) or Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes, Inzymes, amberzymes, and G-cleaver ribozymes, DNAzymes, are nucleic acid decoy molecules and aptemers that bind to HBV reverse transcriptase primer sequences, as well as oligonuclectides that specifically bind the Enhancer I region of HBV DNA. The nucleic acids may be used to modulate the expression of HBV genes and HBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds that modulate the expression and/or replication of HCV. The compounds compounds of the invention are useful for the treatment of degenerative and issease states related to HBV and HCV infection, replication and gene expression such as cirrhosis, liver failure, and hepatocallular carcinoma. The present sequence represents a substrate for one of the HCV DNAzyme or minus strand DNAzyme sequences disclosed in the present
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88.2%; Pred. No. 8.6e+02;
tive 0; Mismatches 2; Indel8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17 BP; 2 A; 9 C; 3 G; 0 T; 3 U; 0 Other;
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08-JUN-2001; 2001US-0296876P.
08-JUN-2001; 2001US-03337055P.
05-DEC-2001; 2001US-0337055P.
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MORRISSEY D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
ses 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ö.
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DRAPER K.
ROBERTS E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAVCO P.
LEE P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLATT L.
MACEJAK D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200281494-A1.
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Gaps

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schizophrenia; ss
                                                                                                                WO2003025176-A2
                                                                                          01-JUL-2003
                                                                                                            Mus musculus.
                                                                                                                                    Telerman A,
                                                                                                                    27-MAR-2003
Draper K,
            infection.
                                                     invention
                                                                                      ACC68140;
                                                            Query Match
                                                                 Matches
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The present invention relates to murine oligonucleotides (ACC62754-ACC68806), which are associated with tumour suppression, tumour reversion, apoptoals and virus resistance. The oligonucleotides are quantifying and/or amplifying uncleic acid, e.g. as one component of agene chip; in vitro as (anti)sense reagents; and (2) for production of recombinant polypeptides. The oligonucleotides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel mutant forms of the rice acetolactate synthase (ALS) gene encoding ALS resistant to pyrimidinyl carboxy herbicides. Plants which may be transformed with the mutant gene include rice, and also maize, barley, wheat, soya, cotton and tobacco. The mutant gene may be useful in the production of herbicide-resistant plants which can be cultivated in the presence of the herbicide-resistant sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rice acetolactate synthase related oligonucleotide 4-83-1 SEQ ID NO:25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ss; rice; acetolactate synthase; ALS; pyrimidinyl carboxy herbicide; herbicide.
                                                                                                                                                                                                                                                                                                                           specifically cancer but also Alzheimer's disease and schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 13.8; DB 1; Length 17; Pred. No. 8.6e+02; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.8%; Score 13.8; DB 1; Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fukuda A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genes of rice origin encoding pyrimidinyl carboxy acetolactate synthase for production of herbicide
                                                                                                                                                                                                                                                                                                                                                                            Seguence 17 BP; 5 A; 4 C; 6 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17 BP; 3 A; 0 C; 9 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kawai K, Nagayama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; SEQ ID NO 25; 96pp; Japanese.
                                                 Disclosure; Page 660; 738pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GATCCAGTGAGAGCCAG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-FEB-2003; 2003WO-JP001917.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAR-2002; 2002JP-00095721.
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.8%;
Best Local Similarity 88.2%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            801 GAGCCAGAGAGACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADD42044 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IND CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
and transfected cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rice and other plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shimizu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-902935/82.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003083118-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADD42044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NAAG-)
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                                                                                                                                                                                                                                       The present invention relates to nucleic acid molecules which modulate the grathesis, expression and/or stability of Hepatitis C virus (HFV) or Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense and enzymeatic nucleic acids such as hammerhead ribozymes, DNAzymes, inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed are uncleic acid decoy molecules and aptamers that bind to HBV reverse transcriptase primer sequences, as well so oligonucleotides that specifically bind the Enhancer I region of HBV genes and dor HBV reverse transcriptase primer sequences, as well as oligonucleotides that specifically bind the Enhancer I region of HBV genes and HBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds that modulate the expression and/or replication of HCV. The compounds and methods of the invention are useful for the treatment of degenerative and disease states related to HBV and HCV infection, replication and gene carcinoma. The present sequence represents a substrate for one of the HCV invention are useful for the compounds and methods of the invention are useful for the treatment of degenerative and carcinoma. The present sequence represents a substrate for one of the HCV invention are useful for the sequence of the HCV invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                             Novel compound useful for treating cirrhosis, liver failure, hepatocellular carcinoma, or condition associated with hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumour suppression; tumour reversion; apoptosis; virus resistance; viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine oligonucleotide associated with tumour supression, SEQ ID 5387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 2 A; 6 C; 8 G; 0 T; 1 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 13.8; DB 1;
Pred. No. 8.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ξ
                                                                                                                                                                                                Claim 1; Page 235; 387pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 gegérégégéeségége 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACC68140 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 880 GAGCACGGGCCCCAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 82.4 nes 14; Conservative
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Roberts E
                                              WPI; 2003-229207/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-333167/31.
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herbicide resistan resistant strains

Tanaka Y;

us10008789-3.rng

RESULT 1347

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A PCR primer (AAT31547) corresponds to nucleotides 22-39 of the thymidine kinase (TK) gene of the wild-type WR strain of vaccinia virus. It was used with a primer (AAT31548) complementary to nucleotides 708-727 of TK for the PCR amplification of the TK gene. The TK gene was used in the construction of a recombinant vaccinia virus vector encoding a VL or VH polypeptide (see also AAR98410 and AAR98411) of monoclonal anti-idiotype antibody 3H1. This was used as a vaccine to protect mice against tumour
                                                   Anti-idiotype; monoclonal antibody; MAb; 3H1; CEA; carcinocherapy; vaccine; carcinocembryonic antigen; cancer; gene therapy; immunotherapy; vaccine; genetic immunisation; vaccinia virus; thymidine kinase; PCR; primer; polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Monoclonal antibody; MAb; 1A7; GD2; immune response; melanoma; neuroblastoma; glioma; soft tissue carcinoma; small cell carcinoma; tumor-associated antigen; TK gene; PCR primer; 86.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant monoclonal anti-idiotype antibody 3H1 sequences - used develop prods. for the detection and treatment of carcinoembryonic antigen-associated diseases, partic. cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.8%; Score 13.8; DB 1; Length 18;
88.2%; Pred. No. 8.9e+02;
ve 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                     Foon KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18 BP; 6 A; 5 C; 6 G; 1 T; 0 U; 0 Other;
                   Vaccinia virus thymidine kinase 5' primer.
                                                                                                                                                                                                                                                                                                                                                                                     Chatterjee SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; Page 85; 121pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TK gene specific forward primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297 TTGCCCCCTTCCATCTG 313
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                                                                                                                                                                                                                                                                                                           94US-00365484.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ31397 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     Chatterjee M, Kohler H,
                                                                                                                                                                                                                                                                                                                                               (KENT ) UNIV KENTUCKY
                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-321850/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JAN-1995;
                                                                                                                                                                                           WO9620277-A2
                                                                                                                                                                                                                                                                                                           28-DEC-1994;
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                                                                                                                                                                                                                                 04-JUL-1996
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                                                                                                                                                       Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      challenge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ31397;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1349
AAZ31397/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence coding for alpha-antitrypsin was fused to an Ig light chain signal sequence. Part of the cloning procedure involved introducing a Sama restriction site downstream of the stop codon of the alpha-antitrypsin coding region. The mutation was created using oligonucleotide TGS66 (AAN97167). The SV40 polyadenylation site could then be inserted into the restriction site. Subsequent manipulations eventually produced plasmid pTG1999, for expression of human alpha-antitrypsin (Arg358 variant) under the control of mouse Ig light chain regulatory sequences. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stable eucaryotic cell lines for expressing specific protein - are tumour or hybridoma cells derived from animals which develop from vector transformed ova.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                     Gaps
                                                                                                                                                                                                                                                                                                                             Mutagenic oligonucleotide TG566 to introduce Smal restriction site.
                                                                                                                                                                                                                                                                                                                                                               Transgenic animal; stable cell line; tumour cell line; polylinker; human alpha-antitrypsin; Arg variant; 3'-UTR; Homo sapiens; immunoglobulin light chain; promoter; ss.
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88.2%; Pred. No. 8.9e+02;
ive 0; Mismatches 2; Indels
                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18 BP; 3 A; 3 C; 11 G; 1 T; 0 U; 0 Other;
ilarity 88.2%; Pred. No. 8.6e+02; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lecocq JP;
                                                         1011 AGATGTGGTTGGGGATG 1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Fig 7; 31pp; French
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                                                                                           1 AGAGGTGGTTGGTGATG 17
                                                                                                                                                                                           AAN97167 standard; DNA; 18 BP
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ID AAT31547 standard; DNA; 18 IX

XX

AC AAT31547;

XX

DT 18-SEP-1996 (first entry)
                                                                                                                                                                                                                                                                     (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Skern T, Courtney M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TRGE ) TRANSGENE SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1989-009862/02.
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ttches 15; Conserv
 Local Similarity
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                                                                                                                                                                                                                                                                     25-MAR-2003
03-PEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-JAN-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                 AAN97167;
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RESULT 1348

Matches

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Gaps

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Chatterjee M;

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The invention provides a monoclonal antibody (MAD) designated 1A7, which elicits an anti-GD2 (tumor-associated antigen) immunological response in humans. MAD 1A7 has defined light and heavy chain variable region sequences. The MAD 1A7 and polypeptides can be used for eliciting an opportivity and the control of the products can be used for treating or purifying anti-GD2 antibody. The products can be used for treating GD2 associated diseases, eg. melanoma, neuroblastoma, glicina, soft tissue carcinoma, and small cell carcinoma. They can be used for palliating the disease or for reducing the risk of recurrence. Sequences AAZ31397-100
                                                                                                  Monoclonal antibody 1A7 and related polynucleotide(s) and polypeptide(s) - useful to treat or palliate a GD2-associated disease, e.g. melanoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thomas WJ, Drayna DT, Feder JN, Gnirke A, Ruddy D, Tsuchihashi Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hereditary haemochromatosis; metal toxicity; diagnosis; gene therapy; prenatal screening; human; oligonucleotide ligation assay; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hereditary haemochromatosis gene 24d1 allele OLA oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                  Sequence 18 BP; 6 A; 5 C; 6 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/note= "3' digoxigenin"
                                                                                                                                                                                                                                                                                                                                       encoding a 1A7 polypeptide fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                             Example 6; Col 56; 74pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-00632673.
96US-00632673.
96US-00652265.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 rreseccerrecarere 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        297 TTGCCCCCTTCCATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT96696 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-APR-1998 (first entry)
                                          Chatterjee SK,
                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 88.2
ses 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note=
               (KENT ) UNIV KENTUCKY.
                                                                       WPI; 1996-354530/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
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                                          Foon KA,
                                                                                                                                glioma.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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ΗB

a "5'-phosphorylated"

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Upstream oligonucleotides 24d1.A (AAT96694) for the common allele, 24d1.B (see AAT96695) for the haemochromatosis allele, and downstream oligonucleotide 24d1.K (see AAT96696) are used in an oligonucleotide 11gation assay (OLM) to detect the 24d1 mutation in the gene (see AAT96690) associated with hereditary haemochromatosis (HH). The 24d1 mutation appears responsible for the majority of HH disease. It comprises a G to A substitution that is present in 86% of affected chromosomes and in 4% of unaffected chromosomes. The mutation results in a Cys to Tyr substitution in the encoded protein (see AAW36499) at a critical disulphide bridge important for secondary structure. OLA allows the differentiation between homozygous and heterozygous individuals for the 24d1 allele, and provides rapid determination of the risk of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primers AAV01514-V01515 were used to PCR amplify the gene encoding the human SR-p70e protein (AAV01503). SR-p70 are transcription factors which may control the activity of p53-regulated genes, and are expressed by
                                                                    Hereditary haemochromatosis gene and variants - useful for diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptide(s) encoded by the SR-p70 tumour suppressor gene - and related nucleic acid, useful for diagnosis and treatment of tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SR-p70; transcription factor; tumour suppressor gene; human; p53; homology; differential splicing; diagnosis; cancer; neuroblastoma; gene therapy; apoptosis; primer; PCR; amplification; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             0.8%; Score 13.8; DB 1; Length 18;
88.2%; Pred. No. 8.9e+02;
iive 0; Mismatches 2; Indels
                                                                                     treatment of hereditary haemochromatosis disease.
                                                                                                                                                                                                                                                                                                                                                                                                          Sequénce 18 BP; 4 A; 6 C; 7 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense primer for human SR-p70e gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 16; Page 81; 136pp; French.
                                                                                                                        Example 1; Fig 5; 115pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1237 CCTGGCTGCTTCACCTG 1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kaghad A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV01515 standard; DNA; 18 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                        24dl allele, and provides individual developing HH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-402550/37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-FEB-1996;
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Wolff RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Length 18; 2; Indels

Score 13.8; DB 1; Pred. No. 8.9e+02; 0; Mismatches 2;

0.8%;

313

Gaps

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The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (VEGF). A patient (preferably human) having a condition associated with the level of the fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour anglogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient. AAX67275 to AAX75752 represent specific examples of nucleic acid molecules from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
tumour suppressor genes related to the p53 gene family. SR-p70 sequences (see AAV01496-V01505) can be used in the diagnosis and monitoring of cancer, especially neuroblastoma. The nucleic acid sequences and corresponding antisense sequences, are also useful in gene therapy, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
fms-like tyrosine kinase 1; kinase insert domain containing receptor;
foetal liver kinase 1; se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid molecule modulating VEGF receptor(s) gene expression or stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient.
                                                                                                                                                                                 ö
                                                                                                                                            Length 18;
                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse flt-1 VEGF receptor hairpin ribozyme substrate #81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escobedo J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18 BP; 6 A; 9 C; 1 G; 0 T; 2 U; 0 Other;
                                                                                                             Sequence 18 BP; 1 A; 4 C; 8 G; 5 T; 0 U; 0 Other;
                                                                                                                                            Score 13.8; DB 1;
Pred. No. 8.9e+02;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 188; 218pp; English.
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0
                                                                                                                                                                                                                   838 GCTGCTGGGGTCTCTGG 854
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AAX75622 standard; RNA; 18 BP
                                                                                                                                              0.8%;
88.2%;
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(CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                  28-JUL-1999 (first entry)
                                                                                                                                            Query Match 0.8
Best Local Similarity 88.2
Matches 15; Conservative
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                                                                          to regulate apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-259017/23.
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                                                                                                                                                                                                                                                                                                                                                                               AAX75622;
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This synthetic oligonucleotide comprises a forward PCR primer corresponding to nucleotides 22-39 of the thymidine kinase (TK) gene of the wild-type WR strain of vaccinia virus (GenBank J02425). It contains an ApaI site. It was used with a reverse primer (see T85158) to amplify the TK gene. The TK gene was incorporated into recombinant vaccinia virus vectors encoding monoclonal anti-iditotype IDD10 polypeptides (see also W27119-20). ILD10 elicits an immune response to human milk fat globule in patients with HMPG-associated tumours such as breast cancer. (Updated on
                                                                                                                                                                                                       Monoclonal antibody 11D10; anti-idiotype antibody; mucin;
human milk fat globule; HMFG; tumour; breast cancer; vaccine;
polymerase chain reaction; PCR; primer; vaccinia virus; thymidine kinase;
vector; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 elicits immune response against tumours, especially breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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88.2%; Pred. No. 8.9e+02;
ative 0; Mismatches 2; Indels
                                                                                                                                                                                            Vaccinia virus thymidine kinase gene forward PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18 BP; 6 A; 5 C; 6 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monoclonal anti-idiotype antibody 11D10 -
human milk fat globule disease associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chatterjee SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 6; Page 84; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003 to correct PR field.)
                                                                                           AAT85157 standard; cDNA; 18 BP
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96US-00766350.
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                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Foon KA,
                                                                                                                                                   (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (KENT ) UNIV KENTUCKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-341690/31.
773 GAGGTGAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 15; Conserv
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                                                                                                                                                                                                                                                                                                                        WO9722699-A2
                                                                                                                                                                                                                                                                                                                                                                               19-DEC-1996;
                                                                                                                                                 25-MAR-2003
04-JAN-1998
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                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                         AAT85157;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer.
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                                                                   RESULT 1353
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Matches
                                                                                 AAT85157,
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                                                                                                          장무염
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Score 13.8; DB 1; Length 18; Pred. No. 8.9e+02; 0; Mismatches 2; Indels

0.8%;

15; Conservative

Query Match Best Local Similarity Matches 15; Conserv

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determining region 3 (CDR3) rearrangements. The rearrangement of immunoglobulin (IG) H genes or the rearrangement of T cell receptor (TCR) genes in a clone is called its clonotypic rearrangement. The sequences are derived from BM plasma cells of patients suffering from multiple myeloma. A novel method is described that identifies clonotypic nucleic acid rearrangements in haematopoietic cells from a patient with (or at risk of) a haematological neoplastic disease. This method comprises isolating a neoplastic haemopoietic cell containing a target clonotypic rearrangement and amplifying a specific segance of the target. The rearrangement is present. The method is especially used to monitor a mapping presponse to treatment of haematological cancer (e.g. multiple myeloma, Hodgkin's disease or acute lymphoblastic leukaemia). The method can also be used to test bone marrow samples, including stem cells, intended for autologous transplant. Other applications include detecting clonotypic cells in premalignant and autoimmune states, identifying cell types representative of the different stages in a malignant clone and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting specific clonotypic nucleic acid rearrangement in
haematopoietic cells - used to monitor treatment of haematological cancer
                                                                                           clonotypic rearrangement; haematopoietic cell; monitor; response; haematological cancer; multiple myeloma; Hodgkin's disease; acute lymphoblastic leukaemia; test; bone marrow; autologous transplant; detection; clonotypic cell; premalignant; autoimmune; PCR primer; ss.
                                      Clonotypic IgH CDR3 sequences from the joining (J) gene pool segment.
                                                                           Rearrangement; gene; immunoglobulin H; IgH; T cell receptor; TCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Forward PCR primer for Thymidine kinase gene amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 18 BP; 3 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    Szczepek AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or to screen bone marrow transplants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 49; 74pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 982 TACTTTGGCCAGTGTGG 998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX89560 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-OCT-1999 (first entry)
03-JUN-1998 (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    Belch AR,
                                                                                                                                                                                                                                                                                                                                                                               (UYAL-) UNIV ALBERTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-042212/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  Pilarski LM,
                                                                                                                                                                                                                           W09746706-A1
                                                                                                                                                                                                                                                                                                   03-JUN-1997;
                                                                                                                                                                                                                                                                                                                                        03-JUN-1996;
                                                                                                                                                                                                                                                                1-DEC-1997
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AAX89560/c
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AC AAX8956(
AC AAX8956(
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DT 06-OCT-1
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The sequence is the forward PCR primer for the amplification of the vaccinia virus TK (Thymidine Kinase) gene. The sequence corresponds to nucleotides 22-39 of the TK sequence. The reverse primer AAX89561 corresponds to nucleotides 727-708 of the TK gene. The amplified sequence is used in the construction of a recombinant vaccinia vector encoding a 1A7 polypeptide fragment. The 1A7 antibody can be used to produce an anti-GD2 T cell or antibody response. The 1A7 peptides and antibodies may be useful for the modulation of ganglioside GD2, and particularly for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treatment of GD2-associated tumours e.g. melanoma, neuroblastoma, glioma, soft tissue sarcoma, and small cell carcinoma (including small cell lung cancer)
                                                                                                                                                                                                                                                                                                          Anti-GD2 immunological peptides useful for the treatment of tumors especially melanomas and small cell carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Secretory peptide-9; Zsig9; human; tumour marker; cancer; therapy; diagnosis; growth enhancer; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 13.8; DB 1; Length 18;
Pred. No. 8.9e+02;
0; Mismatches 2; Indels
PCR primer; TK; thymidine kinase; vaccinia virus; melanoma; recombinant vector; carcinoma: ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 BP; 6 A; 5 C; 6 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Secretory peptide-9 (Zsig9) antisense primer.
                                                                                                                                                                                                                                                      Chatterjee M;
                                                                                                                                                                                                                                                                                                                                                      Example 6; Col 59; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297 TIGCCCCCTICCAICTG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX06978 standard; DNA; 18 BP.
                                                                                                                                                     96US-00752844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.8%;
                                                                                                                                                                               95US-00372676.
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97US-00888088.
                                                                                                                                                                                              96US-00591196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 TIGGGCCCTICCAICIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 88.2
les 15, Conservative
                                                                                                                                                                                                                                                      Foon KA,
                                                                                                                                                                                                                          (KENT ) UNIV KENTUCKY
                                                                                                                                                                                                                                                                                  WPI; 1999-457600/38
                                                                                                                                                                                                                                                      Chatterjee SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9901554-A1
                                                                                                                                                                               17-JAN-1995;
16-JAN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JUL-1997;
                                                                                            US5935821-A.
                                                                                                                         10-AUG-1999
                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX06978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1356
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Nucleotide sequences encoding mycrene synthase, limonene synthase and pinene synthase from Grand fir may be incorporated into any organism (e.g. intact plant, animal, microbe), or derived call culture that produces geranyl diphosphate for the production of the aforementioned enzymes or their products. The sequences when expressed in transfected ealls may also be used for the production or modification of flavour and aroma properties, improvement of defense capablity, and the alteration of other ecological interactions mediated by mycrene, limonene, pinene, or their derivatives. In particular they can be used for the production of plant seeds for the synthase sequences can be used for the conserved regions of the synthase sequences can be used to create degenerate primers which can be used for screening/amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting tumors using antibodies, antagonists and antisense nucleotides to secretory protein-9 (Zsig9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present DNA sequence is the antisense PCR primer, that is used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the chromosomal assignment and placement of Zsig9 gene. The gene was mapped to chromosome 12q15 region, on the integrated LDB chromosome 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secretory protein-9; Human Zsig9; antisense PCR primer; mapping;
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                                                                                                                                                                                                                                                                                             0.8%; Score 13.8; DB 1; Length 18; 88.2%; Pred. No. 8.9e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.8%; Score 13.8; DB 1; Length 18; 88.2%; Pred. No. 8.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense PCR primer used for mapping of human Zsig9 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosomal assignment; chromosome 12q15 region; ss
                                                                                                                                                                                                                                                           Sequence 18 BP; 2 A; 10 C; 2 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18 BP; 4 A; 8 C; 2 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; Page 33; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1570 ACCGTCACCACTGACTG 1586
                                                                                                                                                                                                                                                                                                                                                                      749 GCCCCCACTITCCTCTC 765
                                                                                                                                                                                                                                                                                                                                                                                               1 GCCACCACCTTCCTCTC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ08292 standard; DNA; 18 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCTCCACCACTGACTG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US011107.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                Local Similarity 88.2
nes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-039447/03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VO9960405-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Moore EE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ08292;
                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1358
                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ08292
   X888888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                   New mammalian secretory peptide-9 (Zsig9) - used as a growth enhancer for placenta, liver and heart, and as an indicator of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycrene synthase; limonene synthase; pinene synthase; flavour; monoterpene synthase; aroma; defense; plant seed; oil; meal; primer; PCR;
                                                                                                                                                                                                                                                                                         This antisense primer, and a sense primer (see AAX06977), were used in a PCR designed to determine the chromosomal assignment of Zaig9 (see AAA06968), a gene encoding new secretory peptide-9 (see AAA088469). Zaig9 was mapped to chromosome 12. The invention provides polynucleotides (see AAX06968-70) encoding Zaig9 polypeptides (see AAW88469-77). Zaig9 can used as a growth enhancer for placenta, liver and heart, and as an indicator of cancer. Antisense nucleotides derived from Zaig9 cDNA, and anti-Zaig9 antibodies, can be used to inhibit the growth of tumour cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated gymnosperm monoterpene synthase DNA - obtained from Grand fir (Abies grandis), used to provide plants with modified production of monoterpenes, e.g. mycrene, limonene or pinene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.8%; Score 13.8; DB 1; Length 18; 88.2%; Pred. No. 8.9e+02; ative 0; Mismatches 2; Indels
                                                                                                                              Whitmore TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence 18 BP; 4 A; 8 C; 2 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide derived from pinene synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UNIW ) UNIV WASHINGTON STATE RES FOUND
                                                                                                                            Jaspers SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 11; Page 116; 121pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Croteau RB
                                                                                                                                                                                                                                                           Example 4; Page 72; 85pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1570 ACCGTCACCACTGACTG 1586
98US-00081338.
98US-0085983P.
98US-00099005.
98US-0089899P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX08679 standard; DNA; 18
                                                                                                                              Jelinek LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                      (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bohlmann J, Steele CL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-120396/10.
                                                                                                                                                                 WPI; 1999-106055/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                 that express Zsig9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAW85714.
                                                                                                                            Sheppard PO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JUL-1997;
19-MAY-1998;
19-MAY-1998;
                                                     17-JUN-1998;
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                                    17-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
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region. The move gene encodes a mevalonate kinase enzyme. The enzyme is involved in the mevalonate pathway in the carotenogenic yeast Phaffia rhodozyma. The specification also describes enzymes that are involved in the pathway from isopenteny! pyrophosphate to farnesy! pyrophosphate. The enzymes of the invention are used in the production of isoprenoids and earotenoids, especially astaxanthin. Astaxanthin is useful for the pharmaceutical industry, to protect cells against cancer as it has a strong antioxidation property. Astaxanthin is also useful as a colouring reagent in the farmed fish industry, e.g. salmon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, SRA; steroid receptor RNA activator; cytostatic, antiinflammatory, SRA inhibitor; cancer; infection; antisense oligonucleotide; ss.
                                                                                                                                                  mvk gene; mevalonate kinase; mevalonate pathway; carotenogenic yeast; isopentent) tyrophosphate; farnesyl pyrophosphate; isoprenoid; carotenoid; astaxanthin; cancer; antioxidant; colouring reagent; farmed fish industry; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated DNA sequences encoding enzymes, useful for the production of isoprenoids and carotenoids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR primers AAZ30195-96 were used to amplify the mvk gene 5' adjacent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                      PCR primer Mk17 used to amplify the mvk gene 5' adjacent region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 BP; 10 A; 0 C; 8 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 13.8; DB 1;
Pred. No. 8.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antisense oligonucleotide ISIS# 30411.
                                                                                                                                                                                                                                                                                                                                                                                                  (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 10; Page 15; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Setoguchi
                               BP.
                                                                                                                                                                                                                               Synthetic.
Xanthophyllomyces dendrorhous.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GGAAGAGGAAGAAAA 17
                                                                                                                                                                                                                                                                                                                                         99EP-00107413
                                                                                                                                                                                                                                                                                                                                                                     98EP-00108210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.8%;
                            AAZ30195 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA92592 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 GGAAGAGGAAAAAAA
                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  Ojima K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-001086/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                       26-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                     06-MAY-1998;
                                                                                         11-FEB-2000
                                                                                                                                                                                                                                                                                                          10-NOV-1999
                                                                                                                                                                                                                                                                            EP955363-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                Hoshino T,
                                                           AAZ30195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA92592;
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              AAZ30195
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                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is one of a large number of antisense oligonucleotides which is directed against one of four human steroid receptor RNA activator (SRA) nucleic acid sequences. Two series of antisense oligonucleotides were synthesised. The first series comprised 30 oligodeoxynucleotides with a phosphorothioate backbone. The second series comprised chimeric oligonucleotides, which was flanked on both sides by four-nucleotide wings. The wings were composed of a central gap region, consisting of ten 2'-deoxynucleotides, which was flanked on both sides by four-nucleotide wings. The wings were composed of 2'-methoxyethyl (2'-MOE) nucleotides. Both series contained the same nucleotide sequences. The antisense compounds are useful for research, diagnosis, treatment and prophylaxis to prevent or delay infection, inflammation or tumour formation. Therapeutically the oligonucleotides are highly safe and are effectively administered to humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, SRA, steroid receptor RNA activator, cytostatic, antiinflammatory, SRA inhibitor, cancer, infection, antisense oligonucleotide, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.8%; Score 13.8; DB 1; Length 18; 88.2%; Pred. No. 8.9e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18 BP; 5 A; .5 C; 6 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                    O'malley BW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense oligonucleotide ISIS# 30180.
                                                                                                                                                                                 (ISIS-) ISIS PHARM INC.
(BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Col 42; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            768 AGGCCGAGGTGAAGTCT 784
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                                                                                                                 99US-00280409.
                                                                                                                                                  99US-00280409.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA92513 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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Matches 15, Conservative
                                                                                                                                                                                                                                    Bennett CF,
                                                                                                                                                                                                                                                                   WPI; 2000-586211/55.
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                                                                                                                 29-MAR-1999;
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                                                                                                                                                                                                                                    Cowsert LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-JAN-2001
                                               US6107092-A.
                                                                                22-AUG-2000.
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                 Synthetic.
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(ISIS-) ISIS PHARM INC.

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Antisense compounds targeted to steroid receptor RNA activator useful for diagnosis, prophylaxis and treatment of diseases associated with the steroid activator, such as infection, inflammation or tumor formation.
                                                                                                                                                                                                 The present sequence is one of a large number of antisense oligonuclectides which is directed against one of four human steroid seceptor RNA activator (SRA) nucleic acid sequences. Two series of antisense oligonuclectides were synthesised. The first series comprised 10 oligodeoxynuclectides with a phosphorothicate backbone. The second series comprised chimeric oligonuclectides composed of a central gap region, consisting of ten 2'-deoxynuclectides, which was flanked on both sides by four-nuclectide wings. The wings were composed of 2'-methoxyethyl (2'-MOE) nuclectides. Both series contained the same nuclectide sequences. The antisense compounds are useful for research, diagnosis, treatment and prophylaxis to prevent or delay infection, inflammation or tumour formation. Therapeutically the oligonuclectides are highly safe and are effectively administered to humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cleavage structure; target sequence detection; flap endonuclease; FEN;
Heltest4; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The labelling of nucleic acids for their detection and quantification comprises the formation of a cleavage structure and its cleavage with five' exonuclease-1 or flap endonuclease-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.8%; Score 13.8; DB 1; Length 18; 88.2%; Pred. No. 8.9e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18 BP; 5 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
                                 O'malley BW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Page 22; 81pp; English
(BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                      Claim 3; Col 40; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     768 AGGCCGAGGTGAAGTCT 784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH27102 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AGGCCCAGGAGAGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heltest4 cleavage fragment
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                                   Bennett CF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-328805/34
                                                                   WPI; 2000-586211/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (STRA-) STRATAGENE
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                                   Cowsert LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sorge JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH27102
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This invention relates to a method for generating a signal indicative of

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the presence of a target nucleic acid sequence in a sample. The method comprises the formation of a cleavage structure through the incubation of a sample comprising a target nucleic acid sequence and a nucleic acid polymerase and cleaving the cleavage structure with a 5' exonuclease-1 or flap endonuclease (FEN) to generate the signal. The method is used for the detection and quantification of a target nucleic acid sequence. The present sequence represents a fragment of oligonucleotide Heltest4, which is used in an assay to evaluate the activity of a FEN endonuclease. This sequence is the fragment of Heltest4 which is cleaved off by FEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention provides the primary nucleotide sequence of the WSBV genome (AAM62689), predicted transcript sequences (AAM62689-AAM62833) and encoded proteins (AAG68910-AAG685051) and oligonucleotide sequences (AAM62840-63160) suitable for use as primers or probes. The nucleic acid molecules and proteins of the invention are useful for diagnosis and monitoring viral infection, in screens for antiviral agents and for monitoring viral gene expression or activity during a treatment regimen. The nucleic acid molecules are also useful as antisense constructs to control viral gene expression in infected cells and tissues and to create transgenic viral resistant shrimp. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primary nucleotide sequence of the shrimp white spot Bacilliform virus (WSBV), useful for producing viral polypeptides that can be used to screen for agents that are useful for treating WSBV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shrimp white spot Bacilliform virus; WSBV; diagnosis; viral infection; antiviral agent; gene expression; antisense construct; probe; primer; transgenic viral resistant shrimp; 8s.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shrimp white spot Bacilliform virus (WSBV) oligonucleotide 43.
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                                                                                                                                                                                                                                                                                                                                                                                                                   0.8%; Score 13.8; DB 1; Length 18;
88.2%; Pred. No. 8.9e+02;
tive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                       Sequence 18 BP; 15 A; 0 C; 0 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Fig 3, 626pp, English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1736 AAAAAAAAAAAAAA 1752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВЪ
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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11-SEP-2001
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RESULT 1364

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The invention relates to a method for inhibiting metastasis in a mammal. The method comprises administering an agent which alters the actin-based cytoskeleton of one or more tumour cells in the mammal. It is useful for inhibiting metastatic conditions, such as melanoma and ovarian, prostate, lung, bone, throat, brain, testicular, liver, stomach and pancreatic ancer. The present sequence is a primer used to clone human fibronectin in an example illustrating the invention. The fibronectin gene is one of a group of genes whose activity may be inhibited by the agent of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhibiting metastasis in humans by administering an agent which inhibits activity of genes which function in regulation of tumor cell metastasis, particularly genes which alter actin-based cytoskeleton of tumor cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sample origonucleotide #22 for analysing nucleic acid base sequence.
                                                    Human, fibronectin, cytostatic, metastasis inhibition, cancer, actin-based cytoskeleton, melanoma, PCR primer, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.8%; Score 13.8; DB 1; Length 18; 88.2%; Pred. No. 8.9e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid base sequence analysis; DNA diagnosis; probe;
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                                                                                                                                                                                                                                                                                                                                                                                          Lander ES;
                                                                                                                                                                                                                                                                                                           (WHED ) WHITEHEAD INST BIOMEDICAL RES (MASI ) MASSACHUSETTS INST TECHNOLOGY (DAND ) DANA FARBER CANCER INST INC.
                                                                                                                                                                                                                                                                                                                                                                                          Golub TR, Hynes RO,
                  Human fibronectin PCR primer #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example; Page 26; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1010 AAGATGTGGTTGGGGAT 1026
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                                                                                                                                                                                                                                  11-DEC-2000; 2000WO-US033631.
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                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding monoterpene synthases, for increasing terpene synthesis in plants, e.g. for increasing resistance to pests or for treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides the protein and coding sequences of monoterpene synthases from the grand fir. These include (-)-camphene synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-lipha-pinene synthase, limonene synthase, myrcene synthase and pinene synthase. The sequences can be used to produce transgenic plants expressing high levels of the enzymes, resulting in levels which are useful in protecting against and treating cancers, and to confer insect resistance on plants
                                                                                                                                                                                                                                                                                                                                                        90.
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                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                      Grand fir monoterpene synthase conserved coding sequence SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                      Monoterpene synthase; grand fir; cancer; (-)-camphene synthase; myrcene synthase; (-)-limonene synthase; (-)-pinene synthase; terpinolene synthase; insect resistance; nutrition; ss.
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                  Length 18;
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18.2%; Pred. No. 8.9e+02;
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                                                       Indels
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                0.8%; Score 13.8; DB 1;
88.2%; Pred. No. 8.9e+02;
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                                                                                           380 TACTCCAGCACACGCAG 396
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                                                                                                                                  1 TACCCCAGCACAGGCAG 17
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                Query Match
Best Local Similarity 88.2
Matches 15; Conservative
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Matches

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Gaps

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Example 6; Col 66; 62pp; English.

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acid base sequence. The method comprises preparing a probe array, hybridising with the probe array, measuring the fluorescence yield in the reaction, obtaining a template pattern, producing a sample pattern, and comparing the sample pattern with the template pattern. The method is useful for specifying an unknown base sequence at a defined aite of a target single-stranded nucleic acid, which is useful for analysing a nucleic acid base sequence. The method is applicable in DNA diagnosis and therapy, and is useful in medicine and biology. Measuring the fluorescence yield allows the detection of a one-base mismatch which can be considered to produce high detection accuracy. The hybrid pattern of the DNA probe is used so the difference in thermostability is less important, and the judgement on each spot can be reliably carried out.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention relates to a method of analysing an unknown nucleic
                                                                                                                                                                                                                                                                                          Screening an unknown base sequence at a defined site of a target single-stranded nucleic acid for use in DNA diagnosis and therapy, comprises a DNA chip, fluorescence yield and pattern-based method.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 13; 53pp; Japanese
                                                                                                   Suzuki T;
                                                                                                   Yamamoto N, Okamoto T,
                                                                                                                                                                                            WPI; 2002-372310/40
(CANO ) CANON KK.
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. 0 0.8%; Score 13.8; DB 1; Length 18; 88.2%; Pred. No. 8.9e+02; ative 0; Mismatches 2; Indels Seguence 18 BP; 2 A; 3 C; 8 G; 5 T; 0 U; 0 Other; Local Similarity 88.2 les 15; Conservative Query Match Matchee

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Gaps

482 ATGGGGGTCGGGGTCAT 498 2 Arcecerrecerreir 18 δ 원

ABL54126 standard; DNA; 18 BP ABL54126; 

12-JUL-2002 (first entry)

Cleavage product of FEN nuclease template Heltest4.

FEN; endonuclease; nuclease; template; Heltest4; nucleic acid detection;

Synthetic.

US6350580-B1

26-FEB-2002

11-OCT-2000; 2000US-00686179

Detection of an object component in a sample using an oligonucleotide as detecting probe.

Example 3; Page 19; 25pp; Japanese.

The invention relates to a novel method for detecting a complex formed between a probe and its complex. The method is used for detecting a complex formed between an oligonucleotide of known base sequence and a complementary probe, and for evaluating if the sequence is contained in liquid samples, or the level of binding by using the oligonucleotide as the detecting probe. The sequence represents a probe used in the

0.8%; Score 13.8; DB 1; Length 18;

Sequence 18 BP; 2 A; 3 C; 8 G; 5 T; 0 U; 0 Other;

Invention

Query Match

11-OCT-2000; 2000US-00686179

(STRA-) STRATAGENE

Sorge JA;

WPI; 2002-380832/41.

Detecting a target nucleic acid in a polymerase chain reaction process comprises forming a cleavage structure by incubating with a probe having secondary structure that changes upon binding and cleaving with a nuclease to release a fragment.

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The present sequence is the 18-nucleotide cleavage product of FEN nuclease template 1 oligonucleotide, Heltest4 (see ABL54126), which was unclease template 1 oligonucleotide, Heltest4 (see ABL54126), which was the binds to Mil to determining FEN endonuclease activity. Heltest4 complementary 5' overhang. This duplex forms template 2. Template 3 has an additional primer, FENAS (see ABL54127), bound to Mil and is directly adjacent to Heltest4. In the presence of template 3, FENAS binds the free 5' terminus of Heltest4, migrates to the junction and cleaves Heltest4 to produce the present 18-nucleotide fragment. FEN nuclease is preferred for use in the method of the invention, which relates to generating a signal to detect the presence of a target nucleic acid in a sample. In this method, a nucleic acid is treated with a probe that has a secondary structure which changes upon binding of the probe to a target nucleic acid sequence. The invention also provides a process for detecting or measuring a nucleic acid that allows for concurrent amplification, cleavage and detection of a target nucleic acid sequence
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                                                                                                                                                                                                                                                                                                        Sequence 18 BP; 15 A; 0 C; 0 G; 3 T; 0 U; 0 Other;
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Pred. No. 8.9e+02;
0; Mismatches 2;
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88.2%;
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                                                                                                                                                                                                                                                                             ın a sample
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The sequence represents a two-base mismatch probe designed to detect a variation a specific base in the p53 gene sequence. The invention relates to a novel method for screening for a variation in a nucleic acid sequence. The method involves using a DNA array in which a group of probes which will give strong signals forming hybrids with a normal gene sequence, and a group of probes having sequences expected to form hybrids with gene variants are separately arranged. The method is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Screening for gene variation by using DNA array in which probes giving strong signals forming hybrids with normal sequence, and probes having sequences expected to form hybrids with variants are separately arranged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    absence of a gene variation without need of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       screening for the presence or absence of variation in a nucleic acid sequence. The method is also useful for mass screening to determine
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                               Indels
                                                                                                                                                                                                                                                                                    Human; p53; probe; variation detection; DNA array; ss.
Pred. No. 8.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Suzuki T;
                                                                                                                                                                                                                                                       Human tumour suppressor gene p53 probe #22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expensive apparatus and a complex analysis
                             0; Mismatches
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               88.2%;
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Then 15; Conservative
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Matches 15, Conservative
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                              End-labelled probe array production; probe; 88; target substance capture.
End-labelled probe array production method-related oligonucleotide 22
                                                                                                                                                                                                                                                                                                                                                         invention comprises a method for the synthesis of an end-labelled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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fimune system disease; leukaemia; allergy; inflammatory disease;
tissue damage; allergic rhinitis; osteoarthritis; Crohn's disease;
psoriasis; rheumatoid arthritis; conjunctivitis; primer; ss.
                                                                                                                                                                                                                                                                              Preparation of an end-labelled probe array, for capturing a target
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.8%; Score 13.8; DB 1; Length 18;
88.2%; Pred. No. 8.9e+02;
ive 0; Mismatches 2; Indels
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Best Local Similarity
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                                                                                         JP2002153284-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-2000;
                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Longphre M,
                                                                                                                       28-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JAN-2002
                                                                                                                                                                                                                                                                                              substance
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Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein molecules useful for treating immune system diseases such as asthma, leukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease.

Example 4; Page 73; 209pp; English

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Human; sialic acid-binding Ig-related lectin; SIGLEC; asthma; immune system disease; leukaemia; allergy; inflammatory disease; tissue damage; allergic rhinitis; osteoarthritis; Crohn's disease; psoriasis; rheumatoid arthritis; conjunctivitis; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                        731 CTTCTGGGCCCCTCCCG 747
                                                                                                                                                                                                                                                                                 CIGCIGGCCCCICCIG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-2000; 2000US-0220139P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JUL-2001; 2001WO-US023082.
                                                                                                                                                                                                                                                                                                                                                                     Siglec-BMS, PCR primer #17.
                                                                                                                                                                                                                                                                                                                         ABK43392 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                     05-JUN-2002 (first entry)
                                                                                                                                                                                                                                                        15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Longphre M, Chang H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-241565/29
                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200208257-A2
                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JAN-2002.
                                                                                                                                                                                                                                                                                                                                        ABK43392;
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                                                                                                                                                                                                                                                                                                           RESULT 1372
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Matches
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Gaps

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related lectin) protein (1) Pharmacoutical compositions comprising (I) are useful for treating immune system diseases such as asthma, leukaemia or other allergic or inflammatory diseases. Extracellular domains of (I) represent potential markers for screening, diagnosis, prognosis, follow-cc up assays, and imaging methods. (I) is useful as a target for drugs which inflammation, tissue damage and remodeling in asthma, and inflammation, tissue damage and remodeling in asthma, and inflammation, tissue damage and remodeling in asthma, and inflammation, tissue as allergic rhinitis, osteoarthritis, crohn's disease, psoriasis, rheumatoid arthritis, conjunctivitis, etc. (I) is also useful for monitoring the course of disease or disorders, and for identifying agents that bind with and/or modulate the biological activity of SIGLEC-BMS proteins. The nucleoid acid molecules (II) encoding (I) are useful in disagnosis and/or prognosis methods, and to detect the presence and/or amount of SIGLEC-BMS nucleotides and some of SIGLEC-BMS succession of SIGLEC-BMS succession of SIGLEC-BMS succession of are useful as nucleic acid probes are useful for screening genomic library to isolate a genomic clone of SIGLEC-BMS antibodies are also used to detect, sort or isolate cells the SIGLEC-BMS antibodies are also used to detect, sort or isolate cells are abstant human affects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK43360-ABK43411 represent human SIGLEC coding sequences and PCR primers
Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein molecules useful for treating immune system diseases such as asthma, leukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated SIGLEC (sialic acid-binding Ig-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.8%; Score 13.8; DB 1; Length 18; 88.2%; Pred. No. 8.9e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 BP; 0 A; 9 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                              Example 2; Page 69; 209pp; English
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The invention relates to an isolated SIGLEC (sialic acid-binding Igrelated lectin) protein (I). Pharmaceutical compositions comprising (I) care useful for treating immune system diseases such as asthma, leukaemia or other allergic or inflammatory diseases. Extracellular domains of (I) to passays, and imaging methods. (I) is useful as a target for drugs which cinhibit inflammation, tissue damage and remodeling in asthma, and for inhibit inflammation, tissue damage and remodeling in asthma, and inflammatory diseases such as allergic rhinitis, osteoarthritis, crohn's cliesase, psoriasis, rheumatoid arthritis, conjunctivitis, etc. (I) is also useful for monitoring the course of disease or disorders, and for identifying agents that bind with and/or modulate the biological activity of SIGLEC-BMS proteins. The nucleic acid molecules (II) encoding (I) are useful in diagnosis and/or prognosis methods, and to detect the presence and/or amount of SIGLEC-BMS nucleotide sequences and/or SIGLEC-BMS contains and a biological sample. (II) are useful for screening genemic library to isolate a genomic clone of SIGLEC-BMS antibodies are also used to detect, sort or isolate cells expressing SIGLEC-BMS proteins and in diagnostic imaging technology.

CT he SIGLEC-BMS proteins and in diagnostic imaging technology. The provision of the invarient contains and belongical sample. (II) are useful to sorders associated with SIGLEC coding sequences and PCR primers of hardshology.

Sequence 18 BP; 0 A; 9 C; 5 G; 4 T; 0 U; 0 Other;

of the invention

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Generating a signal indicating presence of a target nucleic acid, for use in a polymerase chain reaction, comprises incubating target nucleic acid with a probe to form a cleavage structure that is cleaved with nuclease.
                          Gaps
                                                                                                                                                                                                                                     hairpin probe; safety pin probe; assay; nucleic acid detection;
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                                                                                                                                                                                                          Cleavage product of Heltest4 after cleavage with FEN nuclease.
0.8%; Score 13.8; DB 1; Length 18; 88.2%; Pred. No. 8.9e+02; ive 0; Mismatches 2; Indel8
                                                 731 CTTCTGGGCCCCTCCCG 747
                                                                        17
                                                                                                                                      B
                                                                                                                                                                                                                                                                                                                                               17-OCT-2001; 2001US-00981621.
                                                                                                                                                                                                                                                                                                                                                                       11-OCT-2000; 2000US-00686179.
                                                                                                                                    ABQ78689 standard; DNA; 18
                                                                                                                                                                                    (first entry)
             Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-682018/73.
                                                                                                                                                                                                                                                                                                                                                                                              (SORG/) SORGE J A
                                                                                                                                                                                                                                                 FEN nuclease; ss.
                                                                                                                                                                                                                                                                                                JS2002102591-A1.
                                                                                                                                                                                    05-DEC-2002
                                                                                                                                                                                                                                                                                                                       01-AUG-2002.
                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                      Sorge JA;
                                                                                                                                                            ABQ78689;
  Query Match
                                                                                                            RESULT 1373
                                                                                                                         ABQ78689
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Whitney G;

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The present sequence represents the cleavage product of an oligonucletide used to test FEN nuclease activity. FEN nucleases are used in the course of the invention. The specification describes a method for generating a signal indicative of the presence of a target nucleic acid sequence in a sample. The method comprises forming a cleavage structure comprising duplex and single-stranded nucleic acid, by incubating the target nucleic acid sequence with a probe having a secondary structure that changes upon binding of the probe to the target nucleic acid sequence, and cleaving the cleavable structure with a nuclease to release a nucleic acid fragment. The method is useful for generating a signal indicative of the presence of target nucleic acid sequence in a sample. It is useful in a polywnerase chain reaction (PCR)-based assay or non-PCR based assay for detecting naturally occurring target nucleic acid sequences in a solution including RNA and DNA that is isolated and purified from cells, tissues, cargets in solution, including RNA or DNA oligonucleotides, and peptide nucleic acids

The sample call organisms, bacteria or viruses, and for detecting synthetic acids and pertide acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the reactivity of a first sample with other samples, in which the second to the 2 plus nth (n is not less than 1) samples having different properties are arranged independently on a substrate, on whose surface the first sample is already present, and the reactivities between the first sample and each of the second to the 2 plus n-th samples are determined. Also described is a tissue sample matrix in which several samples from different sources are present on each matrix divided on a substrate. The method is used for determining simultaneously the reactivity of a first sample with several other differing samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Simultaneous testing of the reactivity of a sample with other different samples, comprises applying to the two samples to a substrate comprising divided matrices.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the present invention describes a method for determining simultaneously
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.8%; Score 13.8; DB 1; Length 18; 88.2%; Pred. No. 8.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18 BP; 15 A; 0 C; 0 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simultaneous determination; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide probe SEQ ID NO:22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 11; 24pp; Japanese.
  6; Page 37; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1736 AAAAAAAAAAAAAAA 1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAATAAATAAAAAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL59657 standard; DNA; 18 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-AUG-2000; 2000JP-00263505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-AUG-2000; 2000JP-00263505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-398978/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CANO ) CANON KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JP2002065299-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL59657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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ABL59657
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\mathtt{ABLS9636} to \mathtt{ABLS9701} represent oligonucleotide probes used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic DNA selling system using the Internet, displays purchase order menu to orderer's terminal and initiates production of selected DNA for the successful bidder.
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                   synthetic DNA selling system; internet; ss; purchase order menu; major histocompatibility complex; MHC.
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                                                                               Length 18;
                                                                                                                                                                                                                                                                                                                                        Synthetic DNA selling system - related oligonucleotide 41.
                                                                                                           Indels
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                                                                          Score 13.8; DB 1;
Pred. No. 8.9e+02;
0; Mismatches 2;
                                               8 G; S T; 0 U; 0 Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 13.8; DB 1;
Pred. No. 8.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                         482 ATGGGGGTCGGGTCAT 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18
                                                                                                                                                                                                                                               ABT06236 standard; DNA; 18 BP
                                                                             0.8%;
88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-AUG-2000; 2000JP-00259715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-AUG-2000; 2000JP-00259715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       482 ATGGGGGTCGGGGTCAT
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                                                                                                                                                                      2 Arccccrccccrrcar
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                                                                                                                                                                                                                                                                                                           (first entry)
                                                 Sequence 18 BP; 2 A; 3 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.8
Best Local Similarity 88.2
Matches 15, Conservative
                                                                                           Local Similarity 88.2
nes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-492955/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CANO ) CANON KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                JP2002074089-A.
                                                                                                                                                                                                                                                                                                           24-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                               ABT06236;
                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK87302
                                                                                                                                                                                                                    RESULT 1375
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                                                                                                             Matches
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                                                                                                                                                                                                                                                  ex 2
    SXXS
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This invention relates to a novel method for detecting/measuring a target incleic acid. The method comprises forming a cleavage structure by incubating the target sequence with a probe comprising a binding moiety and a secondary structure that changes upon binding of the probe to the target, cleaving the cleavage structure to release a mucleic acid fragment, and detecting and/or measuring the fragment captured by binding of the binding moiety to a capture element on a solid support. The method of the invention is useful for detecting or measuring a target nucleic acid and are useful for generating a signal indicative of the presence of the target nucleic acid in a sample. Another method of the invention is useful for simultaneously forming a cleavage structure, amplifying the target nucleic acid in a sample and cleavaing the cleavage structure. The method does not require multiple steps, subsequent amplification process, and allows for concurrent amplification and detection of target nucleic
                                                                                                                                                                                                                                                                                                                                                                                                             Detecting/measuring target nucleic acid, by forming cleavage structure by incubating target nucleic acid with probe having binding moiety, cleaving structure to release nucleic acid and detecting released fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ss, PCR, ganglioside GD2-associated tumour; melanoma, antibody;
anti-idiotype; monoclonal antibody; 1A7; neuroblastoma; glioma; sarcoma;
small cell lung cancer; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sample. The present sequence represents a cleavage product by FEN 1 nuclease shown in an example of the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18 BP; 15 A; 0 C; 0 G; 3 T; 0 U; 0 Other;
                                                                                   ss; nucleic acid detection; FEN nuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaccinia virus TK gene PCR primer #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Page 38; 157pp; English
                                                    FEN 1 nuclease cleavage product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1736 AAAAAAAAAAAAAAA 1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAAAAAAAAAAA 17
                                                                                                                                                                                                                                 26-NOV-2001; 2001WO-US044215.
                                                                                                                                                                                                                                                                   30-NOV-2000; 2000US-00728574.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADA14814 Btandard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-NOV-2003 (first entry)
                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 88.2
hes 15; Conservative
                                                                                                                                                                                                                                                                                                                                        Sorge JA, Whalen AM;
                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-508503/54.
                                                                                                                                                                                                                                                                                                      (STRA-) STRATAGENE
                                                                                                                                                          40200244326-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vaccinia virus
                  24-SEP-2002
                                                                                                                                                                                              36-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acid in a
                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADA14814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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The invention relates to the recurrence and/or development of a ganglioside GD2-associated tumour, e.g. melanoma, in an individual which is delayed by administration of an antibody comprising light and heavy chain variable region sequences of the anti-idiotype monoclonal antibody IA7. The antibody is used for delaying recurrence and/or development of GD2-associated tumour, e.g. melanoma, neuroblastoma, glandividual, or small cell lung cancer, in individual, and for treating individual with GD2-associated tumour. The present sequence is a PCR primer used to clone vaccinia virus sequences in order to construct an expression vector for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Humanin; neuroprotective; cerebroprotective; cytostatic; immunomodulator; antiinfective; cardiant; gene therapy; neurodegenerative disease; cancer; brain dysfunction; immune disease; infection; digestive disease; circulatory disease; endocrine disease; cell death; ds.
                                                                                                                                                                                                                                                                      Delaying recurrence and/or development of ganglioside GD2-associated
tumor in individual, by administering antibody containing light and heavy
chain variable region sequences contained in sequence of specified amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 0.8%; Score 13.8; DB 1; Length 18; Local Similarity 88.2%; Pred. No. 8.9e+02; Pred. 15; Conservative 0; Mismatches 2; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Humanin-like protein related DNA fragment # SEQ ID 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18 BP; 6 A; 5 C; 6 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccinia virus sequences in order to construct a
the cDNA encoding the anti-idiotype antibody 1A7
                                                                                                                                                                                                           Chatterjee SK;
                                                                                                                                                                                                                                                                                                                                                         Example 6; Col 59; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297 ITGCCCCCTTCCATCTG 313
                                                                                                        95US-00372676.
96US-00591196.
96US-00752844.
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01-AUG-2001; 2001JP-00233532.
                                                                            99US-00293533.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABZ59706 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                         Chatterjee M, Foon KA,
                                                                                                                                                                          (KENT ) UNIV KENTUCKY
                                                                                                                                                                                                                                       WPI; 2003-401117/38.
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                JS6509016-B1
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                                                                             15-APR-1999;
                                                                                                            17-JAN-1995;
16-JAN-1996;
                                                                                                                                            21-NOV-1996;
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                                               21-JAN-2003
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Gaps ; 0

0.8%; Score 13.8; DB 1; Length 18; 88.2%; Pred. No. 8.9e+02; tive 0; Mismatches 2; Indels

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The invention relates to a novel humanin-like polypeptide. The activity of the polypeptide of the invention may be described as neuroprotective, cerebroprotective, cytostatic, immunomodulator, antiinfective and cardiant. The polypeptide is applicable in diagnosis and remedies or preventives as well as screening drugs, including for example those for neurodegenerative diseases, cancer, brain dysfunction, immune diseases, infections, digestive diseases, circulatory diseases and endocrine diseases. The polypeptide of the invention also has cell-death inhibitory properties, and may be used in gene therapy. The current sequence represents a humanin-like protein related DNA fragment
                                                                                                             Novel humanin-like polypeptide with cell death-inhibitory activity, applicable in diagnosis and remedies or preventives as well as screening drugs for e.g. neurodegenerative diseases and cancer.
                                                                                                                                                                                                           Disclosure; Page 80; 87pp; Japanese
                                                                 WPI; 2003-167524/16
                        Mori M;
                        Sugo
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Sequence 18 BP; 4 A; 5 C; 8 G; 1 T; 0 U; 0 Other;

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Length 18;
                     2; Indels
Score 13.8; DB 1;
Pred. No. 8.9e+02;
                     0; Mismatches
                                          1121 CCGTGGAGGAGGCCA 1137
                                                                18
0.8%;
                                                                ccercaacaccccccc
                     15; Conservative
           Local Similarity
 Query Match
                       Matches
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Gaps . 0

AAL61062 standard; DNA; 18

BP

(first entry) 22-SEP-2003 AAL61062; 

Humanin, bax, bid; therapy; Alzheimer's disease; Parkinson's disease; neuron cell death; cancer; autoimmune disorder; noctropic; vasotropic; anticonvulsant; tranquilliser; vulnerary; cardiant; autinflammatory; stroke; Huntington's disease; trauma; amyotrophic lateral sclerosis; Human humanin cDNA amplifying reverse PCR primer, HNR. human; PCR; primer; ss

Homo sapiens

WO2003046205-A2

05-JUN-2003.

27-NOV-2002; 2002WO-US038191.

28-NOV-2001; 2001US-0334149P.

(BURN-) BURNHAM INST.

Reed JC,

WPI; 2003-505209/47.

Identifying modulators of apoptosis, in particular binding modulators of humanin to bax or bid, useful for diagnosing and/or treating disorders such as Alzheimer's disease, Parkinson's disease, cancer and inflammatory disorders

Example 3; Page 86; 141pp; English.

The invention relates to method for identifying an effective compound

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that modulates the binding of humanin to bax and/or bid. The method is useful for diagnosing and/or treating disorders associated with the humanin-bax or humanin-bid complex, such as Alzheimer's disease, stroke, Parkinson's disease, Huntington's disease, trauma, amyotrophic lateral esclerosis, neuron cell death, cancer or inflammatory or autoimmune disorders. The present sequence is a PCR primer used for amplifying human humanin cDNA. This sequence is a PCR primer tee for amplifying human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              recruiting a tumor-specific response against glycosphingolipid GD2, useful for treating a GD2-associated disease e.g., melanoma, glioma, soft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a monoclonal antibody 1A7 (an anti-idiotype antibody eliciting an anti-GD2(ganglioside) response). Also included are an antibody producing cell deposited under ATCC Accession No. HB-11786 (or its progeny), a polynucleotide comprising a sequence encoding a polypeptide with immunological activity of 1A7 (where the polypeptide comprises at least 5 consecutive amino acids from a variable region of 1A7), an isolated polynucleotide comprising a region of at least 20 consecutive nucleotides that is capable of forming a stable duplex with a polynucleotide encoding the light or heavy chain variable region of 1A7 under conditions where the region does not form a stable hybrid with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 monoclonal antibody; 1A7; anti-idiotype antibody; ganglioside GD2;
cytostatic; melanoma; neuroblastoma; small cell lung cancer; tumour;
antibody; variable region; VH; VL; glioma; soft tissue sarcoma; vaccine;
ss; primer; viral vector; PCR.
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                                                                                                                                                                                                    0.8%; Score 13.8; DB 1; Length 18; 88.2%; Pred. No. 8.9e+02;
                                                                                                                                                                                                                                       2; Indels
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                                                                                                                                                                Sequence 18 BP; 2 A; 8 C; 2 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vaccinia virus thymidine kinase PCR primer #1.
                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                           1123 GTGGAGGGGGGCATA 1139
                                                                                                                                                                                                                                                                                                                                                                                                      ADC35343 standard; DNA; 18 BP
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96US-00591196.
99US-00293533.
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                                                                                                                                                                                                                                                                                                             18 GTGAAGAGGCGGGCATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                         15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FOON/) FOON K A. (CHAT/) CHATTERJEE S K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHAT/) CHATTERJEE M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-810913/76.
                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2003114398-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vaccinia virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue sarcoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chatterjee M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JAN-1995;
16-JAN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                invention
                                                                                                                                                                                                                                                                                                                                                                                                                                         ADC35343;
                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                  RESULT 1380
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Seguence 18 BP; 6 A; 5 C; 6 G; 1 T; 0 U; 0 Other; Beer spoilage-associated primer SEQ ID 331 Claim 1; SEQ ID NO 331; 88pp; German. 297 TIGCCCCCTTCCATCTG 313 BP. 17 TTGGGCCCTTCCATCTG 1 19-JUN-2002; 2002WO-EP006808 19-JUN-2001; 2001DE-01029410 ADE15136 standard; DNA; 18 29-JAN-2004 (first entry) Conservative Lactobacillus perolens. Beimfohr C, Snaidr J; WPI; 2003-175243/17. (VERM-) VERMICON AG. Local Similarity les 15; Conserv WO2002103043-A2. 27-DEC-2002 Query Match ADE15136; species. RESULT 1381 Matchea ADE15136/ 셤

8x333333 셤 polynucleotide consisting of a variable region encoding sequence appearing as ADC1521 - ADC15370, a host cell comprising the appearing as ADC1521 - ADC15370, a host cell comprising the polynucleotide, a fusion polypeptide comprising 1A7, a humanised antibody comprising to antibodies from the iA7 variable regions and a vaccine comprising the antibodies. The antibodies are useful for eliciting an immune response in an individual, and for treating a GD2 associated disease is another and remember and individual has a clinically detectable tumour, and the method is for palliating the GD2-associated disease. 1A7 is preferably useful for treating a tumour that was previously detected in the individual and has been treated and is clinically undetectable at the time of the administering of 1A7, or for reducing the risk of recurrence of a clinically detectable tumour. 1A7 and the humanised antibody are useful for detecting the presence of an anti-GD2 antibody are construction of a vaccinia virus vector expressing the light or heavy chain variable regions of monoclonal antibody 1A7

; 0 0.8%; Score 13.8; DB 1; Length 18; 88.2%; Pred. No. 8.9e+02; Artive 0; Mismatches 2; Indels

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Gaps

88; primer; detection; beer-spoilage; lactic acid bacteria; Gram-negative bacteria; spoilage bacteria.

New oligonucleotides, useful for rapid detection of beer-spoilage bacteria by in situ hybridization, are specific for type, genus or

The present invention relates to an isolated human olfactory receptor, family 1, subfamily 6, member 1, (ORIG1) polymorlectide comprising a sequence which is a polymorphic variant for a reference sequence for the ORIG1 gene or its fragment, or a polymorphic variant of a reference sequence for a ORIG1 cDNA or its fragment. ORIG1 is useful in studying the expression and function of ORIG1 and in expressing ORIG1 protein for use in screening for candidate drugs to treat diseases related to ORIG1 activity. ORIG1 is useful for therapeutic purposes. The invention is useful for studying expression of the ORIG1 isogenes in vivo, for in vivo screening and testing of drugs targetted against ORIG1 protein, and for testing the efficacy of therapeutic agents and compounds for olfactory sensory deficits, in a biological system. The invention is useful in gene therapy and is located on the . The present sequence is human ORIG1 gene polymorphism detecting ASO (allele specific oligonucleotide) probe

Novel isolated human olfactory receptor, family 1, subfamily G, mem polynuclectide, for therapeutic purposes, for studying expression av function of the polynuclectide and for expressing receptor protein.

Claim 16; Page 13; 96pp; English.

Tanguay DA;

Меввег С,

Kazemi A,

WPI; 2002-269097/31

(GENA-) GENAISSANCE PHARM INC

This invention describes novel oligonucleotides used in a method for detecting beer-spoilage bacteria in a sample. The bacteria detected include lactic acid bacteria of the genera Lactobacillus or Pediococcus, especially the species L. coryniformis, L. perolens, L. buchneri, L. plantarum, L. fructivorans, L. lindheri, L. casei, L. brevis or P. Amannosa or Gram-negative bacteria of the genera Pectinatus and Megasphaera, specifically P. frisingensis, P. cerevisiphilus and M. cerevisiae. The oligonucleotides of the invention provide rapid detection

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Gapa

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0.8%; Score 13.6; DB 1; Length 15; 92.9%; Pred. No. 8.4e+02; tive 1; Mismatches 0; Indels

13; Conservative

Local Similarity

Best Loca Matches

Query Match

Sequence 15 BP; 3 A; 4 C; 4 G; 3 T; 0 U; 1 Other;

ö of spoilage bacteria (typically within 48 hours, compared with 7-12 days for conventional culture methods), can detect all relevant bacteria in parallel, can differentiate between species of the same genus, and are easy to use. ADE14806-ADE15247 represent the oligonucleotides used in the Human; olfactory receptor family 1 subfamily G member 1; ORIG1; therapy; polymorphism; drug screening; olfactory sensory deficit; gene therapy; chromosome 17p13.3; probe; ss. Gaps ö Length 18; 2; Indels duman OR1G1 gene polymorphism detecting ASO probe #13. Sequence 18 BP; 7 A; 7 C; 3 G; 1 T; 0 U; 0 Other; Score 13.8; DB 1; Pred. No. 8.9e+02; 0; Mismatches 1357 TCAGTGTGCGGTGGGGC 1373 BP 03-AUG-2001; 2001WO-US024478. N 03-AUG-2000; 2000US-0222755P. Query Match 0.8%; Best Local Similarity 88.2%; rcagriroccerecrec AAD32456 standard; DNA; 15 (first entry) 15; Conservative method of the invention. NO200212561-A2 Homo sapiens 18-JUN-2002 14-FEB-2002 18 AAD32456; RESULT 1382 Matches AAD32456
AAD32456
AAC3456
AAC346
AAC3456
AAC346
AAC3 Best Local Similarity

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The present invention describes genetic variants of the human glutathione reductase (GSR) gene (1). (1) has antianaemic activity and can be used in gene therapy. (1) can be used in screening for drugs targeting (1) that are useful for treating heemolytic anaemia. Methods from the present invention can be used: for improving the efficiency and reliability of several steps in the discovery and development of drugs for treating diseases associated with GSR activity; for haplotyping, which is also used by the pharmaceutical research scientist to validate GSR as a candidate target for treating a specific condition or disease predicted to be associated with GSR activity, e.g. haemolytic anaemia, and in the consist of clinical trials for treating a specific condition of disease condidated with GSR activity, and for screening compounds targeting GSR. (1) is useful in studying the expression and function of GSR. and in the expression of the waitain on the biological activity of GSR activity. (1) is also useful in studying the condidate drugs are treatment of the binding affinity of candidate drugs targeting GSR for the treatment of the binding affinity of candidate drugs targeting GSR for the treatment of the exemplification of the present sequence represents an allele specific of lagewing a single nucleotide polymorphism) in the present invention)

Constitution of the present invention. N.B. The polymorphic base (showing a single nucleotide polymorphism) in the present invention)
                                                                                                                                                                                                                                                                                              Human; glutathione reductase; GSR; enzyme; haemolytic anaemia; SNP; gene therapy; antianaemic; polymorphic; single nucleotide polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New genetic variants of Glutathione reductase isogenes, useful for improving efficiency and reliability in drug development for treating hemolytic anemia.
                                                                                                                                                                                                                                                       Human GSR allele specific oligonucleotide primer SEQ ID NO:39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/note= "polymorphic base"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bieglecki KM, Sanchis A, Sausker EA,
                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 14; Page 14; 137pp; English.
                                                                                                                                  ABN87920 standard; DNA; 15 BP
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1149 CTGCTACGTGGCCA 1162
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                      2 CTGCTAYGTGGCCA 15
                                                                                                                                                                                                                12-AUG-2002 (first entry)
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misc_feature
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                     primer; 88
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0.8%; Score 13.6; DB 1; Length 15;

Query Match

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                                                                                                                                                                                                                                                                                                   Human; single nucleotide polymorphism; SNP; ADORA3; haplotyping;
chromosome 1p21-p13; adenosine A3 receptor; genotyping)
pathophysiological heart condition; myocardial ischaemia;
chronic heart failure; allele-specific oligonucleotide; ASO; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to novel single nucleotide polymorphisms (SNPs) in the human adenosine A3 receptor (ADORA3) gene located on chromosome 1p21-p13, and methods for haplotyping and/or genotyping the ADORA3 gene. The methods of the invention make use of allele-specific oligonucleotides (ASOB) as probes and primers and/or primer-extension oligonucleotides for detecting the ADORA3 gene polymorphisms. The polymucleotides and screened compounds are useful for the treatment of diseases associated with ADORA3 activity, such as pathophysiological conditions of the heart e.g. myocardial isohaemia and chronic heart failure. ABK92603-ABK92628 represent ASO primers for detecting human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel genetic variants of the adenosine A3 receptor, useful therapeutically and in screening for drugs to treat diseases related ADORA3 activity e.g., myocardial ischemia and chronic heart failure.
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                 Gaps
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                 Indels
                                                                                                                                                                                                                                                                    ASO primer #4 to detect human ADORA3 gene polymorphisms.
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92.9%; Pred. No. 8.4e+02;
ive 1; Mismatches 0;
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                                                                                                                                                                    ABK92606 standard; DNA; 15 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENA-) GENAISSANCE PHARM INC.
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                                                1736 AAAAAAAAAAAA 1749
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                                                                                                                                                                                                                                    (first entry)
                                                                                14 WAAAAAAAAAA 1
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               13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gilson CR, Kazemi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                     ABK92606;
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                 Matches
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This invention describes novel derivatised solid supports of formula S'-L-Z-GIZCH2-R, where: S' = a solid support; L = a bond or an (in) organic linker; Z = SOZ or S-S; R = OH, an H-phosphonate, alkanephosphonate, phosphotriester, phosphite triester, phosphorame, or phosphorame, or an optionally substituted or modified nucleotide (N'), or an oligonucleotide of formula (N') SR2; g = 1-200; R1 = a protecting group; R2 = an H-phosphonate, alkanephosphorate, phosphorate, p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSCHEMIZER/CHEMIZER AND MENTIONE AND MENTIONE AND CONTRIBUTION OF A CONTRIBUTION OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Derivatised solid supports and reagents for oligo:nucleotide synthesis and new oligo:nucleotide phosphoramidate conjugates.
                                                                                                                                                                                                                                                                                                             (SLOK ) SLOAN KETTERING INST CANCER RES. (ZWBI-) ZW BIOMEDICAL RES AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 44; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT86603 standard; DNA; 15 BP
                                                                                                                                                        95WO-US006379.
                                                                                                                                                                                                                                   94US-00242664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 864 AAGAGGAAGAGGAGG 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                             Watanabe KA, Ren W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-010846/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
WO9531434-A1
                                                                                                                                                        12-MAY-1995;
                                                                                                                                                                                                                                   13-MAY-1994;
                                                                              23-NOV-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New genetic variants comprising haplotypes of the cyclin-dependent kinase 4 (CDK4) gene, useful in improving the efficiency drug screening protocols for compounds targeting CDK4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated polynucleotide comprising fragments and haplotypes of the cyclin-dependent kinase 4 (CDK4) gene. Human CDK4 gene is located on chromosome 12q13 and contains 8 exons. The haplotypes and polymorphisms of CDK4 gene are useful for validating whether CDK4 is a suitable target for drugs to treat cancer, melanoma and disorders associated with impaired protein synthesis in cells, screening for such drugs and reducing bias in clinical trials of such drugs. Haplotype information would be useful in improving the efficiency and output of several steps in the drug discovery and development process, including target validation, identifying lead compounds, early phase clinical trials. The present secening for compounds targetting CDK4 to treat a specific condition or disease predicted to be associated with the condition or disease predicted to be associated with the present sequence is a ASO primer used for detecting
                                                                                                                                                                                     Human, cyclin-dependent kinase 4; CDK4; chromosome 12q13; therapy; cancer; melanoma; protein synthesis disorder; drug screening; primer; ASO; allele-specific oligonucleotide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                               Human CDK4 gene polymorphism detecting ASO primer #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 15 BP; 3 A; 4 C; 4 G; 3 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sausker EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 16; Page 13; 58pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIV-1 proviral DNA fragment 10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX56927 standard; DNA; 15 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENA-) GENAISSANCE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-MAY-2001; 2001WO-US016350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAY-2000; 2000US-0205867P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human CDK4 gene polymorphism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2003 (revised)
15-JUL-1999 (first entry)
                                 26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kazemi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-083072/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200190115-A2.
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX56927;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide separated by capillary affinity gel electrophoresis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Capillary afinity gel electrophoresis; separation; polymer-gel;
                                                                                                                     ö
                                                   ch 0.8%; Score 13.4; DB 1; Length 15; 1 Similarity 93.3%; Pred. No. 8.9e+02; 14; Conservative 0; Mismatches 1; Indels
Sequence 15 BP; 6 A; 0 C; 9 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polyacrylamide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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Human immunodeficiency virus 1.

RESULT 1386

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Amixture of oligonucleotides (AAT86601-3) were separated by a new process using capillary affinity gel electrophoresis. The invention relates to selective separation of electrically charged target molecules in an analytical mixture. It comprises capillary affinity gel electrophoresis using a capillary tube which is at least partly filled with a polymer agel. Receptors for target molecules are covalently bound to the polymer. An electric field of at least 50 volts/cm is applied. The capillary tube is charged with the analytical mixture. In a first separation stage, the target molecules in the mixture are bound to the receptors and the remaining components are eluted, optionally whilst components are eluted, optionally whilst splitting open. In a second stage, the elution conditions are changed, optionally in stages, so that the affinity of the target molecules for the receptor is eliminated and the target molecules are eluted and detected, optionally whilst splitting open. The process is useful for selective separation and/or determination of charged organic compounds, such as oligonucleotides, peptides or carbohydrates. It may be used, e.g. for isolation of specific proteins and DNA molecules, purification of antibodies, analysis of antisense compounds or screening for enzyme inhibitors. The process achieves higher resolution and selectivity than prior art processes, especially in the case of complex biological canalytical mixtures. It has high sensitivity, even with small amounts of samples. The derivatised polymers may be synthesised specifically using espandard methods
                                                                                                                                                                                                                                                                                                                               Separation of electrically charged target molecules - by capillary affinity gel electrophoresis using polymer-gel to which receptors for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15 BP; 14 A; 0 C; 0 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                            Example D2; Page 25; 41pp; English.
                                                                                             97WO-EP002647
                                                                                                                                         96CH-00001320
                                                                                                                                                                                                                                                                                                                                                                                target molecules are bound
                                                                                                                                                                                                                                    Paulus A,
                                                                                                                                                                                                                                                                                  WPI; 1998-041763/04.
                                                                                                                                                                                     (NOVS ) NOVARTIS AG
                                                                                                                                                                                                                                                                                                                                                       gel
                                                                                             23-MAY-1997;
                                                                                                                                           24-MAY-1996;
  WO9745721-A1
                                              04-DEC-1997
                                                                                                                                                                                                                                      Muscate A,
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ö Gaps ö Query Match 0.8%; Score 13.4; DB 1; Length 15; Best Local Similarity 93.3%; Pred. No. 8.9e+02; Matches 14; Conservative 0; Mismatches 1; Indels 1736 AAAAAAAAAAAA 1750 ઠ

1 AAAAAATAAAAA 15 පු

AAA11718 standard; DNA; 15 BP 14-JUL-2000 (first entry) AAA11718; RESULT 1388 

Human MIF gene D5k region primer #2.

MIF; migration inhibitory factor; D5k region; human; macrophage; diagnosis; primer; adenocarcinoma; metastasis; cancer; tumor cell; ss.

Homo sapiens

US6043044-A.

28-MAR-2000

97US-00893204. 15-JUL-1997;

97US-00893204. 15-JUL-1997; 

HUDSON P B. (HUDS/) HUDSON P (HAKK/) HAKKY S I (SIEG/) SIEGLER K (HAKK/) HAKKI A.

HAKKY S I. SIEGLER K M.

Siegler KM,

Hakki A;

SI, Hudson PB, Hakky

A new method useful for diagnosing human adenocarcinoma and measuring metastatic potential comprises determining the levels of macrophage migration inhibitory factor within tumor cells. WPI; 2000-292363/25.

Claim 11; Col 7-8; 6pp; English.

This invention describes a novel method for diagnosing adenocarcinoma and determining metastatic ability of human cancer in an individual by determining the increased levels of macrophage migration inhibitory factor (MIP) within tumor cells. The method is useful for diagnosing human adenocarcinoma, as well as for its prognosis. The method is also useful for measuring levels of macrophage migration inhibitory factor within tumor cells. The method provides better and more accurate prognostic markers for cancer. The method is also capable of alstinguishing histological tumors from clinical cancers. This sequence represents a primer used to detect the human MIF gene D5k region which is

Sequence 15 BP; 0 A; 1 C; 0 G; 14 T; 0 U; 0 Other;

Gaps ö 0.8%; Score 13.4; DB 1; Length 15; 93.3%; Pred. No. 8.9e+02; ive 0; Mismatches 1; Indel8 Best Local Similarity 93.3 Matches 14; Conservative Query Match

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à 원 RESULT 1389

AAF46740 standard; DNA; 15 BP **AAF46740/** 

AAF46740;

30-MAR-2001 (first entry)

IGFBP3 oligonucleotide #160.

Antisense therapy; antiproliferative; antinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFB-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; sclaroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition of the retina; ss. 

Homo sapiens.

WO200078341-A1

28-DEC-2000.

21-JUN-2000; 2000WO-AU000693.

99US-0140345P 11-JUN-1999; (MURD-) MURDOCH CHILDRENS RES INST.

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Edmondson SR;

Werther GA,

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WPI; 2001-041421/05
                                                                                      WO200078341-A1
                                                                                               21-JUN-1999;
 Wraight CJ,
                                                              AAF49276;
                                           Query Match
                                                        RESULT 1390
                                              Matches
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administering
cleic acid that
                                                                                                                                                                                                                                                                                                                                                                                                       ekin disorders. The method comprises contacting the skin will an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFB]-2 or IGFBP], which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, hyperneovascular condition such as a neovascular condition of the retina brain or skin, growth factor-mediated malignancies, other sclerotic
                                                                                                                                                                                                                                                                                                                                                                 present invention relates to a method for ameliorating the effects of
Ameliorating the effects of a disorder, e.g. psoriasis, by administer (UV (ultra-violet) treatment (optional) and an antisense nucleic acid inhibits or reduces growth factor mediated cell proliferation and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15 BP; 0 A; 7 C; 6 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                           Example 7; Page 45; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vessels or any other hyperplasia
                                                                                                                                                                      inflammation.
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                                 Gaps
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0
0.8%; Score 13.4; DB 1; Length 15; 93.3%; Pred. No. 8.9e+02; vative 0; Mismatches 1; Indels
                                 14; Conservative
                    Local Similarity
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AAF49276 standard; DNA; 15 BP

IGF-I oligonucleotide #236. 30-MAR-2001 (first entry)

cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated call proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition of the retina; ss. Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;

Homo sapiens

28-DEC-2000.

21-JUN-2000; 2000WO-AU000693.

(MURD-) MURDOCH CHILDRENS RES INST.

99US-0140345P

Wraight CJ, Werther GA, Edmondson SR;

WPI; 2001-041421/05

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                                                                                                                                                                                                                                                                                  The present invention relates to a method for ameliorating the effects of akin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF$151 and AAF$153-F$151). The method is useful for ameliorating the effects of psoriasis, ichthyosis, picyriasis, unb, pilaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperpoliferation of the inside of blood
Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.8%; Score 13.4; DB 1; Length 15; 33.3%; Pred. No. 8.9e+02; Ved. 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15 BP; 3 A; 5 C; 5 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                  Example 8; Page 62; 201pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ressels or any other hyperplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   762 TCTCCCAGGCCGAGG 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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BP AAF45532/c ID AAF45532 standard; DNA; 15 RESULT 1391

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AAF45532;

IGFBP2 oligonucleotide #371. 30-MAR-2001 (first entry)

Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; Keloid; skin discorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keatosis; neoplasta; sclaroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neoblastic disease; neoblastic of the retina; ss. 

Homo sapiens.

WO200078341-A1.

21-JUN-2000; 2000WO-AU000693.

21-JUN-1999; 99US-0140345P.

(MURD-) MURDOCH CHILDRENS RES INST.

Edmondson SR; Wraight CJ, Werther GA,

WPI; 2001-041421/05.

Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or

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present invention relates to a method for ameliorating the effects

Mon Aug 16 16:46:36 2004

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The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonuclectide, (for Insulin-like Growth Factor [IGF]-1 creeptor, IGF binding protein [IGFP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, coligonuclectide which can be used to design the antisense oligonuclectide which can be used to design the antisense oligonuclectide which can be used to design the affects of portagis, coligonuclectide which ameliorating the effects of psoriasis, replaying the method is useful for ameliorating the effects of psoriasis, chhyosis, pitziasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic condition of the inside of blood
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                                                                                                                                                                                                                                                                                                        Sequence 15 BP; 0 A; S C; 7 G; 3 T; 0 U; 0 Other;
                              Example 6; Page 36; 201pp; English.
                                                                                                                                                                                                                                                                             vessels or any other hyperplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                    Local Similarity 93.3
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inflammation
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0.8%; Score 13.4; DB 1; Length 15; 33.3%; Pred. No. 8.9e+02; ve 0; Mismatches 1; Indels
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                            93.3%;
                                                                                                                                         188 AGCAGCCGGAGCCCG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGFBP3 oligonucleotide #303.
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                                                                                                                                                                                                          15 AGCAGCCGCAGCCCG 1
                                                                                                                                                                                                                                                                                                                                                                                    AAF46883 standard; DNA; 15
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Example 7; Page 46; 201pp; English

inflammation.

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               skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-Ike Growth Factors [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBPB), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotide of the present invention (see AAF45151 and AAF45153-F4516). The method is useful for ameliorating the effects of psoriaais, ichthyosis, pityriasis, ruba, pilaris, serbornhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antisense therapy, antiproliferative, antinflammatory, antipsoriatic, cytostatic, dermatological, cardiant, virucide, ophthalmological, keloid, skin disorder, Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein, IGFB-2; IGFBP3; inflammation, psoriasis; pilatis; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition of the retina; ss.
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                                                                                                                                                                                                                                                                                                                                                                           / Match 0.8%; Score 13.4; DB 1; Length 15; Local Similarity 93.3%; Pred. No. 8.9e+02; nes 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                    Sequence 15 BP; 0 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF46741 standard; DNA; 15 BP.
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inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF4151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, hyperneovascular condition such as a neovassular condition of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood
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      8x388888888x8
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Sequence 15 BP; 0 A; 7 C; 6 G; 2 T; 0 U; 0 Other;

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0.8%; Score 13.4; DB 1; Length 15; 93.3%; Pred. No. 8.9e+02; arive 0; Mismatches 1; Indels
                                                        CGCCCACGGAGCAG 268
                            Conservative
            Local Similarity
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Gaps

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AAF46738 standard; DNA; 15 RESULT 1394

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30-MAR-2001 (first entry) AAF46738;

IGFBP3 oligonucleotide #158.

Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriaais; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriaais; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition of the retina; ss.

Homo sapiens.

WO200078341-A1.

28-DEC-2000

21-JUN-1999;

21-JUN-2000; 2000WO-AU000693

99US-0140345P.

(MURD-) MURDOCH CHILDRENS RES INST.

Wraight CJ, Werther GA, Edmondson SR;

WPI; 2001-041421/05.

Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.

Example 7; Page 45; 201pp; English.

The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, infilammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense of the present invention (see AAF45151 and AAF45153-

The present invention relates to a method for ameliorating the effects of antisense oligonucleotide, (for Insulin-like Growth Factor [IGF] receptor, IGF binding protein [IGFBP] or IGFBPB), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, ruba, planis, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina,

Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or

Example 7; Page 45; 201pp; English.

inflammation.

Edmondson SR;

Wraight CJ, Werther GA, WPI; 2001-041421/05.

(MURD-) MURDOCH CHILDRENS RES INST

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                                                                                                                                                                                                                                                                                                                                                                                                            Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGF8P-2; IGF8P2; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; seleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition; byperplasia; kidney disease;
                                            the retina,
F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pitytiasis, ruba, pilaris, seraborhosa, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina bain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperpoliferation of the inside of blood vessels or any other hyperplasia
                                                                                                                                                                      Gaps
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                                                                                                               Sequence 15 BP; 0 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                    BP.
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                                                                                                                                                                                                  257 CCCACGGAGCAGCAC 271
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AAF46739 standard; DNA; 15
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Best Local Similarity 93.3'
Matches 14; Conservative
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effects of therapeutic agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to a polynucleotide sequence that is a polymorphic variant of the human prostaglandin-endoperoxide synthase 2 (PTGS2) gene also referred to as cyclooxygenase 2. The human PTGS2 gene sequence AAP80896 contains 27 single nucleotide polymorphisms (SNPB). AAP80896 and AAP80897 represented by AAB72199. The invention includes PCR and sequencing primers, and probes represented in AAP80898 - AAP81151 which are used to isolated and characterise the PTGS2 gene sequence, and to coate the positions of the SNPB. PTGS2 proteins and polymucleotide sequences are used to express variant PTGS2 proteins, for structural analysis or drug-binding studies and also in gene therapy (either sepressing PTGS2 or inhibitory RNA). Antibodies raised against PTGS2 are useful for diagnosis, prognosis and therapy and analysis of the new, and known, polymorphisms and used to determine PTGS2 palotype and genecype, especially for determining association between a particular trait, e.g. clinical response to drugs that target PTGS2 but also disease of inscending diagnostic testes and treatments for immune-related disorders such as arthritis and inflammation. The polymorphisms may also be used to study expression and biological function of PTGS2. Transgenic animals that express PTGS2 are used to study expression and biological function of PTGS2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; prostaglandin-endoperoxide synthase 2; PTGS2; cyclooxygenase 2; single nucleotide polymorphism; SNP; immune-related disorder; arthritis; inflammation; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid containing polymorphisms in the cyclooxygenase-2 gene, for gene therapy of inflammation and for establishing a genotype or
                                                                                                                                                                                                       Gaps
brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia
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                                                                                                                                                Length 15;
                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTGS2 allele specific oligonucleotide probe SEQ ID 25.
                                                                                                  Sequence 15 BP; 0 A; 6 C; 6 G; 3 T; 0 U; 0 Other;
                                                                                                                                              0.8%; Score 13.4; DB 1;
93.3%; Pred. No. 8.9e+02;
ative 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 21; 118pp; English
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                                                                                                                                                                                                                                                   256 GCCCACGGAGCAGCA 270
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                                                                                                                                              Query Match
Best Local Similarity 93.34
Matches 14; Conservative
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AAF80919/AAF80919/AAF80919/AAF80919/AAF80919/AAF80919/AAF80919/AAF80919/AAF80919/AAF80919/AAF80919/AAF80919/AAF80919/AAF80919/AAF80919/AAF8090/AAF8000/CCC AAF80CCC  AAF80CCC AAF80CC
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This invention relates to oligonucleotide analogues comprising a protein nucleic acid molecule (DNA) monomer. They are used in the detection and separation of nucleic acid molecules and as probes, primers, linkers, adapters and antisense agents on solid supports. Modifications enhance their use as capture and detection probes e.g. by the incorporation of blotin, digoxigenen, radioisotopes, fluorescent labels such as fluorescent and reporter molecules such as alkaline phosphatese. They are closed for enhancing or inhibiting the activity of an enzyme or also used for enhancing or inhibiting the activity of an enzyme or cellular activity. The polyamide backbone of PNAs is resistant to both nucleases and proteases. PNAs bind nucleic acid molecules with greater affinity than DNA or RNA concentration. The compounds are relatively simple to synthesize and are used in a wide variety of applications. This sequence represents a DNA oligoner which is used to represent the effect of single base mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleotide sequence of oligomer # 12 used to compare mismatches.
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                                                                 0.8%; Score 13.4; DB 1; Length 15; 93.3%; Pred. No. 8.9e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archdeacon D, Archdeacon J; kova A, Choob M, Hondorp K;
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Sequence 15 BP; 1 A; 0 C; 0 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein nucleic acid molecule; PNA; ds.
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Chakhmakhcheau O, Buryakova A,
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                                                                                                                                                                                                                                                                    15 AAAAAAAAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JUN-2002 (first entry)
                                                Query Match
Best Local Similarity 93.3<sup>3</sup>
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Matches 14; Conservative
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Best Local Similarity
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15 AAAAAAGAAAAAA 1
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ABK98166 standard; DNA; 15 07-OCT-2002 ABK98166; 

(first entry)

Triple helix forming associated oligonucleotide #36.

Triple-helix formation; purine-rich target sequence; double-helix DNA gene expression; regulatory sequence; pathogenic double-stranded DNA; pathogenic bacteria; virus; replication; virulence; cancer; cancer; oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

Synthetic.

US6403302-B1

11-JUN-2002.

9305-00168920 16-DEC-1993;

92US-00946976 17-SEP-1992;

(CALY ) CALIFORNIA INST OF TECHNOLOGY.

Beal PA; Dervan PB,

WPI; 2002-536030/57.

A triple-helix comprising a double helical nucleic acid (DHNA) and an oligonucleotide which binds in parallel and antiparallel orientation, respectively, for targetting sequences on alternate strands of DHNA to control gene expression.

Example 6; Fig 20A; 108pp; English

The present invention relates to methods and oligonucleotides for forming a triple-helix comprising a double helical nucleic acid comprising first and second substantially complementary strands, and an oligonucleotide bound to a purine-rich target sequence within the double helical nucleic acid, where the oligonucleotide binds in a parallel and antiparallel or ienteation, respectively, to target sequences on alternate strands of the double helical nucleic acid. The method has therapeutic applications, where gene expression is controlled by selective triple-helix formation within expression regulatory sequences of a target gene. The oligonucleotides can be used to form triple-helices, and are useful to detect the presence or absence of specific sequences within genomic DNA for diagnostic and therapeutic purposes. The oligonucleotides can be selected to specifically bind to pathogenic double-stranded DNA including specific sequences required by pathogenic bacteria or viruses for replication or virulence, reducing their pathogenicity. Alternatively, creplication or virulence, reducing their pathogenicity. Alternatively, pathogen which is not found in the genome of pathogen; shows of triple-helix oligonucleotides can be used in cancer treatment by way of triple-helix suppression of specific oncogenes including those of endogenous or virule. origin. Such therapeutic oligonuclectides are capable of forming triple-helices with such sequences in cancerous cells containing the activated oncogene, so preferentially killing or repressing the cancer causing so preferentially killing or repressing the cancer causing present sequence represents an oligonucleotide used in the methods of the present invention

Sequence 15 BP; 0 A; 1 C; 0 G; 14 T; 0 U; 0 Other;

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Score 13.4; DB 1; Length 15;
Pred. No. 8.9e+02;
0; Mismatches 1; Indels
0.8%;
                         14; Conservative
Query Match
Best Local Similarity
                        Matches
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Gaps

|||||||| ||||||| 15 AAAAAAGAAAAAA

RESULT 1399 ABK98185,

ABK98185 standard; DNA; 15 BP

ABK98185;

(first entry) 07-OCT-2002 Triple helix forming associated oligonucleotide #49.

Triple-helix formation; purine-rich target sequence; double-helix DNA; gene expression; requiatory sequence; pathogenic double-stranded DNA; pathogenic bacteria; virus; replication; virulence; cancer; concegene suppression; cancerus cell; cytostatic; antimicrobial; ss.

Synthetic.

US6403302-B1.

11-JUN-2002.

93US-00168920 .6-DEC-1993; (CALY ) CALIFORNIA INST OF TECHNOLOGY.

92US-00946976.

17-SEP-1992;

Dervan PB, Beal PA; WPI; 2002-536030/57. A triple-helix comprising a double helical nucleic acid (DHNA) and an oligonucleotide which binds in parallel and antiparallel orientation, respectively, for targetting sequences on alternate strands of DHNA to control gene expression.

Example 7; Fig 24A; 108pp; English

The present invention relates to methods and oligonucleotides for forming a triple-helix comprising a double helical nucleic acid comprising first and second substantially complementary strands, and an oligonucleotide bound to a purine-rich target sequence within the double helical nucleic acid, where the oligonucleotide binds in a parallel and antiparallel corientation, respectively, to target sequences on alternate strands of the double helical nucleic acid. The method has therapeutic applications, where gene expression is controlled by selective triple-helix formation within expression regulatory sequences of a target gene. The oligonucleotides can be used to form triple-helixes, and are useful to detect the presence or absence of specific sequences within genomic DNA for diagnostic and therapeutic purposes. The oligonucleotides can be used to form to pathogenic bacteria or viruses for selected to specifically bind to pathogenic bacteria or viruses for replication or virulence, reducing their pathogenicity. Alternatively, the oligonucleotide can be chosen to target a unique sequence of the oligonucleotides can be used in cancer treatment by way of triple-helix suppression of specific oncogenes including those of endogenous or viral or oligonucleotides are capable of forming triple-helix suppression of specific oncogenes including those of endogenous or viral or origin. Such therapeutic oligonucleotides are capable of forming triple-helix oncogene, so preferentially killing or repressing the cancer causing capable. methods of the present invention

Sequence 15 BP; 0 A; 1 C; 0 G; 14 T; 0 U; 0 Other;

Gaps ö 0.8%; Score 13.4; DB 1; Length 15; 13.3%; Pred. No. 8.9e+02; ve 0; Mismatches 1; Indels 93.3%; 14; Conservative Best Local Similarity Matches 14; Conserv

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(first entry)

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Adaptor molecule; nucleic acid cloning; nucleic acid ligating; internal deletion mutagenesis analysis; cloning vehicle; ss.
                                                                                                  Nucleic acid cloning associated adaptor molecule #143.
            ACD82442 standard; DNA; 15 BP.
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                                                                                                                                                                                                                                                               13-JUN-2001; 2001US-00880313.
                                                                                                                                                                                                                                                                                                                        (FLEM/) FLEMINGTON E
                                                                                                                               Adaptor molecule;
                                                                                                                                                                                                     US2003044791-A1.
                                                                                                                                                                                                                                                                                                                                                     Flemington EK;
                                                                    19-SEP-2003
                                                                                                                                                                                                                                  06-MAR-2003
                                                                                                                                                                         Synthetic.
                                         ACD82442;
ACD82442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention discloses a method for identifying a candidate polymorphic repeat within a coding sequence (expressed sequence tag, EST), which comprises detecting tandem repeats in a target coding sequence, scoring the repeats for polymorphic probability and generating a dataset correlating the repeats with polymorphic probability to identify a candidate polymorphic repeat. The computational methods (polymorphic candidate polymorphic repeat. The computational methods (polymorphic cuscul for identifying and detecting candidate polymorphic repeats in cuscul for identifying and detecting candidate polymorphic repeats in classases, predictions or adverse drug-treatment reactions. Examples of diseases linked to nucleotide repeats are Machado-Joseph, Haw River syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis, syndrome, Eredreich's ataxis, spinal and bulbar atrophy and spinocerebellar ataxia. The sequences presented in ABX7967-ABX80022 are the polymorphic repeats identified for a search of human ESTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for
                                                                                                                                                                                                                EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat; polymorphic marker prediction of ubiquitous simple sequences; POMPOUS; Rep-X; human; genetic disease; drug-treatment; Machado-Joseph; Haw River syndrome; Huntington's disease; fragile-X syndrome; Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia; spinal atrophy; bulbar atrophy; spinocerebellar ataxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying a candidate polymorphic repeat within a coding sequence, funderstanding or treating genetic disease, comprises detecting tandem repeats in a target coding sequence and scoring the repeats for polymorphic probability.
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                                                                                                                                                                                       EST polymorphic DNA repeat polynucleotide #164.
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1736 AAAAAAAAAAAAA 1750
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                                                                                                  ABX79839 standard; cDNA; 15
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                                                                                                                                                          (first entry)
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                          15 AAAAAAAGAAAAAA
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                                                                                                                                                            17-APR-2003
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                                                                                                                               ABX79839;
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                                                                      RESULT 1400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mutagenesis analysis. The adaptor molecules are ligated to a cioning vehicle, making the cloning procedure more rapid and efficient, and less error-prone. This sequence represents a nucleic acid cloning associated
                                                     New adaptor molecules, useful for cloning nucleic acid molecules that does not require the design and synthesis of oligonucleotides or PCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.8%; Score 13.4; DB 1; Length 15; 33.3%; Pred. No. 8.9e+02; ve 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15 BP; 2 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                            Claim 12; Fig 3; 100pp; English.
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WPI; 2003-521745/49.
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ACD82604
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Synthetic

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RESULT 1401

93.3%;

Best Local Similarity 93.3 Matches 14; Conservative

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                                                                                                                                                                                                                                                                                                    13-JUN-2001; 2001US-00880313.
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                                                                                                                                                                                                                                                                                                                                                                                           (FLEM/) FLEMINGTON E K.
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US2003044791-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Flemington EK;
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                                                                                            06-MAR-2003
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The invention relates to a novel method of inhibiting the expression of one or more genes or RNA transcripts by administering at least one oligonucleotide analogue that includes at least one hydroxyproline nucleic acid (HypNA) monomer to a cell or organism or their extracts. Throlloging sene expression, respiration, secretion, signalling, innectance channel activity, cell motility, developmental phenotype and tumour regression. Furthermore, they may be utilised to determine the effects of particular genes, as antisense or homologous recombination constructs e.g. for creating animal models of disease and finally, for increasing the activity of some enzymes, such as polymerases. The current sequence is that control of the single-base mismatch oligonucleotide SEQ ID 12 DNA of the invention. This sequence may also comprise a peptide nucleic acid (PNA), a phosphono-PNA (PPNA) or a HypNA.
                                                                     useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Target; Human Immunodeficiency Virus; AIDS; triplex; hepatitis; herpes; malignancy; ds.
                                                                  Method of inhibiting expression of genes or RNA transcripts, useful f
therapy and determining effects of genes, by administering oligomers
containing hydroxyproline nucleic acid.
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               Archdeacon D, Archdeachon J,
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                                                                                                                                                                                                                                                                                                                                                                               Sequence 15 BP; 0 A; 1 C; 0 G; 14 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Purine rich HIV target duplex sequence.
                                                                                                                               Disclosure; Page 234; 240pp; English.
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91US-00643382.
91US-0068544.
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91US-00686546.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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Best Local Similarity 93.3
Matches 14; Conservative
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               Fernandez J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GILE-) GILEAD SCI INC
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                                          WPI; -2003-689653/65.
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07-DEC-1992
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The sequence depicts a HIV viral duplex sequence which contains a purinerich region concentrated on one chain of the duplex. The sequence may be prepd. by standard DNA synthesis. The HIV duplex sequence is used as a target for novel oligomers which are capable of forming a triplex at physiological pH by coupling into the major groove of the DNA duplex. Three such oligomers HIV141 -HIV143 are capable of forming a triplex with this sequence. The oligomers are used in the diagnosis and therapy of HIV infection. Similar oligomers are used in the diagnosis and therapy of HIV infection. Similar oligomers may be used to target viral DNA duplexes specific for hepatitis, herpes and malignancy. The triple helices form under mild conditions thus assays may be carried out without subjecting the test specimen to harsh conditions. The oligomer is able to inhibit gene expression, as verified by in vitro systems See also AAQ23452-25551 and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    viable Cryptosporidium parvum cells - in 18S rRNA, useful as probe or primer
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oligomers contg. modified bases - which form a triplex with G-C blet in a DNA duplex, for treating and diagnoging HIV, hepatitis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.8%; Score 13.4; DB 1; Length 16; 93.3%; Pred. No. 9.2e+02; ve 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cryptosporidium parvum 18S rRNA gene primer/probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16 BP; 7 A; 0 C; 9 G; 0 T; 0 U; 0 Other;
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                                                                         herpes malignancy and inflammation.
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                                                                                                                                               Claim 11; Page 63; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vesey G, Veal D, Williams KL,
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(SYDN-) SYDNEY WATER CORP
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                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide array; genotyping; single base extension reaction; SBE; PCR primer; polymorphic locus; single nucleotide polymorphism; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Universal array of oligonucleotides tags attached to a solid substrate along with locus-specific tagged oligonucleotides useful in genotyping using single base extension reactions.
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dead cells, because RNA degrades too quickly in such cells, or other Cryptosporidium species that are not pathogenic to humans
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                                                                            0.8%; Score 13.4; DB 1; Length 16; 93.3%; Pred. No. 9.2e+02; ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                       Forward primer #66 used in multiplexing PCR/SBE assay.
                                                Seguence 16 BP; 2 A; 0 C; 1 G; 13 T; 0 U; 0 Other;
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99US-0140359P.
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Ryder T, Sklar P;
                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200058516-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified,
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dermatclogical; antidepressant; tranquilliser; antidiflammatory; eczema, antiulcer; antimigraine; neuroprotective; antiparkinsonian; analgesic; antiulcer; antimigraine; neuroprotective; antiparkinsonian; analgesic; gynaecological; virucide; vulnerary; antiarthritic; antipsoriants; cold; antimicrobial; cytostatic; litholytic; pathological disorder; depression; abnormal appetite; hypertension; hypercholesterolaemia; hyperlipidaemia; erectile dysfunction; anxiety; stress; inflammatory bowel syndrome; ulcerative colitis; Crohn's disease; renal stone; gall stone; migraine; constipation; headache; seizure; multiple sclerosis; polymyositis; fibromyalgia; Parkinson's disease; amyotrophic lateral sclerosis; trauma; chronic fatigue syndrome; sinusitis; carpal tunnel syndrome; chronic fatigue syndrome; rosacea; arthritis; psoriasis; prostatis; inflammation; heart burn; infection; colon cancer; malignant melanoma; skin disorder; antisense oligonucleotide; ss.

Human; pharmacological; hypotensive; antilipaemic; vasotropic; laxative;

Human Ghrelin antisense oligonucleotide SEQ ID NO:38.

(first entry)

09-OCT-2003

ACF63316;

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The present sequence is that of a single mismatch target sequence for a molecular beacon comprising an oligonucleotide probe (see ABL57069) covalently attended at the 3' end to fluorescent dye and at the 5' end to conformation with hybridised termini. The probe forms a hairpin conformation with hybridised termini. The probe forms a hairpin and quencher (gold nanoparticle) in the molecular beacon results in little or no detectable fluorescence. Upon hybridisation of the central complementary stretch of the probe to a target sequence, such as the present sequence, the hairpin undergoes a conformational change resulting in an increase in fluorescence, the extent of which is proportional to the amount of target sequence present Experiments with the present sequence and a perfectly-matched target (see ABL57071) showed that hybridisation was very specific to the matched target. The invention relates generally to the use of metal surface quenchers such as particles or films for high sensitivity applications in, for example, detection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sensitively detecting proximity changes in a system that utilizes an interacting fluorophore and quencher, for high sensitivity applications, involves utilizing a metal surface as quencher.
                                                                                                                                                                              Molecular beacon; fluorophore; nanoparticle; nucleic acid detection; ss.
                                                                                                                                             Molecular beacon target sequence (single mismatch).
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                                                                                                                                                                                                                                                                                       /*tag= a
/note= "mismatch site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Calame M, Libchaber A;
                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Page 30; 62pp; English.
                                   ABL57076 standard; DNA; 16 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-AUG-2000; 2000US-0228728P.
30-MAR-2001; 2001US-0280350P.
                                                                                                                                                                                                                                                                                                                                                                                                                 29-AUG-2001; 2001WO-US041941
                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-404569/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnostic systems
                                                                                                                                                                                                                                                                                                                                             WO200218951-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dubertret B,
                                                                                                          22-JUL-2002
                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                07-MAR-2002
                                                                                                                                                                                                                  Synthetic
                                                                        ABL57076
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The present invention describes a composition (I) suitable for administration in a mammal, which comprises a modified oligonucleotide containing 7 or more contiguous ribose groups [III] of 7-75 nucleotides containing 7 or more contiguous ribose groups condified oligonucleotide is complementary to a region of a gene associated with a pathological disorder. Also described: (I) a comprising (II), where the modified oligonucleotide is complementary to a region of a gene associated with a skin disorder. (I) and (II) can have hypotensive, antilipaemic, vasotropic, dermatological, antidepressant, tranquilliser, antiliflammatory, antilucer, laxative, antimigraine, neuroprotective, antiparkinsonian, analgesic, gynaecological, virucide, vulnerary, antiarthritic, antimicrobial, cytostatic and litholytic activities (I) can be used for treating a patient with a pathological disorder selected from abnormal appetite, hypertension, hypercholesterolaemia, hyperligidaemia, erectile dysfunction, eczema, depression, anxiety, stress, inflammatory bowel syndrome, ulcerative colitis, Crohn's disease, renal stones, gall stones, constipation, colds, migraine headache, seizure, multiple sclerosis, polymyostis, sinustis, chronic pain, pre-menstrual syndrome, trauma, carpal tunnel syndrome, chronic fatigue syndrome, rosacea, arthritis, psoriasis, prostatis, inflammation, heart burn, infection, poison ivy, colon cancer, malignant mealanome, and malignant masal polype. The nutritional supplementic number of the supparance of the shin in an engage of the skin in an engage of the skin in an engage of the skin in an engage of the shin in an engage of the skin in a second enga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     individual with a skin disorder. ACP63279 to ACF63410 represent
nucleotide sequence given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 17; Page 8; 173pp; English
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Gaps

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0.8%; Score 13.4; DB 1; Length 16; 93.3%; Pred. No. 9.2e+02; tive 0; Mismatches 1; Indels

1736 AAAAAAAAAAAAA 1750

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14; Conservative

Matches

Local Similarity

Query Match

AAAAAACAAAAAA 16

ACF63316 standard; DNA; 16 BP.

RESULT 1408 ACF63316/c ID ACF6331 XX

Composition with a modified oligonucleotide useful for treating a patient with a pathological disorder such as abnormal appetite, hypertension,

Thompson T;

WPI; 2003-221709/21. Dale RMK, Arrow A,

(OLIG-) OLIGOS ETC INC.

10-JUL-2002; 2002WO-US021664. 10-JUL-2001; 2001US-0303820P.

WO2003006478-A1

3-JAN-2003

sapiens.

Homo

Synthetic.

eczema, anxiety, stress, and cancer

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A novel method for the detection of plant pathogenic strains of fungine. Septoria nodorum, S. tritici, Pseudocercosporella herpotrichoides, Mycosphaerella fijiensis, M.musicola or Fusarium spp, involves the PCR amplification of sequences found in the internal transcribed region (ITS) of the 18S, 5.8S and 28S ribosomal RNA genes by the primers AAQ94359-93 and AAT05379-72. These primers are derived from the ITS sequences of these fungi (AAT05394-T05404 and AAQ94389) and are strain specific. The amplification products of the reactions using these primers can be used with the capture primers AAT05378-93 in colourimetric assays. The primers and ITS DNAs can be used for the detection of specific fungal pathogen isolates and in monitoring disease development in plant populations
                                                          Plant pathogen; fungus; Septoria nodorum; Septoria tritici; Fusarium; Pseudocercosporella herpotrichoides; Mycosphaerella fijiensis; PCR; Mycosphaerella musicola; amplification; primer; ribosomal RNA gene; internal transcribed region; strain; capture; colourimetric assay; isolate; development; population; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding intervening transcribed sequence - used for detection of plant fungal pathogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.8%; Score 13.4; DB 1; Length 17; ilarity 93.3%; Pred. No. 9.6e+02; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum; MSA-1 gene; recombinant poxvirus; multicomponent multistage malarial vaccines; immunogens; malaria diagnosis; PCR primer C008; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17 BP; 2 A; 2 C; 9 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum MSA-1 gene PCR primer C008.
                         Septoria tritici ITS primer JB446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 15; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ81619 standard; DNA; 17 BP.
                                                                                                                                                                                                                                                                                                           95WO-US004712.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              612 CCCCACTCCAGCCTC
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                                                                                                                                                                                                                                                                                                                                                                                      (CIBA ) CIBA GEIGY AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-383005/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                Beck JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                         WO9529260-A2
                                                                                                                                                                                                                                                                                                           19-APR-1995;
                                                                                                                                                                                                                                                                                                                                                 25-APR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
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30-AUG-1995
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                                                                                                                                                                                                                                                                   02-NOV-1995
                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                              Ligon JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ81619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a method for detecting interactions between biological components using a nonlinear optical technique. The invention is used for screening candidate binding partner(s) for binding to test molecule. It can also be used to detect changes in orientation or conformation of the probe and/or target. The present sequence is a target oligonucleotide used in nonlinear optical technique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Screening candidate binding partner(s) for binding to test molecule by applying external force field to sample in homogeneous phase, illuminating sample with light beam(s) at fundamental frequencies, and
                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                    Target oligonucleotide #3 used in nonlinear optical technique.
                                           Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.8%; Score 13.4; DB 1; Length 16; 93.3%; Pred. No. 9.2e+02;
                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16 BP; 14 A; 1 C; 1 G; 0 T; 0 U; 0 Other;
Sequence 16 BP; 3 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
                                     Query Match

0.8%; Score 13.4; DB 1;
Best Local Similarity 93.3%; Pred. No. 9.2e+02;
Matches 14; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            Nonlinear optical technique; screening; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Fig 20-B; 146pp; English.
                                                                                                                                                                                                                                                                 H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              measuring physical properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1736 AAAAAAAAAAAAA 1750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUL-2001; 2001US-0306040P.
23-OCT-2001; 2001US-0347821P.
06-FEB-2002; 2002US-0354668P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JUL-2002; 2002WO-US022681
                                                                                                                       167 GGCCCACCTGGCTGC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 AAAAAACAAAAAA 16
                                                                                                                                                             16 ĠĠĊĊĊĄĊĊŢĠŦĊŢĠĊ 2
                                                                                                                                                                                                                                                               AAD57846 standard; DNA; 16
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                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 93.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SALA/) SALAFSKY J S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-646172/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003064991-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                                                                                               20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salafsky JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-AUG-2003
                                                                                                                                                                                                                                                                                                       AAD57846;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                         RESULT 1409
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Gaps

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Matches

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                                                                                                                                                                              AAQ81619 and AAQ81620 are a pair of primers for the PCR amplification of the P. falciparum MSA-1 gene, used in the production of new recombinant povairuses containing either the SERA, ABRA, Pfhsp70, AMA-1, Pfs25, Pfs16, CSP, PfSSP2, LSA-1, LSA-1 repeatless, MSA-1, MSA-1 (N-terminal p83 or C-terminal gp42) genes, or combinations of these in non-essential regions of their genomes. These poxviruses (pref. with a virulence reducing genomic deletion or disruption) can be used as vaccines against malaria and for the prodn. of Plasmodium immunogens. These viruses provide multicomponent, multistage vaccines due to their expression of sporozite, liver stage, blood stage and sexual stage proteins. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New enzymatic nucleic acid molecules - cleave RNA produced by e.g. c-myb,
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                       DNA in non-essential region for prodn. of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human c-myb hammerhead ribozyme target sequence (nt. position 52).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enzymatic nucleic acid; hammerhead; ribozyme; cleavage; human;
smooth muscle cell; hyperproliferation; restenosis; cancer; c-myb;
                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                               0.8%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 9.6e+02; ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stinchcomb DT, Draper K, Mcswiggen J, Jarvis T;
                                                                                                                                                                                                                                                                                                            Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                       Recombinant poxvirus contg. Plasmodium useful in vaccines against malaria and
                                                                                                                                                               Example 44; Page 107; 183pp; English.
                                                                                Tine JA;
                                                                                                                                                                                                                                                                                                                                                                        1096 CAGCTTCGCGGCCAG 1110
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT81052 standard; RNA; 17 BP.
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                              93US-00075783.
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95US-00373124
         94WO-US006652
                                                                                                                                                                                                                                                                                                                                                                                           17 cagcrrcgaggccag 3
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                                                                                De Taisne C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-SEP-1997 (first entry)
                                                            (VIRO-) VIROGENETICS CORP
                                                                                                                                                                                                                                                                                                                               Query Match 0.8
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coronary angioplasty; ss.
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                                                                                                    WPI; 1995-036113/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-MAY-1995;
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          10-JUN-1994;
                              11-JUN-1993;
                                        39-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo варіепв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09531541-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-NOV-1995.
                                                                               Paoletti E,
                                                                                                                                             fmmunogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT81052;
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                                                                                                                      The present sequence represents the preferred target sequence for an enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves the human c-myb sequence at the base position indicated in the descriptor line. The c-myb sequence was screened for optimal ribozyme target sites using a computer folding algorithm, and regions of the mRNA which did not form secondary folding structures and contained potential ribozyme activities optimised by either varying the length of the binding arms or by modification to prevent degradation by nucleases. The ribozymes cleave the c-myb sequence and can be used to prevent smooth muscle cell hyperproliferation in restenosis, especially after coronary angioplasty,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This primer is an example of a "bumper" primer, for the gag gene of HIV It is used in a modified version of thermophilic strand displacement amplification (tSDA) to amplify double stranded DNA in situ.

Amplification primers (see AATR8932-3) are hybridised to both strands of the gene, and are extended. Both primers have a restriction endonuclease (RED recognition site, and the products will also contain these sites. The products are displaced from the target sequence, by extension of the bumper primers, which anneal upstream of the amplification primers, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detection of nucleic acids in cells - by in situ amplification of target sequences by thermophilic strand displacement amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIV; gag; HLA-DQ-alpha; human acute myelogenous leukaemia; AML; PCR;
primer; thermophilic strand displacement amplification; tSDA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.8%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 9.6e+02; tive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17 BP; 1 A; 9 C; 1 G; 0 T; 6 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bumper primer 2 for the gag gene of HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 16; 37pp; English.
for treating restenosis or cancer.
                                                              Claim 1; Page 64; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT88942 standard; DNA; 17 BP
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95US-00531749.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 864 AAGAGGAAGAGGAGG 878
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made double stranded by synthesising complementary strands. Making the products double stranded causes "nicks" to be created (via the RE recognition sites). Furthur extension occurs from the nicks, thereby displacing a copy of the target sequence from the double stranded amplification primer extension products. The nicking, extending and displacing steps are repeated, and the target sequence amplified in situ. The method can be used for the amplification of DNA in situ in cells in suspension, on slides or in tissues, with speed, sensitivity and specificity. In situ tSDA also remains compatible with immunochemical techniques in spite of the increased reaction temperature so both amplification of DNA and immunological staining (see AAT88934 for an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (VEGF). A patient (preferably human) having a condition associated with the level of the fms-like tyrosine kinase 1 (ILL-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase 1 (Ilk-1) (e.g. tumour angiogenesis, coular diseases, psoriasis and rheumatoid arthritis) can be tracted by administering the nucleic acid molecule or the expression vector to the patient. AAX67275 to AAX75752 represent specific examples
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1; MSD; hammerhead ribozyme; hairpin ribozyme; cleavage; tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease; fms-like tyrosine kinase 1; kinase insert domain containing receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                          amplification of DNA and immunological staining (see AAT88934 for a example of a detector probe) can be performed on the same specimen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17 BP; 3 A; 5 C; 3 G; 6 T; 0 U; 0 Other;
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96US-00584040.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX70026 standard, RNA; 17
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11-JAN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                               Vascular endothelial growth factor receptor; VBGF receptor; flt-1; flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage; tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease; fms-like tyrosine kinase 1; kinase insert domain containing receptor; foetal liver kinase 1; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient.
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                                                                 0.8%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 9.6e+02; tive 0; Mismatches 1; Indels
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of nucleic acid molecules from the present invention
                                Seguence 17 BP; 2 A; 4 C; 1 G; 0 T; 10 U; 0 Other;
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                                                                                                                                                                                                                                                             AAX70027 standard; RNA; 17 BP.
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96US-00584040.
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                                                                                   Local Similarity
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RESULT 1416

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Sequences AAV62507 to AAV62566 represent species specific PCR primers for various fungal isolates used for fungal detection in the course of the invention. The primers are designed based on the internal transcribed spacer (ITS) sequences of the various fungal species. The invention provides a DNA molecule isolated from the ribosomal RNA gene region of fungal pathogen, where the DNA molecule consists of an ITS sequence selected from ITS and ITS of Fusarium culmorum, Pusarium graminearum, Fusarium moniliforme, Septoria avenae or Microdochicum mivale. A method for detecting F graminearum, F. moniliforme, F. poae, F. avenaceum and M. nivale isolates is also provided which comprises isolating DNA from a plant leaf infected with at least one of the above pathogenical pathogens and amplifying parts of the ITS sequence of the pathogen(s) by PCR using specific primers from within these sequences. The pathogen(s) by are detected by visualising the amplified part of the ITS sequence
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                    Internal transcribed spacer; ITS; ribosomal RNA; Fusarium avenaceum; Fusarium culmovum; Fusarium graminaerum; Fusarium moniliforme; plant; Septoria avenae; Microdochicum nivale; Fusarium poae; fungal pathogen; PCR; nucleic acid detection; PCR primer; 88.
                  spacer; ITS; ribosomal RNA; Fusarium avenaceum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA isolated from fungal RNA, and its internal transcribed spacer sequence - used for detecting fungal pathogens in plant tissue.
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nes 14; Conservative
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                                                                                                                                                  Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (VEGF). A patient (preferably human) having a condition associated with the level of the fims-like tyrosine kinase 1 (flt-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase i (flk-1) (e.g. tumour angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be treated by administering the nucleic acid molecule or the expression vector to the patient. AAX67275 to AAX75752 represent specific examples
                                                                                                                                                                                                                                                                                                  Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
                                                                                                                                                                                                                                                                                                                       KDR; hammerhead ribozyme; hairpin ribozyme; cleavage; tumour anglogenesis; psoriasis; rheumatoid arthritis; ocular disease; fems-like tyrosine kinase 1; kinase insert domain containing receptor; foetal liver kinase 1; se
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                                                                                                                                                                                                                                             Human flt1 VEGF receptor hammerhead ribozyme substrate #1323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.8%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 9.6a+02; ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tor to the patient. AAX67275 to AAX75752 represent nucleic acid molecules from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17 BP; 2 A; 4 C; 1 G; 0 T; 10 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escopedo J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stinchcomb D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 86; 218pp; English
                                                                                              AAX70028 standard; RNA; 17 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95US-0005974P.
96US-00584040.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 AGGAAAAAAAAGG 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (RIBO-) RIBOZYME PHARM INC. (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 AGGAAAAAAAAGAGC 1
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                                                                                                                                                                                              28-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 93.33
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pavco P, Mcswiggen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-259017/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-OCT-1995;
11-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ното варіеня
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9715662-A2
                                                                                                                                             AAX70028;
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Septoria tritici species specific primer JB446.

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AAX30261/
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                                                                                                                                                                                                                                                                                                                                                         The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl cleaving activity, which specifically cleave RNA encoded by an aryl cleaving activity, which specifically cleave RNA encoded by an aryl collegion and integrin subunit beta 3 gene, an integrin subunit beta 3 gene, an integrin subunit beta 3 corresponding target sequences for Tie-2 gene AAA1565 to AAA19156 and AAA1185 and AAA11958 represent their corresponding target sequences for Tie-2, and AAA19187 to AAA1922 represent their corresponding target sequences; AAA1922 to AAA1922 represent their corresponding target sequences; AAA1922 to AAA2168 represent their corresponding target sequences; AAA1168 to AAA2168 to AAA2168 represent their corresponding target sequences; AAA2168 to AAA2168 represent their corresponding target sequences; AAA2168 to AAA2168 are present their corresponding target sequences; AAA2168 to AAA2168; and AAA2163 and AAA2163 to AAA23343 to for integrin subunit beta 3, and AAA23476 to AAA23343; to stability of an mRNA encodulating the synthesis, expression and/or stability of an mRNA encodulating the synthesis, expression and/or cespecially used to treat cancer, diabetic retinopathy, age related macular degeneration (ARM), inflammation, and arthritis, as well as corresponding of tuberous scleoneration, psoriasis, verruca vulgaris, and other syndrome, Kippel-Trenaunay-Weber spot-wine stains, Sturge Weber cynthesis, and other syndrome stains, there are all diseases related to the levels of ARNI, Tie-2, and other syndromes and diseases related to the levels of ARNI, Tie-2, and other syndromes and diseases related to the levels of ARNI, Tie-2, and other syndromes and diseases related to the levels of ARNI, Tie-2, and other syndromes are lated to the levels of ARNI, Tie-2, and other syndromes are lated to the levels of ARNI, Tie-2, and other syndromes are lated to the levels of ARNI, Tie-2, and other syndromes are lated.
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                                                                                                                                                                                                                                                                                     Novel ribozymes for modulating the synthesis, expression and/or stability
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, aryl hydrocarbon nuclear transport; ARNT, TIE-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
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                                                                                                                                                                                                                        Coeshott C, Mcswiggen JA;
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Pred. No. 9.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Integrin subunit beta 3 substrate sequence SEQ ID NO:6314.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      integrin subunit alpha-6, or integrin subunit beta-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17 BP; 1 A; 3 C; 3 G; 0 T; 10 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                      of an mRNA encoding an angiogenic factors.
                                                                                                                                                                                                                                                                                                                                   Claim 54; Page 261; 305pp; English.
                                                                                                                                                                                                                          Jarvis T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8;
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                                                                                                                           99WO-US006507.
                                                                                                                                                           98US-0079678P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 UUUCUCUUCUGGAGU 15
                                                                                                                                                                                        (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA23088 standard, RNA, 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                        Pavco PA, Roberts E,
                                                                                                                                                                                                                                                      WPI; 1999-591315/50.
                                 Homo sapiens.
                                                                                                                                                           27-MAR-1998;
                                                             WO9950403-A2
                                                                                                                           24-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUN-2000
                                                                                          07-OCT-1999
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The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl cleaving activity, which specifically cleave RNA encoded by an aryl cleaving activity, which specifically cleave RNA encoded by an aryl cleaving activity, which specifically cleave RNA encoded by an aryl gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to AAA17165 to AAA1765 and AAA1885 and AAA19087 to Corresponding target sequences; and AAA19155 to AAA1915 to AAA1915 to AAA1768 to AAA1915 to AAA1915 to AAA1915 to AAA1915 to AAA1915 to AAA2165 and AAA1915 to AAA2165 and AAA2165 and AAA2165 and AAA2165 and AAA2165 to AAA2165 and AAA2165 to AAA2165 and AAA2169 to AAA2168 represent their corresponding target sequences; AAA21689 to AAA2165 and AAA2167 to AAA21689 to AAA21689 represent their corresponding target sequences for integrin subunit beta 3, and AAA2347 to AAA23343 to Corresponding target sequences for integrin subunit beta 3, integrin subunit beta 3, integrin subunit beta 3, integrin subunit beta 3, integrin subunit beta 6 integrin subunit beta 7, integrin subunit beta 8 integrin subunit beta 9 integrin subunit beta 9 integrin subunit beta 8 int
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors.
                                        dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; verruea vulgaris; angiofibroma; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coeshott C, Mcswiggen JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.8%; Score 13.4; DB 1; Length 17; [0.0%; Pred. No. 9.6e+02; ve 8; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               integrin subunit alpha-6, or integrin subunit beta-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 17 BP; 2 A; 3 C; 3 G; 0 T; 9 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 54; Page 261; 305pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jarvis T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX30261 standard; DNA; 17 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US006507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :::|:::|:|||:
2 UUUCUCUUCUGGAGU 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUN-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-591315/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9950403-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-OCT-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX30261;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                detection assay to determine the presence, absence or amount of a target analyte in a sample. The method and kit may be used to detect amplification of nucleic acid molecules in real time using fluorescence quenching for example. The assays may be used to detect the presence of nucleic acids from pathogens in samples of body fluid from patients. The kit allows a homogeneous nucleic acid amplification and real time nucleic acid probe detection assay to be carried out with minimal complexity which yields a consistent reliable fluorescent detection signal. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single nucleotide polymorphism; SNP; human; genetic disease; disease susceptibility; cardiovascular system; endocrine system; neurological system; forensic testing; paternity testing; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lelds a consistent reliable fluorescent detection signal. The sequence represents a primer used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                            HIV; gag; bumper primer; amplification primer; probe; detection; fluorescence quenching; Chlamydia trachomatis; Neisseria gonorrheae; human; placental DNA; pathogen; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a kit for conducting a fluorescence
                                                                                                                                                                                                                                                                                                                                                      New method for real-time fluorescence-detection assays useful fo
detecting nucleic acids from pathogens in samples from patients.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17 BP; 3 A; 5 C; 3 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single nucleotide polymorphism PCR primer #1575.
                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 8; 16pp; English.
                                                                                                                                                                                                                                                        (BECT ) BECTON DICKINSON & CO.
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                                                                                                                                                                                          98EP-00120832
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HIV gag bumper primer B2.
                                                                                                                                                                                                                                                                                        Vonk GP;
                                                                                                                                                                                                                                                                                                                        WPI; 1999-265943/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-1999;
                                                                                                                                                                                          03-NOV-1998;
                                                                                                                                                                                                                          04-NOV-1997;
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                                                                                                                                                          12-MAY-1999
                                                                                                                                                                                                                                                                                        Little MC,
                                                                                             Synthetic
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AAC72533/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Single nucleotide polymorphism; SNP; human; genetic disease; disease susceptibility; cardiovascular system; endocrine system; neurological system; forensic testing; paternity testing; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid selected from one of 106 genes comprising single nucleotide polymorphisms, allele-specific oligonucleotides to the genes are useful for phenotypic correlations, forensics, paternity testing, medicine and genetic analysis.
                                                                                                                                                                                                                                                                   Nucleic acid selected from one of 106 genes comprising single nucleotide polymorphisms, allele-specific oligonucleotides to the genes are useful for phenotypic correlations, forensics, paternity testing, medicine and genetic analysis.
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Sklar P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17 BP; 6 A; 6 C; 4 G; 1 T; 0 U; 0 Other;
                                                                                                                    Ireland JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single nucleotide polymorphism PCR primer #1569.
                      WHITEHEAD INST BIOMEDICAL RES. AFFYMETRIX INC.
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                                                                                                                 Cargill M, Daley GQ,
Patil N, Sklar P;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; Fig 5; 214pp; English.
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Patil N, S
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                                                                                                                                                                                                            WPI; 2000-611722/58
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les 14; Conserv
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                                                                                                              Altshuler D,
Lipshutz RJ,
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                         (WHED )
(AFFY-)
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Matches
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Gaps

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0.8%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 9.6e+02; ive 0; Mismatches 1; Indels

Conservative

Local Similarity

Query Match

14;

Matches

Sequence 17 BP; 6 A; 6 C; 4 G; 1 T; 0 U; 0 Other;

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(WHED ) WHITEHEAD INST BIOMEDICAL RES. (AFFY-) AFFYMETRIX INC.
     Claim 8; Fig 5; 214pp; English
                                                                                                                                                                                                                                                                                                                         Claim 8; Fig 5; 214pp; English.
                                                                                                  1461 GTGTGGCTGCTGCT 1475
                                                                                                                                                                                                                                 30-MAR-2000; 2000WO-US008440.
                                                                                                                                     AAC72521 standard; DNA; 17
                                                                                                                                                          (first entry)
                                                                                 Local Similarity 93.3
1es 14; Conservative
                                                                                                           16 Grérééécrécrecr
                                                                                                                                                                                                                                                                     Cargill M,
Patil N, S
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                                                                                                                                                                                                                                                                                                               genetic analysis.
                                                                                                                                                                                                             WO200058519-A2.
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Lipshutz RJ,
                                                                                                                                                                                                    Homo sapiens
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                                                                             Query Match
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Matches
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invention. It was used to normalise the CDNA sequences in a sample for study, which then enabled the PCR amplification of 'rare' sequences i.e. those which are not found most often in the sample. This is useful in procedures such as gene identification, particularly those genes itenscribed at low levels, therapeutic protein identification, to variations within the human genome such as single nucleotide polymorphisms, identification of differences between normal and diseased tissue and analysis of differential gene expression between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is an adaptor sequence used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identification of novel nucleic acid sequences used to identify variations within the human genome including in diseased tissues
                                                                                                                                                                                                                                                                                                                                                                                                                              DNA synthesis; nucleic acid identification; primer; adaptor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.8%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 9.6e+02; vismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17 BP; 4 A; 8 C; 2 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Predki P,
                                                                                                                                                                                                                                                                                                                                                                                       DNA synthesis adaptor sequence NR17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 18; 45pp; English.
                                                                                                                                                                                                                                            BB
                                                                              1461 GTGTGGCTGCTGCT 1475
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14; Conservative
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                                                                                                                                                                                                                                            AAA70335 standard; DNA; 17
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13-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                           AAA70335;
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AC AAF81
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The present invention is concerned with a number of human single nuclectide polymorphisms (SNPs) which the inventors identified in human genes. These SNPs can be used in disease diagnosis and prediction of an individual's susceptibility to disease, in forensic and paternity testing and in genetic mapping. In particular, the SNPs of the invention can be used to diagnose susceptibility to diseases of the cardiovascular, endocrine and neurological systems, such as coronary artery disease, echizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Single nucleotide polymorphism; SNP; human; genetic disease; disease susceptibility; cardiovascular system; endocrine system; neurological system; forensic testing; paternity testing; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleotide polymorphisms (SNPs) which the inventors identified in human genes. These SNPs can be used in disease diagnosts and prediction of an individual's susceptibility to disease, in forensic and paternity testing and in genetic mapping. In particular, the SNPs of the invention can be used to diagnose susceptibility to diseases of the cardiovascular, endocrine and neurological systems, such as coronary artery disease, echizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
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                                                                                                                                                                                                                                                                                                                                         Gaps
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Sklar P;
                                                                                                                                                                                                                                                                                        0.8%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 9.6e+02;
                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                          Sequence 17 BP; 6 A; 6 C; 4 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single nucleotide polymorphism PCR primer #1567.
                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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Shimkets RA;

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Gaps

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diseases

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The present invention describes a recombinant vaccinia or avipox virus (RV1) containing DNA coding for Plasmodium falciparum (Pf) merozoite surface antigen 1 (MSA1) or its subfragment, operably linked to a promoter for controlling expression of the DNA. The subfragment of Pf (1) consists of an N-terminal 83 kDa fragment or the N-terminal 83 kDa fragment of Pf MSA1. Also described are: (1) a recombinant vaccinia or aripox virus (RV2) containing a DNA coding for a subfragment of Plasmodium MSA1 of the Uganda Palo-Alto isolate of Pf, operably linked to promoter for controlling expression of DNA, the subfragment of Plasmodium MSA1 of the Uganda Palo-Alto isolate of Pf, operably linked to promoter for controlling expression of DNA, the subfragment of plasmodium MSA1 of the Uganda Palo-Alto isolate of cacids 1-752 and 1333-1726 of Plasmodium MSA1; (2) an immunological composition for inducing an immunological response in a composition for inducing an immunological response incertie; and (3) producing Plasmodium MSA1 or its subfragment invention can have antimalarial activity, and can be used in vaccine production. RV1 or RV2 is useful for inducing an immunological response in a host eaginst Plasmodium infections such as malaria. The present sequence represents a PCR primer for the MSA1 N-terminal, which is used in an example from the present for the combinants of N-terminal fragments of MSA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful for inducing immunological response in host against Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel recombinant vaccinia or avipox virus containing DNA encoding
Plasmodium falciparum merozoite surface antigen 1 or its subfragment,
                                                                  Vaccinia virus; merozoite surface antigen 1; MSA1; plasmodium; recombinant poxvirus; vaccine; immunological response; mutagenesis; antimalarial; malaria; PCR primer; ss.
                                        MSA1 N-terminal fragment PCR primer C008 SEQ ID NO:16.
                                                                                                                                                                                                                                                                                                                                                                                                                  (INMR ) PASTEUR MERIEUX SERUMS & VACCINS SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chang S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 5; Col 11; 15pp; English.
                                                                                                                                                                                                                                                                                                             98US-00083366.
                                                                                                                                                                                                                                                                                                                                                                         94US-00178476.
                                                                                                                                                                                                                                                                                                                                                      91US-00724109
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYHA-) UNIV HAWAII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-280989/29.
                                                                                                                                                               Vaccinia virus
                                                                                                                                                                                                                             US6214353-B1
                                                                                                                                                                                                                                                                                                             21-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                      01-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                         07-JAN-1994;
15-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Paoletti E,
                                                                                                                                                                                                                                                                      10-APR-2001
                                                                                                                                                                                    Synthetic.
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Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Gaps ô 0.8%; Score 13.4; DB 1; Length 17; 33.3%; Pred. No. 9.6e+02; ve. 0; Mismatches 1; Indels 93.3%; Local Similarity 93.3 les 14, Conservative Query Match **datches** 

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ABK03736 standard; RNA; 17 BP 12-MAR-2002 (first entry) ABK03736; ABK03736
ID ABK0
XX
AC ABK0
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DT 12-M

RESULT 1426

Human CD20 Amberzyme #85.

cerebroprotective; nootropic; neuroprotective; antiparkingonian; muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; Parkinson's disease; huntington's disease; taxia; Huntington's disease; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease. Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;

Homo sapiens

Synthetic.

WO200159103-A2

16-AUG-2001.

09-FEB-2001; 2001WO-US004273

Siddigui WA;

Hui G,

11-FEB-2000; 2000US-0181797P. 28-FEB-2000; 2000US-0185516P. 06-MAR-2000; 2000US-0187128P.

RIBOZYME PHARM INC. BLATT L. MCSWIGGEN J. RIBO-) BLAT/)

MCSW/)

CHOWRIRA B M. CHOM/) Chowrira BM; Blatt L, Mcswiggen J,

WPI; 2001-607195/69.

Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 game or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury.

Claim 30; Page 168; 200pp; English.

expression of a cucleic acid molecule which down regulates expression of a nucleic acid molecule which down regulates expression of a nucleic acids molecule which down regulates expression of a nucleic acids (e.g. a ribozyme or a nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a nucleic acids may be enzymatic nucleic acid cleaving a an RNA molecule possessing an NCH motif), a G-cleaving RNA with a NYN motif) propessessing an NCH motif), a G-cleaving RNA with a NYN motif) propessessing an NCH motif), a G-cleaving RNA with a NYN motif) propessessing an NCH motif). The CD2-targetting nucleic acid is used to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg-2+.

C of CD20 in the presence of a divalent cation that is preferably Mg-2+.

C but any be contacted with a cell to reduce CD20 activity of the cation appears the use of one or more the call and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more the call and treatmaia, HV (human immunodeficiency virus) associated NHL, lymphoma, HV (human immunodeficiency virus) associated NHL, lymphoma, immune thrombocytopaenia, and inflammatory arthropathy. The NOGO cat argetting nucleic acid is used to cleave RNA of the NOGO gene in the immunodeficiency arthropathy. The NOGO cat a divalent cation that is preferably Mg-2+. Furthermore, the contacted with a cell to reduce NOGO activity of the nucleic acid may be contacted with a cell to reduce NOGO activity of the nucleic acid may be contacted with a cell to reduce NOGO activity of the nucleic acid may be contacted with a cell to reduce NOGO activity of the nucleic acid may be contacted with a cell to reduce NOGO activity of the nucleic acid may further comprise the use of one or more contacted with a cell to reduce NOGO activity of the nucleic acid may be contacted with a cell to reduce NOGO activity of the nucle nucleic acid may be contacted with a cell to reduce NOGO activity of the nucle nucleic acid may therapies. In particular, the NOGO-targetting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy.induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob The invention relates to a nucleic acid molecule which down regulates

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NOGO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNAzyme) an Inozyme (an endolyptic nucleic acid cleaving a an RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr
                                                                                                                                                                                                                                                                                                        Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; nootropic; neuroprotective; antiparkinsonian; muscular; D20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNAzyme; incyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia; inflammatory arthropathy; central nervous system injury; cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis; chemotherapy:induced neuropathy; amyotrophic lateral sclerosis; ALS; Parkinson's disease; ataxia; Huntingcon's disease; Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury.
           states which respond to the modulation of NOGO expression. The present sequence is an amberzyme molecule of the invention
                                                                                                 Gaps
muscular dystrophy, and/or other neurodegenerative disease
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                                                                      Score 13.4; DB 1; Length 17;
Pred. No. 9.6e+02;
3; Mismatches 1; Indels
                                               Sequence 17 BP; 4 A; 1 C; 8 G; 0 T; 4 U; 0 Other;
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                                                                                                                      1009 GAAGATGTGGTTGGG 1023
                                                                                                                                                                                                           ABK02365 standard; RNA; 17 BP
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28-FEB-2000; 2000US-0185516P.
06-MAR-2000; 2000US-0187128P.
                                                                        0.8%;
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                                                                                 73.3%;
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1 GAAGAAGUGGUUGGG 15
                                                          Guery Match
Best Local Similarity 73.3%,
Best Local 11, Conservative
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                                                                                                                                                                                                                                                           12-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                   Human NOGO Amberzyme #37.
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MCSWIGGEN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-607195/69.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                    ABK02365;
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                                                                                                                                                                                     RESULT 1427
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an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA cc confoct of the presence of a divalent cation that is preferably MG<sup>2</sup>+.

Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CC of CD20. The treatment may further comprise the use of one or more cherapies. In particular, the CD20 targetting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular noncervative lymphoma (MCL), immunocytoma [IMC], small B-cell lymphocytic lymphomy, concervative lymphoma, manunocytoma [IMC], small B-cell lymphocytic lymphoma, concervative lymphocytic lymphoma, manunocytoma inflammatory arthropathy. The NOGO-c targetting nucleic acid is used to cleave RNA of the NOGO gene in the presence of a divalent cation that is preferably MG<sup>2</sup>+. Furthermore, the cargetting nucleic acid may be contacted with a cell to reduce NOGO activity of the conclain and treat a patient having a condition associated with the level of NOGO. The treatment may further comprise the use of one or more cell and treat a patient having a condition associated with the level of the NOGO. The treatment may further comprise the use of one or more cell and treat a patient aving a condition associated with the level of creat central nervous system (CNS) injury and cerebrovascular accident (CNA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (MS), parkinson's disease, muscular dystrophy, and/or other neurodegenerative disease contacted to the nodulation of NOGO expression. The present contacted to the nodulation of NOGO expression. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence is an amberzyme molecule of the invention
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27-MAR-2000; 2000US-0192179P.
01-JUN-2000; 2000US-0208538P.
30-OCT-2000; 2000US-024989P.
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ABA80561
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The present invention provides single-stranded oligonuclectides which can be used for the targeted alteration of genomic sequences, where the oligonuclectide has at least one mismatch compared with the genomic sequence to be altered. In particular, these sequences are directed at the following genes: adenosine deaminase, p53, beta-globin, retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A (CDKNZA), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6, apolipoprotein E (APOB), LDL receptor (LDLR), UDP-glucuronosyltransferase (UGTI), amyloid precursor protein (APC), presentiln-1 (PSENI) and presentiln-2 (PSENI2). These can be used in the gene therapy of diseases such as cancer, adenosine deaminase deficiency, cystic fibrosis, haemoghila, hypercholseterolaemia, thalassaemia, sickle cell anaemia, chalmier's disease, melanoma, adenomatous polyposis of the colon and various syndromes. The present sequence is one of the gene correcting coligonuclectides of the invention
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                                                                         Oligonucleotide for targeted alterations of genetic sequences and for treating cystic fibrosis, comprises at least one mismatch and chemical modification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
                                                                                                                                                           Claim 7; Page 231; 294pp; English
Rice MC
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ABA80560 standard; DNA; 17 BP
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2000US-0192179P.
2000US-0208538P.
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Gamper HB,
                                     WPI; 2001-639230/73.
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Kmiec EB,
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The present invention provides single-stranded oligonucleotides which can be used for the targeted alteration of genomic sequences, where the oligonucleotide has at least one mismatch compared with the genomic sequence to be altered. In particular, these sequences are directed at the following genes: adenosine deaminase, p53, beta-globin, retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A (CDKN2A), APC, Factor VIII, Factor IX, haemoglobin alpha locus (CDKN2A), APC, Factor VIII, Factor IX, haemoglobin alpha locus (CDKN2A), APC, haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6, apolipoprotein B (APOB), LDL receptor (LDLR), UDP-glucuronosyltransferase (UGT1), amyloid precursor protein (APC), presenilin. 1 (PSEN1) and presenilin-2 (PSEN2). These can be used in the gene therapy of diseases such as cancer, adenosine deaminase deficiency, cystic fibrosis, hypercholesterolaemia, thalassaemia, sickle cell anaemia, hampinia, hypercholesterolaemia, thalassaemia, sickle cell anaemia, various syndromes. The present sequence is one of the gene correcting oligonucleotides of the invention
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                                                                                     Oligonucleotide for targeted alterations of genetic sequences and for treating cystic fibrosis, comprises at least one mismatch and chemical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 0.8%; Score 13.4; DB 1; Length 17; Local Similarity 93.3%; Pred. No. 9.6e+02; nes 14; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                               Claim 7; Page 231; 294pp; English.
                 Rice MC;
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                 Gamper HB,
                                                    WPI; $2001-639230/73
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                                                                                                                          modification.
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The sequence represents a downstream PCR primer used in a DDRT-PCR experiment (and in cDNA synthesis), demonstrating the method of the invention. The method relates to evaluating a cellular response to an environmental compound, comprising determining or comparing the environmental compound, comprising determining or comparing the environmental compound, comprising determining or comparing the environmental compounds that act on the level of endogenous gene adapted to identify compounds that act on the level of endogenous gene expression through activating nuclear receptors. The method is useful in toxicological analysis, diagnostics, for diagnosing cancer (e.g. cryptorchism and/or allergy, and endometrium), asthma, hypospadia, cryptorchism and/or allergy, and for evaluating the efficiency of a treatment for hormonal deficiency or hormonal replacement therapy, in a treatment for hormonal deficiency or hormonal replacement therapy, in cryptorchism and/or allergy, and for evaluating the efficiency of a treatment such as a post-menopausal female. The method is also useful for identifying environmental chemicals or pharmaccutical compositions that capitally using a sensitive technique, and for detecting chemicals that pose a rapidly using a sensitive technique, and the expression of any gene can be monitored. The assays are far more informative than the currently used assays, and significantly reduces the number of animals required for the company of the c
  toxicological analysis, involves determining or comparing the expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shigella; Salmonella; differentiation; determination; primer; probe; detection; microorganism; bacterium; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.8%; Score 13.4; DB 1; 93.3%; Pred. No. 9.6e+02;
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                       levels of at least one endogenous gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 group will respond to the compound
                                                                           Example 3; Page 27; 77pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAI71138 standard; DNA; 17 BP.
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es 14; Conservative
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The present invention describes a method for differentiating bacteria by

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using primers or probes having different base sequences. The method can be used for the differentiation or detection of Shigella flexneri, Shigella boydii, Shigella connei or Salmonella typhi, Salmonella parathyphia, Salmonella typhimurium, Salmonella chester, Salmonella enterfitdis, and Salmonella cranienburg spp. bacteria. The method can be used for rapid differentiation of 9 lines of bacteria for prevention, diagnosis and treatment of diseases caused by these bacteria. The present sequence represents a detection probe which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.
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                                                                                                                                                                                       0.8%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 9.6e+02; tive 0; Mismatches 1; Indels
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                                                                                                                                                            Sequence 17 BP; 3 A; 6 C; 0 G; 8 T; 0 U; 0 Other;
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nucleic acids can be used as probes to detect, characterise and quantify nucleic acids can be used as probes to detect, characterise and quantify to browner; nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 crowled initial substrates for the recombinant engineering of hGDMLP-1 capture improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption insistion, as therefore an acid in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The concentration and skeletal muscle disorders. hGDMLP-1 may be used for diagnosing a clisorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.

The present sequence in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO car fitp.wipo.int/pub/published_pct_sequence
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muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
skeletal muscle disorder; amplicon; screening; ss.
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2000US-0236359P
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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids can be used as probes to detect, characterises and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to hGDMLP-1 nucleic acids in samples, as amplification substrates, to hGDMLP-1 proteins as immunosens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specific biomolecule and/or amount specifically of hGDMLP proteins, as specific biomolecule and/or amount specifically of hGDMLP proteins, as specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The polymucleotide sequences encoding hGDMLP-1 may be used for dagnosing a disorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders, hGDMLP-1 is localised to chromosome 22.

The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO
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                                                       New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
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                                                                                                                                       Disclosure; SEQ ID NO 10503; 214pp; English.
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27-SEP-2000; 2000US-023539P.
07-SCT-2000; 2000US-003539P.
30-JAN-2001; 2001WO-US000661.
30-JAN-2001; 2001WO-US000663.
30-JAN-2001; 2001WO-US000663.
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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynuclectide sequences of hGDMLP-1 (can be used in gene therapy and vaccine production. The hGDMLP-1 cucleic acids can be used as probes to detect, characterise and quantify chicked acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ioniation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The polymuclectide sequences encoding hGDMLP-1 and statement sequence expression of hGDMLP-1, in particular heart of showing-1 sequence represents an oligomer used in the screening of the hGDMLP-1 sequence exemplification of the present invention. N.B. The sequence data for this parent did not form part of the printed and the exemplification of the present invention.
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                    30-JAN-2001; 2001WO-US000666.
30-JAN-2001; 2001WO-US00667.
30-JAN-2001; 2001WO-US000668.
30-JAN-2001; 2001WO-US000669.
30-JAN-2001; 2001WG-US000670.
05-FEB-2001; 2001US-0266860P.
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                                    Match 0.8%; Score 13.4; DB 1; Length 17; Local Similarity 93.3%; Pred. No. 9.6e+02; es 14; Conservative 0; Mismatches 1; Indels
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1 GCCCCGTGCTCCCAG 15

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ABN07888 standard; DNA; 17
                   29-MAY-2002 (first entry)
             ABN07888;
RESULT 1435
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Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7880.

Human, genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.

ABN10289 standard; DNA; 17 BP

RESULT 1436

29-MAY-2002 (first entry)

ABN10289;

ABN10289/o ID ABN1 XX AC ABN1 XX DT 29-M

Homo sapiens

WO200192524-A2

06-DEC-2001

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The present invention describes a human genome-derived myosin-like protein 1 (hdDMLP-1). The protein and polynucleotide sequences of hdDMLP-1 can be used in gene therapy and vaccine production. The hdDMLP-1 nucleic acids can be used as probes to detect, characterise and quantify hdDMLP-1 nucleic acids in samples, as amplification substrates to hdDMLP-1 protein tenintial substrates for the recombinant engineering of hdDMLP-1 protein variants having desired phenotypic improvements, and for capture proteins. The hdDMLP-1 proteins or polypeptides may be used as immunospes to raise antibodies that specifically recognise hdDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hdDMLP proteins as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as therefore the partial proteins or for replacement therapy. The production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production and in vaccines or for replacement therapy. The characteristic sequences encoding hdDMLP-1 may be used for diagnosing a disorder associated with the expression of hdDMLP-1, in particular hart and skeletal muscle disorders hdDMLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the screening of the hdDMLP-1 sequence data for this patent did not form part of the printed capture.
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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids in samples, as amplification substrates, to hGDMLP-1 nucleic acids in samples, as amplification substrates, to hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP-1 proteins, as specific biomolecule and/or amount specifically of hGDMLP-1 proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionication, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.

The present sequence in the exemplification of the present invention. N.B. hGDMLP-1 sequence data for this patent did not form part of the printed production in the screening of the heart section of the present invention.
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                                      Human, genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.
Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10281.
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Shannon ME;

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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polymucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 call a caids can be used as probes to detect, characterise and quantify nucleic acids in samples, as amplification substrates, to protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as specifically recognise hGDMLP-1 proteins, as specifically recognise hGDMLP-1 proteins, as specific blomclecule and to and for amount specifically of hGDMLP proteins, as specific blomclecule capture probes for surface-enhanced laser desorption ionisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production and in vaccines or for replacement therapy. The production and unsacle disorders hGDMLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed
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                                                                                                                                                                       Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
skeletal muscle disorder; amplicon; screening; 88.
                                                                                                                                   fuman GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10283.
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04-0CT-2000; 2000US-0234585P.
04-0CT-2000; 2000US-0234585P.
04-0T-2000; 2000US-0234585P.
30-JAN-2001; 2001WO-US000661.
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30-JAN-2001; 2001WO-US000666.
30-JAN-2001; 2001WO-US0006670.
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                    ABN10291 standard; DNA; 17 BP
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Query Match 0.8%; Score 13.4; DB 1; Length 17; Best Local Similarity 93.3%; Pred. No. 9.6e+02; Matches 14; Conservative 0; Mismatches 1; Indels

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specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequence
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                                                                     Sequence 17 BP; 6 A; 5 C; 2 G; 4 T; 0 U; 0 Other;
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27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000B-00024263.
30-JAN-2001; 2001WO-US000661.
30-JAN-2001; 2001WO-US000663.
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and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-therapeutic supplement in patients having specific deficiency in hGDMLP-therapeutic supplement in patients having specific deficiency in hGDMLP-therapeutic supplement in patients having specific deficiency in hGDMLP-1 may be used for diagnosing a disporder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip. wipo.int/pub/published_pct_sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17 BP; 5 A; 3 C; 9 G; 0 T; 0 U; 0 Other;
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30-JAN-2001; 2001WO-US000665.
30-JAN-2001; 2001WO-US000666.
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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polymucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 calcided acids in samples, as amplification substrates, to hGDMLP-1 nucleic acids in samples, as amplification substrates, to protein variants having desired phenotypic improvements, and for protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The groundlectide sequences encoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart of and skelatal muscle disorders. hGDMLP-1 is localised to chromosome 22. The sequence represents an oligomer used in the acreening of the hGDMLP-1 for the present invention. N.B. The sequence data for this patent did not form part of the printed for this patent did not form part of the printed for the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequence
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Disclosure, SEQ ID NO 6391; 214pp; English.
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05-FEB-2001; 2001US-0266860P.
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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 mucleic acids in samples, as amplification substrates, to hGDMLP-1 nucleic acids in samples, as amplification substrates, to hGDMLP-1 nucleic acids in samples, as amplification substrates, to hGDMLP-1 protein variants having desired phenotypic improvements, and for correspond to raise antibodies that specifically recognise may be expressing the proteins. The hGDMLP-1 proteins or polypeptides may be can simmunospens to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP-proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as therapulate proteins or for replacement therapy. The production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production and in vaccines or for replacement therapy. The concentration and skeletal muscle disorders, hGDMLP-1 is localised to chromosome 22.

The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence of this patent did not form part of the printed capture data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO cat fig...
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                                                                                                                                            New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
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0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
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                                                            Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR,
                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 7881; 214pp; English
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New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
                                                                                                                              Hanzel DK, Rank DR, Chen W,
                                                                                                                                                                                                      Disclosure; SEQ ID NO 6390; 214pp; English
                                  30-JAN-2001; 2001WO-US000665.
30-JAN-2001; 2001WO-US000666.
30-JAN-2001; 2001WO-US000667.
30-JAN-2001; 2001WO-US000667.
                           30-JAN-2001; 2001WO-US000664.
                                                                        30-JAN-2001; 2001WO-US000669.
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         30-JAN-2001; 2001WO-US000663
30-JAN-2001; 2001WO-US000663
                                                                                                                               Gu Y, Ji Y, Penn SG,
                                                                                                                                                WPI; 2002-179446/23.
                                                                                                             (AEOM-) AEOMICA INC.
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Shannon ME;

The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used as probes to detect, characterise and quantify nucleic acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as specific biomolecule and/or amount specifically of hGDMLP proteins, as specific biomolecule and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as the respective supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The production and in vaccines or for replacement therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence data for this patent did not form part of the printed appearance in the exemplification of them part of the printed appearance or the present invention. N.B. The sequence data for this patent did not form part of the printed appearance in the capture of the printed appearance or the present sequence or the patence or the present did not form part of the printed appearance. Gaps ö 0.8%; Score 13.4; DB 1; Length 17; 33.3%; Pred. No. 9.6e+02; ve 0; Mismatches 1; Indels Sequence 17 BP; 3 A; 8 C; 4 G; 2 T; 0 U; 0 Other; specification, but was obtained in electron
at ftp.wipo.int/pub/published_pct_sequence l Similarity 93.3%; 14; Conservative Best Local Similarity Query Match Matches

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Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.
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                              BP.
                             ABN07884 standard; DNA; 17
                                                                                   29-MAY-2002 (first entry)
                                                        ABN07884;
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Homo sapiens

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ABN10509 standard; DNA; 17 BP.

RESULT 1443 ABN10509

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The present invention describes a human genome-derived myosin-like

protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1

can be used in gene therapy and vaccine production. The hGDMLP-1

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hGDMLP-1 nucleic acids in samples, as amplification substrates, to

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protein variants having desired phenotypic improvements, and for

concern and the proteins. The hGDMLP-1 proteins or polypeptides may be

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production askeletal muscle disorders, hGDMLP-1 is localised to chromosome 22.

The present sequence represents an oligomer used in the screening of the

CC The present sequence in the exemplification of the present invention. N.B.

CT he sequence data for this patent did not form part of the printed

can ftp.wipo.int/pub/published_pct_sequence

cat ttp.wipo.int/pub/published_pct_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rank DR,
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                                                                                                      25-MAY-2001; 2001WO-US016981
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2000US-0236359P.
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05-FEB-2001; 2001US-0266860P
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Gaps

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WPI; 2002-179446/23.
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                          Homo sapiens
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ABN10509;
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The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 claim be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP-1 proteins, as specifically of hGDMLP proteins, as specific blomolecule capture probes for surface-enhanced laser desorption ionisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The polynucleotide sequences encoding hGDMLP-1, may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
skeletal muscle disorder; amplicon; screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                   Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10020.
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Mismatches
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30-JAN-2001; 2001WO-US000665.
30-JAN-2001; 2001WO-US000666.
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05-FEB-2001; 2001US-0266860P.
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  Matches 14; Conservative
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                                                                                                                                                                                     RESULT 1444
                                                    S'''원
                                                                                                                                                                                                                                                                    The present invention describes a human genome-derived myosin-like protein 1 (hGMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used as probes to detect, characterise and quantify nucleic acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunosquas to raise antibodies that specifically recognise hGDMLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specific biomolecule and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as theorem or for replacement therapy. The production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The polymucleotide sequences encoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.

The present sequence in the exemplification of the present invention. N.B. heavened at a for this patent did not form part of the printed production.
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                                                                                                                                                 Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
skeletal muscle disorder; amplicon; screening; ss.
                                                                                                        -Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10501.
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05-FEB-2001; 2001US-0266860P
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                                                    29-MAY-2002 (first entry)
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Best Local Similarity
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Shannon ME

Chen W,

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and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.
                                                                                                                                                                                   Gaps
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Conservative 0; Mismatches 1; Indels
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                                                                                                                 Sequence 17 BP; 1 A; 4 C; 8 G; 4 T; 0 U; 0 Other;
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27-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
04-OCT-2000; 2000US-023639P.
04-OCT-2000; 2001WO-US000661.
30-JAN-2001; 2001WO-US000663.
30-JAN-2001; 2001WO-US000664.
30-JAN-2001; 2001WO-US000665.
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                                                                                                                                                              Local Similarity
les 14; Conserv
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                                                                                                                                                 Query Match
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protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP receips, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The production, and in vaccines or for replacement therapy. The polymucleotide sequences encoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders, hGDMLP-1 is localised to chromosome 22.

The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence in the screening of the hGDMLP-1 sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO te fip. wipo.int/pub/published_pct_sequence
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initial substrates for the recombinant engineering of hGDMLP-1
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30-JAN-2001; 2001WO-US000664.
30-JAN-2001; 2001WO-US000665.
30-JAN-2001; 2001WO-US000665.
30-JAN-2001; 2001WO-US000668.
310-JAN-2001; 2001WO-US000669.
23-WAY-2001; 2001US-00864761.
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Best Local Similarity
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The present invention relates to human testis expressed Patched like protein (HTPL, see ABV78759 to ABV78752 and ABS98519 to ABB98520). HTPL has two isoforms, with a few single base pair changes introduces a between the two. One of the single base pair changes introduces a premature stop codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL shares an overall structure organisation with the Patched protein. The shares an overall features strongly inply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL is important in regulating male germ cell development, and the HTPL gene was mapped to human chromosome lopp.1. HTPL and its coding sequence are therapy and manufacture of a medicament for treatment or prevention of such disorder associated with decreased expression or activity of human HTPL. Such disorders include disorders of testis, or adrenal, adult and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           foetal liver, bone marrow, brain, kidney, lung, placenta, prostate, skeletal muscle or colon function. HTPL proteins and nucleic acids are clinically useful diagnostic markers and potential therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an example from the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1; human testis expressed Patched like protain; testis; adrenal; liver; male germ cell development; bone marrow; brain; kidney; lung; placenta; prostate; skeletal muscle; colon; male infertility; cancer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.8%; Score 13.4; DB 1; Best Local Similarity 93.3%; Pred. No. 9.6e+02; Matches 14; Conservative 0; Mismatches 1
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ID ABV79403/C

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ABV79403;
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ABV79403;
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DT 03-JAN-2003 (first entry)
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Human HTPL scanning oligonucleot
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Human, gene therapy; tumour supp
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Human, gene therapy; tumour supp
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Human testis expressed Patched 1
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Homo sapiens.
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O7-AUG-2002.
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PD 07-AUG-2002.
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PD 07-AUG-2002.
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PP 30-JAN-2001; 2001W0-US000663.
PR 30-JAN-2001; 2001W0-US000664.
PR 30-JAN-2001; 2001W0-US0006664.
PR 30-JAN-2001; 2001W0-US0006669.
PR 30-JAN-2001; 2001W0-US0006669.
PR 30-JAN-2001; 2001W0-US0006669.
PR 30-JAN-2001; 2001W0-US0006669.
PR 30-JAN-2001; 2001W0-US000669.
PR 30-JAN-2001 JAN-2001W0-US000069.
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PR 30-JAN-200
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Novel isolated human testis expressed Patched like protein (HTPL), useful for identifying agonist and antagonist and specific binding partners, and for treating subjects having defects in HTPL.

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The present invention relates to human testis expressed Patched like protein (HTPL, see ABV7875 to ABV78762 and ABB9819 to ABB98520). HTPL thas two isoforms, with a few single base pair differences between the two. One of the single base pair changes introduces a premature stop codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL shares an overall structure organisation with the Patched protein. The shares an overall structure organisation with the Patched protein. The shared structural features strongly imply that HTPL plays a role similar to that of Patched, and is a potential tumour suppressor. HTPL is important in regulating male germ cell development, and the HTPL gene was mapped to human chromosome lolpl2.1. HTPL and its coding sequence are useful for diagnosing a disorder caused by mutation in HTPL, and in therapy and manufacture of a medicament for treatment or prevention of such disorders include disorders of testis, or adrenal, and the HTPL. Such disorders include disorders of testis, or adrenal, and the cotal liver, bone marrow, brain, kidney, lung, placenta, prostate, cotal liver, bone marrow, brain, kidney, lung, placenta, prostate, cotal miscally useful diagnostic markers and potenial therapeutic agents for male infertility and cancer. The present oligonucleotide was used in an example from the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.8%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 9.6e+02; ive 0; Mismatches 1; Indels
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Example 2; Page 148; 718pp; English.
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nes 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-082995/11.
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Claim 4; Page 122; 149pp; English

The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for treating conditions selected from cancer, lymphoma, Ewing's sarcoma, malanoma, conditions selected from cancer, lymphoma, Ewing's sarcoma, malanoma, tumour angiogenesis, diabetic retinopathy, macular degeneration, culgarist, angiofibroma of tuberrous sclerosis, port-whise stains, Sturge Conditions, Kippel-Trenaunay-Weber syndrome, Obler-Weber-rendu (Weber syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for treating a patient having a condition associated with the level of ERG, by contacting cells of the patient with (I) under conditions suitable for the treatment. Leukaemia or tumour angiogenesis is treated by administering (I) to the patient in conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with an evel (I) is useful for reducing ERG activity in a cell, by contacting the cell with (I) (I) is useful for cleaving RNA of ERG gene, by contacting the expression of ERG, and as diagnostic tool to examine genetic drift and mutations within diseased cells or to detect CC the presence of ERG RNA in a cell. (I) is useful for specifically ctargeting genes that share homology with ERG gene or ERG fusion genes. ARK1354-ABK22719 represent nucles which regulate expression of ERG, and and ensymmatic nucleic acide, including antisense and ensymmatic nucleic acide molecules which regulate expression of ERG, and ensymmatic nucleic acide, including antisense and ensymmatic nucleic acide, including antisense of ensymmatic nucleic acide, including antisense of ensymmetric profession of the invented of the invent related PCR primers of the invention

Sequence 17 BP; 2 A; 3 C; 9 G; 0 T; 3 U; 0 Other;

Query Match

Matches

/ Match 0.8%; Score 13.4; DB 1; Length 17; Local Similarity 93.3%; Pred. No. 9.6e+02; les 14; Conservative 0; Mismatches 1; Indels 613 CCCACTCCAGCCTCT 627 16 cccacrccaccacr 2 ઠે ద

ABK18235 standard; RNA; 17

ABK18235;

(first entry) 09-APR-2002

Human ERG hammerhead ribozyme target sequence, Seq ID No 882.

Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic; ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic; vulnerary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis; tumour angiogenesis; diabetic retinopathy; macular degeneration; neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris; angiofibroma of tuberous selerosis; port-wine stain; wound healing; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss; Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme; amberzyme. 

Homo sapiens.

WO200188124-A2.

22-NOV-2001.

16-MAY-2001; 2001WO-US015866.

16-MAY-2000; 2000US-00572021.

(RIBO-) RIBOZYME PHARM INC. (GLAX ) GLAXO GROUP LTD.

Mclaughlin F, Mcswiggen JA, Von Carlowitz I, WPI; 2002-082995/11. Jarvis T,

Novel polynucleotide which down regulates expression of Ets-related genuuseful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.

Claim 4; Page 75; 149pp; English.

The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for treating conditions selected from cancer, lymphoma, Ewing's sarcoma, metanoma, tumour angiogenesis, diabetic retinopathy, macular degeneration, tumour angiogenesis, diabetic retinopathy, macular degeneration, cumour angiogenesis, diabetic retinopathy, macular degeneration, verruca vulgaris, angiofibroma of tubberous sclerosis, port wine stains, Sturge vulgaris, angiofibroma of tubberous sclerosis, port wine stains, Sturge Weber syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for treating a patient having a condition associated with the level of ERG, by contacting cells of the patient with (I) under conditions suitable for the treatment. Leukaemia or tumour angiogenesis is treated by administering (I) to the patient in angiogenesis is treated by administering (I) to the patient in conjunction with one or more of other therapies such as radiation or chemotherapy treatment. (I) is useful for reducing ERG activity in a cell, by contacting the cell with (I). (I) is useful for cleaving RNA of ERG gene, by contacting (I) with RNA, in the presence of advalent cation such as Mg2+. (I) is useful for diagnosis of conditions and diseases related to the expression of ERG, and as diagnostic tool to examine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically targeting genes that share homology with ERG gene or ERG fusion genes. ARX.7354-ABKZ2719 represent nucleic acide, including antisense and enzymetic nucleic acide, including antisense and enzymetic nucleic acide molecules which regulate expression of ERG, and related PCR primers of the invention 

Sequence 17 BP; 2 A; 9 C; 3 G; 0 T; 3 U; 0 Other;

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Gaps

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ö 0.8%; Score 13.4; DB 1; Length 17; 80.0%; Pred. No. 9.6e+02; tive 2; Mismatches 1; Indels Local Similarity 80.0 les 12; Conservative Query Match Matches

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Gaps

699 2 CCAGCCCUCCCCGUG 16 655 CCAGCCTTCCCCGTG g ઠ

RESULT 1450

ABK17536 standard; RNA; 17 BP ABK17536; 

(first entry) 09-APR-2002

Human ERG hammerhead ribozyme target sequence, Seq ID Nó 183.

Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic; ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic; vulnerary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis; tumour angiogenesis; diabetic retinopathy; macular degeneration; neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris; angiofibroma of tuberous sclerosis; port-wine stain; wound healing; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss; Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme; amberzyme.

Homo sapiens

WO200188124-A2.

22-NOV-2001

Randi AM;

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The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for treating conditions selected from cancer, lymphoma, Ewing's sacroma, melanoma, tumour angiogenesis, diabetic retinopathy, macular degeneration, thousand all abetic retinopathy, macular degeneration, neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca vulgaris, angiofibroma of tubbarous sclerosis, port-wine stains, Sturge Weber syndrome, Rippel-Trenaunay-Weber syndrome, Osler-Weber-rendu Syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for treating a patient having a condition associated with the level of ERG, by contacting cells of the patient with (I) under conditions suitable for the treatment. Leukaemia or tumour angiogenesis is treated by administering (I) to the patient in conjunction with one or more of other therapies such as radiation or chemotherapy treatment. (I) is useful for reducing ERG activity in a cell, by contacting (I) with RNA, in the presence of a divalent cation such as Mg2+. (I) is useful for diagnosis of conditions and diseases related to the expression of ERG, and as diagnostic tool to examine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically the presence of ERG RNA in a cell. (I) is useful for specifically cargeting genes that share homology with ERG gene or ERG fusion genes. ABK17354-ABK22719 represent nucleic acids, including antisense and enzymmatic nucleic acid molecules which regulate expression of ERG, and enzymmatic nucleic acid molecules which regulate expression of ERG, and enzymmatic nucleic acid molecules acids, including antisense and enzymentic nucleic acid molecules acids, including antisense and enzymmatic nucleic acid molecules acids, including antisense and enzymmatic nucleic acid molecules acids, including antisense and enzymmatic nucleic acid which regulate expression of ERG, and enzymmatic nucleic acids under a cide and 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 62; 149pp; English.
   16-MAY-2001; 2001WO-US015866.
                                                             16-MAY-2000; 2000US-00572021
                                                                                                                                                                                                                Jarvis T, Von Carlowitz I,
                                                                                                                      (RIBO-) RIBOZYME PHARM INC (GLAX ) GLAXO GROUP LTD.
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Gaps ö Query Match 0.8%; Score 13.4; DB 1; Length 17; Best Local Similarity 80.0%; Pred. No. 9.6e+02; Matches 12; Conservative 2; Mismatches 1; Indels Sequence 17 BP; 2 A; 10 C; 3 G; 0 T; 2 U; 0 Other; 655 CCAGCCTTCCCCGTG 669

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1 CCAGCCCUCCCCGUG 15

ABK19388 standard; RNA; 17 BP 09-APR-2002 (first entry) ABK19388; 

Human ERG Amberzyme target sequence Seq ID No 2035.

Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic; ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic; vulnerary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis; tumour angiogenesis; diabetic retinopathy; macular degeneration; neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris; angiofibroma of tuberous sclerosis; port-wine stain; wound healing; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss; Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme; amberzyme

conditions selected from caneer, lymphone, Ewing's sarcome, melanoma, the conditions selected from caneer, lymphone, Ewing's sarcome, melanoma, theorems and conditions selected from caneer, lymphone, Ewing's sarcome, melanoma, theorems selected from caneer, lymphone, conditions selected from caneer, lymphone, contended the stains of the selected where syndrome, Osler-Weber-rendu syndrome, leukemaia, osteoporosis and wound healing. (I) is useful for treating a patient having a condition associated with the level of ERG, by contacting cells of the patient with (I) under conditions suitable for the treatment. The method comprises the use of one or more therapies under conditions suitable for the treatment. Leukemia or tumour angiogenesis is treated by administering (I) to the patient in a conjunction with one or more of other therapies such as radiation or compunction with one or more of other therapies such as radiation or compunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjuncting the cell with (I). (I) is useful for cleaving RNA of ERG gene, by contacting (I) with RNA, in the presence of advalent coll with (I). (I) is useful for specifically diseases related to the expression of ERG, and as diagnostic coll to examine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically the presence of ERG RNA in a cell. (I) is useful for specifically examine genetic drift and mutations within diseased cells or conditions and cargeting genes that share homology with ERG gene or ERG fusion genes. ARK1334-ABK22719 represent nucleic acide molecules which regulate expression of ERG, and carginate of the invention Novel polynucleotide which down regulates expression of Ets-related gene, useful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome. The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for treating Gaps Von Carlowitz I, Mcswiggen JA, Mclaughlin F, Randi AM; ö Length 17; 1; Indels Seguence 17 BP; 7 A; 1 C; 9 G; 0 T; 0 U; 0 Other; Score 13.4; DB 1; Pred. No. 9.6e+02; 93.3%; Prea. .... Claim 4; Page 127; 149pp; English. 16-MAY-2001; 2001WO-US015866. 16-MAY-2000; 2000US-00572021. 861 AGGAAGAGGAAGAGG 875 2 AGGAGGAGGAAGAGG 16 (RIBO-) RIBOZYME PHARM INC. 14; Conservative (GLAX ) GLAXO GROUP LID Query Match Best Local Similarity WPI; 2002-082995/11. WO200188124-A2 Homo sapiens. 22-NOV-2001 Jarvis T, RESULT 1452 ABK19205, 8 요

Human, hammerhead ribozyme; cytostatic; antitumour; antidiabetic; ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic; Human ERG Amberzyme target sequence Seq ID No 1852. ВР 1205/c ABK19205 standard, RNA; 17 (first entry) 09-APR-2002 ABK1,9205; **4444444** 

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WO200188124-A2
       Homo sapiens.
           22-NOV-2001
                    Jarvis T,
     amberzyme.
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Gaps ö Length 17; 1; Indels Sequence 17 BP; 2 A; 2 C; 10 G; 0 T; 3 U; 0 Other; 0.8%; Score 13.4; DB 1; 93.3%; Pred. No. 9.6e+02; 0; Mismatches Local Similarity 93.3%; 14; Conservative Query Match Matches

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ABK19389 standard; RNA; 17 ABK19389 ABK19389 ID ABK1 XX AC ABK1

RESULT 1453

vulnerary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis; tumour angiogenesis; diabetic retinopathy; macular degeneration; neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris; angiofibroma of tuberous sclerosis; port-wine stain; wound healing; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss; Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme; Von Carlowitz I, Mcswiggen JA, Mclaughlin F, Randi AM; 16-MAY-2001; 2001WO-US015866. 16-MAY-2000; 2000US-00572021 (RIBO-) RIBOZYME PHARM INC. (GLAX ) GLAXO GROUP LID.

Novel polynucleotide which down regulates expression of Ets-related gen useful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome. WPI; 2002-082995/11.

Claim 4; Page 122; 149pp; English

related PCR primers of the invention

861 AGGAAGAGGAAGAGG 875 1 AGGAGGAGGAAGAGG 15 Matches ð 유

09-APR-2002 (first entry)

Human ERG Amberzyme target sequence Seq ID No 2036.

Human, hammerhead ribozyme, cytostatic; antitumour; antidiabetic; ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic; vulnerary; cancer; lymphoma; Ewing's earcoma; melanoma; psoriasis; tumour angiogenesis; diabetic retinopathy; macular degeneration; neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris; angiofibroma of tuberous sclerosis; port-wine stain; wound healing; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss; Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme; amberzyme.

Homo sapiens.

WO200188124-A2.

22-NOV-2001.

16-MAY-2001; 2001WO-US015866.

16-MAY-2000; 2000US-00572021.

(RIBO-) RIBOZYME PHARM INC.

GLAX ) GLAXO GROUP LTD

Von Carlowitz I, Mcswiggen JA, Mclaughlin F, Randi AM; Jarvis T,

WPI; 2002-082995/11.

useful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome. Novel polynucleotide which down regulates expression of Ets-related

Claim 4; Page 127; 149pp; English.

The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for treating conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma, tumour angiogenesis, diabetic retinopathy, macular degeneration, the angiogeneration, wyopic degeneration, arthritis, psoriasis, verruca vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for treating a patient having a condition associated with the level of ERG, the treatment with (I) under conditions suitable for the treatment. Leukaemia or tumour conditions with one or more of other therapies such as radiation or chemotherapy treatment. (I) is useful for reducing ERG activity in a coll, by contacting (I) the passence of adiavalent cation such as Mg2+. (I) is useful for diagnostic tool to the expression of ERG, and as diagnostic tool to the examine genetic driffe and muteutions within diseased cells or to detect the conditions and colls or to detect the conditions and colls or to detect the conditions within the colls of the colls of the colls or to detect the coll with the colls of the colls or to detect the coll with the colls of the colls or to detect the colls or to detect the colls or the colls or the colls or to detect the coll or the colls or the colls or to detect the coll or the colls or the colls or to detect the coll or the colls or the colls or to detect the coll or the the presence of ERG RNA in a cell. (I) is useful for specifically targeting genes that share homology with ERG gene or ERG fusion genes. ABK17354-ABK22719 represent nucleic acids, including antisense and enzymatic nucleic acid molecules which regulate expression of ERG, and related PCR primers of the invention

Sequence 17 BP; 7 A; 1 C; 9 G; 0 T; 0 U; 0 Other;

ö 0.8%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 9.6e+02; tive 0; Mismatches 1; Indels Local Similarity 93.3 les 14; Conservative Query Match

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Gaps

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Human, hammerhead ribozyme; cytostatic; antitumour; antidiabetic; ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic; vulnerary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis; tumour angiogenesis; diabetic retinopathy; macular degeneration; neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris; angiofibroma of tuberous sclerosis; port-wine setain; wound healing; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss; Ogler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;
                                                                           Human ERG hammerhead ribozyme target sequence, Seq ID No 646.
                                                                                                                                                                                                                                                       16-MAY-2001; 2001WO-US015866.
                                                                                                                                                                                                                                                                           16-MAY-2000; 2000US-00572021.
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          999/c
ABK17999 standard; RNA; 17
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                                                       09-APR-2002
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                                                                                                                                                                            amberzyme.
                                    ABK17999;
RESULT 1454
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useful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome. Novel polynucleotide which down regulates expression of Ets-related useful for treating cancer, diabetic retinopathy, macular degenerati

Randi AM;

Mcswiggen JA, Mclaughlin F,

Claim 4; Page 70; 149pp; English

conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma, conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma, cumour angiogenesis, diabetic retinopathy, macular degeneration, neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge Weber syndrome, Nippel-Trenaunay-Weber syndrome, Osler-Weber-rendu sclerosis and wound healing. (I) is useful for treating a patient having a condition associated with the level of ERG, by contacting cells of the patient with (I) under conditions suitable for the treatment. Leukaemia or tumour conjunction with one or more of other therapies such as radiation or chemotherapy treatment. (I) is useful for reducing ERG activity in a cell, by contacting the cell with (I). (I) is useful for cleaving RNA of ERG gene, by contacting (I) with RNA, in the presence of advalent cation such as Mg2+. (I) is useful for diagnostic fool to examine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for ERG gene or ERG fixed or ERG fusion genes.

CHE TREE CHE CHE CHE STRA in a cell. (I) is useful for specifically caracting genes that share homology with ERG gene or ERG fusion genes.

CHE STRATASA-ABK22719 represent nucleic acids, including antisense and encymentation of the presence of encymentation of ERG and and encymentation The invention relates to a nucleic acid molecule (I) which down regulates related PCR primers of the invention

Sequence 17 BP; 2 A; 2 C; 10 G; 0 T; 3 U; 0 Other;

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                                                                                                                                                                                                       Human, hammerhead ribozyme, cytostatic; antitumour; antidiabetic; ophthalmological; antiatthritic; antipsoriatic; virucide; osteopathic; vulnerary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis; tumour angiogenesis; diabetic retinopathy; macular degeneration; neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris; angiofibroma of tuberous sclerosis; port-wine stain; wound healing; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; se; osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNAzyme; inozyme;
                        Gaps
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                                                                                                                                                                                     Human ERG hammerhead ribozyme target sequence, Seq ID No 834.
   Length 17;
                         IndelB
   0.8%; Score 13.4; DB 1;
93.3%; Pred. No. 9.6e+02;
iive 0; Mismatches 1;
                                                                                                                     ABK18187 standard; RNA; 17 BP
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                                            613 CCCACTCCAGCCTCT 627
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                                                                 17 cccacrccaccr 3
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             Best Local Similaria,
Matches 14; Conservative
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                amberzyme.
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The invention relates to a nucleic acid molecule (I) which down regulates expression of an Ets-related gene (ERG). (I) is useful for treating conditions selected from cancer, lymphoma, Ewing's sarcoma, malanoma, conditions selected from cancer, lymphoma, Ewing's sarcoma, malanoma, tumour angiogenesis, diabetic retinopathy, macular degeneration, tumour angiogenesis, diabetic retinopathy, macular degeneration, convocation, mayopic degeneration, arthritis, psoriasis, verruca vulgaris, angiofibroma of tuberous sclerosis, port wine stains, Sturge Weber syndrome, Rippel-Trenaunay-Weber syndrome, Oller-Weber-rendu Syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for treating a patient having a condition associated with the level of ERG, by contacting cells of the patient with (I) under conditions suitable for the treatment. Leukaemia or tumour angiogenesis is treated by administering (I) to the patient in angiogenesis is treated by administering (I) to the patient in conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or conjunction with one or more of other therapies such as radiation or cell, by contacting the cell with (I). (I) is useful for cleaving RNA of ERG gene, by contacting (I) with RNA, in the presence of a divalent carlon such as Mg2+. (I) is useful for diagnosis of conditions and diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically

Novel polynucleotide which down regulates expression of Ets-related genuseful for treating cancer, diabetic retinopathy, macular degeneration, arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.

Claim 4; Page 74; 149pp; English.

Randi AM;

Jarvis T, Von Carlowitz I, Mcswiggen JA, Mclaughlin F,

WPI; 2002-082995/11.

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                   ABKI7354-ABK22719 represent nucleic acids, including antisense and enzymatic nucleic acid molecules which regulate expression of ERG, and related PCR primers of the invention
  targeting genes that share homology with ERG gene or ERG fusion genes.
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                                                                                                                                       0.8%; Score 13.4; DB 1; Length 17;
86.7%; Pred. No. 9.6e+02;
tive 1; Mismatches 1; Indels
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                                                                                                 Sequence 17 BP; 3 A; 10 C; 3 G; 0 T; 1 U; 0 Other;
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                                                                                                                                                                                    13; Conservative
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ABK18234
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chemotherapy treatment. (I) is useful for reducing ERG activity in a cell, by contacting the cell with (I). (I) is useful for cleaving RNA of ERG gene, by contacting (I) with RNA, in the presence of a divalent cation such as Mg2+. (I) is useful for diagnosis of conditions and diseases related to the expression of ERG, and as diagnostic tool to examine genetic drift and mutations within diseased cells or to detect the presence of ERG RNA in a cell. (I) is useful for specifically targeting genes that share homology with ERG gene or ERG fusion genes. ABRIT3514 PEREZEIT represent nucleic acid molecules which regulate expression of ERG, and related PCR primers of the invention
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80.0%; Pred. No. 9.6e+02;
.ive 2; Mismatches 1; Indels
                                                                                                                                                                             Sequence 17 BP; 1 A; 10 C; 3 G; 0 T; 3 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human CLCAl gene enzymatic nucleic acid #2137.
                                                                                                                                                                                                                                                                                                                                                                   ABK57766 standard; RNA; 17 BP
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                                                                                                                                                                                                                        Similarity
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The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) genes by cleaving RNA derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, hence, are useful for treatment of a patient having a condition

Enzymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma.

WPI; 2002-217145/27.

Claim 4; Page 135; 152pp; English.

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associated with the level of CLCA1, where the invention further comprises
                      the use of one or more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of CLCAI RNA in a cell. This sequence represents an enzymatic nucleic acid molecule of the invention
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Seguence 17 BP; 3 A; 6 C; 5 G; 0 T; 3 U; 0 Other;

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Score 13.4; DB 1; Length 17; Pred. No. 9.6e+02; in Indels
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 0.8%;
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 Query Match 0.8
Best Local Similarity 93.3
Matches 14; Conservative
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Gaps

15 AGCCTCCCGAGGATG 1

ABK56032 standard; RNA; 17 BP RESULT 1458 ABK56032 

ABK56032;

Human CLCA1 gene enzymatic nucleic acid #403. 02-JUL-2002 (first entry)

Human, chloride channel calcium activated 1, CLCA1, se; antiasthmatic, antinflammatory; chronic obstructive pulmonary disease; COPD; asthma; chronic bronchitis; cystic fibrosis; obstructive bowel syndrome; oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic; acetylcysteine.

Homo sapiens.

WO200211674-A2.

14-FEB-2002

09-AUG-2001; 2001WO-US024970.

09-AUG-2000; 2000US-0224383P.

(RIBO-) RIBOZYME PHARM INC. (SYNT ) SYNTEX USA LLC. (THOM/) THOMPSON J.

Szymkowski DE; Thompson J, Mcswiggen J, Mckenzie T, Ayers D, Grupe A;

WPI; 2002-217145/27.

channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma. chloride Enzymatic polynucleotide that down regulates expression of

Claim 4; Page 60; 152pp; English.

The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) genes by cleaving RNA derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, hence, are useful for treatment of a patient having a condition associated with the level of CLCA1, where the invention further comprises the use of one or more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids,

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antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of CLCA1 RNA in a cell. This sequence represents an enzymatic nucleic acid molecule of the invention
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                                                                                            Query Match

0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
                                                                         Sequence 17 BP; 4 A; 5 C; 5 G; 0 T; 3 U; 0 Other
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                                                                                                                                               908 AGCCTCCAGAGGATG 922
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The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) genes by clearing RNA derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic ibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, hence, are useful for treatment of a patient having a condition casociated with the level of CLCA1, where the invention further comprises the use of one or more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, cartifacterials, vaccinations, acetylcysteine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect Claim 4; Page 135; 152pp; English.

Enzymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma.

Thompson J, Mcswiggen J, Mckenzie T, Ayers D, Szymkowski DE;

(THOM/) THOMPSON J.

WPI; 2002-217145/27

Grupe A;

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New nucleic acid sequences associated with tumor suppression, regression, apoptosis or virus resistance are useful to diagnose and treat viral disease, development of tumor cells and cell degeneration.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       with tumour suppression or regression, apoptosis or virus resistance. invention relates to these sequences or sequences having at least 80% identity to them, and polypeptides encoded by the sequences or polypeptides having 80% identity to the polypeptide sequences. The invention is used to diagnose or treat viral disease or disease characterized by development of tumour cells or cellular degeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents an isolated nucleic acid sequence associated
                                                                                                                               ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
tumour regression; apoptosis; virus resistance; diagnosis;
cellular degeneration.
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                                                                                       Human tumour suppressor sequence #1078.
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                                           (first entry)
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                                                                                                                                                                                                                     Homo sapiens,
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      ACC52311;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents an isolated nucleic acid sequence associated
                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ss; tumour suppressor; antitumour; cytostatic; tumour suppression; tumour regression; apoptosis; virus resistance; diagnosis; cellular degeneration.
the presence of CLCA1 RNA in a cell. This sequence represents an enzymatic nucleic acid molecule of the invention
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                                                               Sequence 17 BP; 3 A; 6 C; 5 G; 0 T; 3 U; 0 Other;
                                                                                                       0.8%; Score 13.4; DB 1;
93.3%; Pred. No. 9.6e+02;
tive 0; Mismatches 1;
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Best Local Similarity 93.3%,
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ACC52311/c
ID ACC5231
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regulates expression of a sequence encoding a subunit of nuclear factor kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme configuration. The earzymatic nucleic acid molecule is adapted to treat cancer and is useful for down-regulating REL-A activity in a cell, for treating a patient having a condition associated with the level of REL-A. (I) is useful for clearing RNA comprising a sequence of REL-A gene, in the presence of a divalent cation, especially MG^2+. The enzymatic and antisense nucleic acid molecules are useful for treating breast, lung, prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic, cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or multidrug resistant cancer. The method involves use of other drug therapies such as monoclonal antibodies, REL-A specific inhibitors or chemotherapy including paclitaxel, docetaxel, cisplatin, methoticxate, cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate, cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate, cyclophosphamide are also useful for treating inflammatory disease such as cheumatoid arthritis, restenosis, athama, Crohn's disease such as observed and molecules are also useful for treating inflammatory disease such as observed and molecules are also useful for treating inflammatory disease such as cheumatoid arthritis, restenosis, athama, Crohn's disease, diabetes, observed the content of the co
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allergic airway inflammation; inflammatory bowel disease; infection; ss.
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                                                                                                                                                                                                                                                                                 92US-00987132.
94US-00245466.
94US-00291932.
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                                                                                                             JS2002177568-A1
                                                        Homo sapiens
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18-MAY-1994;
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ö Gaps ö 0.8%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 9.6e+02; tive 0; Mismatches 1; Indels Local Similarity 93.3 Query Match Best Loca Matches

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704 GCCCACCCAGGCGGG 718
                          GCCCACCCAGGCUGG 17
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RESULT 1463

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ACA07733 standard; RNA; 17
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ACA07733/C
ID ACA077
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AC ACA077
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DT 03-JUN
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(first entry) 03-JUN-2003

G-cleaver, ambergyme, cancer; REL-A activity; breast cancer; human; obsophageal cancer; colorectal cancer; brain cancer; colorectal cancer; brain cancer; cervical cancer; prostate cancer; colorectal cancer; pancreatic cancer; cervical cancer; head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor; chemotherapy; paclitaxed; docetaxed; cisplatin; methotrexxate; cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexxate; gencitabine; radiation therapy; inflammatory disease; asthma; diabetes; rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia; gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis; transplant/graft rejection; reperfusion injury; glomerulonephritis; allergic airway inflammatory bowel disease; infection; se. Snzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme; NFKB sub-unit modulating zinzyme substrate #132.

Homo sapiens.

JS2002177568-A1.

28-NOV-2002

23-MAY-2001; 2001US-00864785

07-DEC-1992; 18-MAY-1994;

92US-00987132. 94US-00245466. 94US-00291932. 96US-00777916. 15-AUG-1994; 23-DEC-1996;

STINCHCOMB D T. MCSWIGGEN J. DRAPER K G. (STIN/) (DRAP/) MCSW/)

Draper KG; Mcswiggen J, Stinchcomb DT,

WPI; 2003-340953/32.

Novel enzymatic nucleic acid molecules which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B useful for treating cancer, inflammatory disorders and autoimmune diseases.

Claim 3; Page 39; 72pp; English.

The invention describes an enzymatic nucleic acid molecule (I) which down regulates expression of a sequence encoding a subunit of nuclear factor Kappa B (MPKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme configuration. The enzymatic nucleic acid molecule is adapted to treat cancer and is useful for down-regulating REL-A activity in a cell, for treating a patient having a condition associated with the level of REL-A. (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in the presence of a divalent cation, especially MG'2+. The enzymatic and antisense nucleic acid molecules are useful for treating breast, lung, prostate, colorectal, brain, oesophagaal, stomach, bladder, pancraatic, cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or multidrug resistant cancer. The method involves use of other drug therapies such as monoclonal antibodies, REL-A-specific inhibitors or chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate, cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate, gemcitabine or radiation therapy. The enzymatic and antisense nucleic acid molecules are also useful for treating inflammatory disease such as rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, gene therapy applications, ischemia/reperfusion injury a novel enzymatic sepsis, allergic airway inflammation, inflammatory bowel disease or infection. This sequence represents the substrate of a novel enzymat (CNS) and myocardial), glomerulonephritis, (central nervous system nucleic acid molecule

Sequence 17 BP; 3 A; 10 C; 2 G; 0 T; 2 U; 0 Other;

ö Gapa ö 0.8%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 9.6e+02; tive 0; Mismatches 1; Indels Local Similarity 93.3 Query Match Best Loca Matches

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The invention describes an enzymatic nucleic acid molecule (I) which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B (NFRA), where (I) is an inozyme, zinzwe, G-cleaver or amberzyme configuration. The enzymatic nucleic acid molecule is adapted to treat cancer and is useful for down-regulating REL-A activity in a cell, for treating a patient having a condition associated with the level of REL-A. (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in the presence of a divalent cation, especially Mg-2 +. The enzymatic and antisense nucleic acid molecules are useful for treating breast, lung, prostate, colorectal, brain, oseophageal, stomach, plandder, pancreatic, cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or multidrug resistant cancer. The method involves use of other drug therapies such as monoclonal antibodices, REL-A-specific inhibitors or chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate, cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate, cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate, cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,
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94US-00245466.
94US-00291932.
96US-00777916.
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1023 GGATGGGGCTGGGGT 1037
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15-AUG-1994;
23-DEC-1996;
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acid molecules are also useful for treating inflammatory disease such as rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclarosis, transplant/graft rejection, gene therapy applications, ischaemia/reperfusion injury (central nervous system (CNS) and myocardial), glomerulonephritis, sepsis, allergic airway inflammation, inflammatory bowel disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G-cleaver, ambergyme; cancer; REL-A activity; breast cancer; human; lung cancer; prostate cancer; colorectal cancer; brain cancer; human; lung cancer; prostate cancer; colorectal cancer; brain cancer; cervical cancer; seasonach cancer; badder cancer; melanoma; lymphoma; glioma; multidrug resistant cancer; REL-A-specific cancer; cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate; gencitabine; radiation therapy; inflammatory disease; aethma; diabetes; rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia; gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis; transplant/graft rejection; reperfusion injury; glomerulonephritis; allergic airway inflammatory bowel disease; infection; ss.
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                                                                                                                   infection. This sequence represents the substrate of a novel enzymatic
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Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1
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94US-00245466.
94US-00291932.
96US-00777916.
                                                                                                                                                                                                                                                                                                                                                                                                                            ACA09009 standard; RNA; 17 BP
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                                                                                                                                                                                                                                                                                            1022 GGGATGGGGCTGGGG 1036
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                                                                                                                                           nucleic acid molecule
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2002177568-A1.
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18-MAY-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACA09009;
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configuration. The enzymatic nucleic acid molecule is adapted to treat cancer and is useful for down-regulating REL-A activity in a cell, for treating a patient having a condition associated with the level of REL-A. (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in the presence of a divalent cation, especially Mg^2+. The enzymatic and antiense nucleic acid molecules are useful for treating breast, lung, prostate, colorectal, brain, oeophageal, stomach, bladder, pancreatic, cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or multidrug resistant cancer. The method involves use of other drug therapies such as monoclonal antibodies, REL-A-specific inhibitors or chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate, cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate, cyclophosphamide, and and asease, lupus, multiple sclerosis, transplant/graft rejection, gene therapy applications, ischaemid/reportuse, or processes, ranges, ranges, especial subtances, mydered, central nervous system (CNS) and myocardial), glomerulonephritis, sepace or radiation contents and second contents and seco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents the substrate of a novel enzymatic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid molecule
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0.8%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 9.6e+02; tive 0; Mismatches 1; Indels 705 CCCACCCAGGCGGG 719 Query Match
Best Local Similarity 93.33
Matches 14, Conservative ઠે

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Gaps ; 0

> ACA06875 standard; RNA; 17 BP 1 cccacccagecuese 15 ACA06875; RESULT 1466 ACA06875 셤

NFKB sub-unit modulating inozyme substrate #694. 03-JUN-2003 (first entry)

G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human; lung cancer; prostate cancer; colorectal cancer; brain cancer; oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer; cervical cancer; head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor; chemotherapy; pachitaxael; docetaxael; cisplatin; methotrexxate; cyclophosphamide; doxorubin; fluorouracil carboplatin; edatexate; gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes; rheumatoid arthritis; restenosis; Crohn's disease; obesity; lachaemia; gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis; transplant/graft rejection; reperfusion injury; glomerulonephritis; allergic airway inflammatory bowel disease; infection; ss. Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;

Homo sapiens

US2002177568-A1.

28-NOV-2002

23-MAY-2001; 2001US-00864785.

94US-00245466. 94US-00291932. 96US-00777916. 92US-00987132 07-DEC-1992; 18-MAY-1994; 15-AUG-1994; 23-DEC-1996;

(STIN/) STINCHCOMB D T. (MCSW/) MCSWIGGEN J.

regulates expression of a sequence encoding a solunit of nuclear factor kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme configuration. The enzymatic nucleic acid molecule is adapted to treat cancer and is useful for down-regulating REL-A activity in a cell, for treating a patient having a condition associated with the level of REL-A.

(I) is useful for cleaving RNA comprising a sequence of REL-A gene, in the presence of a divalent cation, especially MG2+. The enzymatic and antisense nucleic acid molecules are useful for treating breast, lung, prostate, colorectal, brain, ossophageal, stomach, bladder, pancreatic, cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or multidrug resistant cancer. The method involves use of other drug therapies such as monoclonal antibodies, REL-A-specific inhibitors or chemotherapy including paciltaxel, docetaxel, cisplatin, methotrexate, cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate, cyclophosphamide, and universate, content and enthritis, restenosis, asthma, Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, gene therapy applications, inflammatory bowel disease or multiple sclerosis, transplant central nervous system (CNS) and myocardial) plomerulonephritis, epsis, allergic airway inflammation, inflammatory bowel disease or multiple sclerosis, and not an action of a n Novel enzymatic nucleic acid molecules which down regulates expression of invention describes an enzymatic nucleic acid molecule (I) which down Gape a sequence encoding a subunit of nuclear factor kappa B useful for treating cancer, inflammatory disorders and autoimmune diseases. ö 0.8%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 9.6e+02; tive 0; Mismatches 1; Indels Sequence 17 BP; 8 A; 3 C; 3 G; 0 T; 3 U; 0 Other; Draper KG; Claim 3; Page 37; 72pp; English. Stinchcomb DT, Mcswiggen J, 14; Conservative nucleic acid molecule VPI; 2003-340953/32. (DRAP/) DRAPER K G. Query Match Best Local Similarity Matches 

1636 CTTTGATTGATCACT 1650 16 crirgariericaci 2 ઠે 셤

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RESULT 1467

ACA07620 standard; RNA; 17 BP. 03-JUN-2003 (first entry) ACA07620; ACA07620 

NFKB sub-unit modulating zinzyme substrate #19.

rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia; gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis; transplant/graft rejection; reperfusion injury; glomerulonephritis; allergic airway inflammation; inflammatory bowel disease; infection; ss. Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme; G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human; lung cancer; prostate cancer; colorectal cancer; brain cancer; cespobageal cancer; stomach cancer; bladder cancer; pancreatic cancer; ecvical cancer; stomach cancer; ovarian cancer; melanoma; lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor; chemotherapy; paclitaxel; doctaxel; doctaxel; cisplatin; methotrexate; cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate; gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;

Homo sapiens

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Novel enzymatic nucleic acid molecules which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B useful for treating cancer, inflammatory disorders and autoimmune diseases.
                                                                                                                                                         Draper KG;
Mon Aug 16 16:46:36 2004
                                                                                                                                                                                                                Claim 3; Page 38; 72pp; English
                                                                                               94US-00245466.
94US-00291932.
96US-00777916.
                                                                                                                                                        Stinchcomb DT, Mcswiggen J,
                                                                          23-MAY-2001; 2001US-00864785.
                                                                                       92US-00987132
                                                                                                                           (STIN/) STINCHCOMB D T.
                                                                                                                                          DRAPER K G.
                                                                                                                                                                      WPI; 2003-340953/32.
                                                                                                                                    MCSWIGGEN
                                             US2002177568-A1
                                                                                       07-DEC-1992;
                                                                                                18-MAY-1994;
15-AUG-1994;
                                                                                                              23-DEC-1996;
                                                           28-NOV-2002
                                                                                                                                   (MCSW/)
(DRAP/)
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The invention describes an enzymatic nucleic acid molecule (I) which down regulates expression of a sequence encoding a subunit of nuclear factor sequlates expression of a sequence encoding a subunit of nuclear factor of kappa B (NFKB), where (I) is an inozyme, Zinzyme, G-cleaver or amberzyme configuration. The enzymatic nucleic acid molecule is adapted to treat cancer and is useful for down-regulating REL-A activity in a cell, for treating a patient having a condition associated with the level of REL-A. (I) is useful for cleaving RNA comprising a sequence of REL-A gane, in the presence of a divalent cation, especially MG^2+. The enzymatic and antisense nucleic acid molecules are useful for treating breast, lung, corrical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or multidrug resistant cancer. The method involves use of other drug cervicals as monoclonal antibodies, REL-A-specific inhibitors or chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate, cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate, colornation therapy. The enzymatic and antisense nucleic acid molecules are also useful for treating inflammatory disease such as content and antisense nucleic acid molecules are also useful for treating inflammatory diseases such as content and antisense nucleic acid molecules are also useful for treating inflammatory disease such as rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, gene therapy applications, ischaemia, repertication injury (central nervous system (CNS) and myocardial), glomerulonephitis, sepsis, allergic airway inflammation, inflammatory bowel disease or This sequence represents the substrate of a novel enzymatic nucleic acid molecule

Sequence 17 BP; 4 A; 4 C; 7 G; 0 T; 2 U; 0 Other;

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0.8%; Score 13.4; DB 1; Length 17; 00.0%; Pred. No. 9.6e+02; ve 2; Mismatches 1; Indels
Query Matcn
Best Local Similarity 80.0%; Pre
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Gaps

1445 GTTACAAGTGCGAGG 1459 GCUACAAGUGCGAGG 16

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ACA07621 standard; RNA; 17 BP 

ACA07621;

NFKB sub-unit modulating zinzyme substrate #20.

03-JUN-2003 (first entry)

Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;

G-cleaver, amberzyme, cancer, REL-A activity; breast cancer; human; lung cancer; prostate cancer; colorectal cancer; brain cancer; coseophageal cancer; scancer, blancer; plancarer; pancreatic cancer; cervical cancer; sead and neck cancer; ovarian cancer; melanoma; lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor; chemocherapy; paclitaxel; docetaxel; cisplatin; methotrexate; cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate; gencitabine; radiation therapy; inflammatory disease; athma; diabetes; rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia; gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis; transplant/graft rejection; reperfusion injury; glomerulonephritis; allergic airway inflammation; inflammatory bowel disease; infection; ss.

Homo sapiens.

US2002177568-A1.

28-NOV-2002.

23-MAY-2001; 2001US-00864785.

94US-00245466. 94US-00291932. 96US-00777916. 92US-00987132. 07-DEC-1992; 18-MAY-1994; 15-AUG-1994

23-DEC-1996;

STINCHCOMB D T. MCSWIGGEN J. DRAPER K G. STIN/) (DRAP/) MCSW/)

Stinchcomb DT, Mcswiggen J, Draper KG;

WPI; 2003-340953/32.

Novel enzymatic nucleic acid molecules which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B useful for treating cancer, inflammatory disorders and autoimmune diseases.

Claim 3; Page 38; 72pp; English.

The invention describes an enzymatic nucleic acid molecule (I) which down regulates expression of a sequence encoding a subunit of nuclear factor regulates expression of a sequence encoding a subunit of nuclear factor regulates expression of a sequence configuration. The enzymatic nucleic acid molecule is adapted to treat configuration. The enzymatic nucleic acid molecule is adapted to treat cancer and is useful for down-regulating REL-A activity in a cell, for treating a patient having a condition associated with the level of REL-A. (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in the presence of a divalent cation, especially Mg^2+. The enzymatic and antisense nucleic acid molecules are useful for treating breast, lung, prostate, colorectal, brain, oesophageal, stomach, bladder, panoreatic, cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or multidrug resistant cancer. The method involves use of other drug therapies such as monoclonal antibodies, REL-A-specific inhibitors or chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate, cyclophosphamich, docetaxel, cisplatin, methotrexate, cyclophosphamich, docetaxel, cisplatin, methotrexate, cyclophosphamich, docetaxel, cisplatin, edatrexate, cyclophosphamich docetaxel, asthma, crohn's disease such as acid molecules are also useful for treating inflammatory disease such as relection, gene therapy applications, ischaemia/reperfusion injury (central nervous system (CNS) and myocardial), glomerulonephritis, cepsis, allergic airway inflammation, inflammatory bowel disease or inflection, englated represents the substrate of a novel enzymatic nucleic acid molecule 

Sequence 17 BP; 4 A; 4 C; 7 G; 0 T; 2 U; 0 Other;

Gaps ö Query Match

0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 9.6e+02;
Matches 12; Conservative 2; Mismatches 1; Indels

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1447 TACAAGTGCGAGGAG 1461

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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                             )5-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADB02200;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteins and their coding sequences: MD24, MD24, MD27, MD212. MD23 is encoded at chromosome 7921.1, MD24 is encoded at chromosome 6921.3-22.2, MD27 is encoded at chromosome 1691.0 in the foremasome for in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MD23, MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic acused by altered expression of MD23, MD24, MD27, or MD212. The nucleic acide can also be used as probes to detect and characterize gross alterations in MD23, MD27, or MD212 genetic locus. The probes are
                                                                                                                                                                                                                                                                                                                   Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger proctein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
developmental disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful in constructing microarrays for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as vaccines. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                     Human MDZ3 scanning oligonuclectide SEQ ID 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 8; SEQ ID NO 1077; 103pp; English.
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                                                                                                                    ADB00091 standard; DNA; 17 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gu Y, Nguyen C;
2 UACAAGUGCGAGGGG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-NOV-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            852 TGGCCCTGCAGGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP1281758-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shannon M,
                                                                                                                                                                     ADB00091;
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The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is concoded at chromosome 7q22.1, MD24 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome cor in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MD23. MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic acids and also be used as probes to detect and characterize gross alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are useful in constructing microarrays for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as cuccines. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                               Cytostatic; immunostimulant; gene therapy; vaccine; human; zinc finger protein; MDZ3; MDZ4; MDZ12; chromosome 7q22.1; chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer; developmental disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence 17 BP; 8 A; 0 C; 9 G; 0 T; 0 U; 0 Other;
                                                                     Human MDZ4 scanning oligonucleotide SEQ ID 3187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human MDZ4 scanning oligonucleotide SEQ ID 3186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 8; SEQ ID NO 3187; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MDZ4, MDZ7 or MDZ12, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-AUG-2001; 2001US-00922181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADB02200 standard; DNA; 17 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUL-2002; 2002EP-00016874.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 AGGAGGAAGAGGAGG 16
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gu Y, Nguyen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-423107/40
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A CARCING AS TO

ADB02201

developmental disorder;

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The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MDZ3, MDZ4, MDZ12, MDZ12. MDZ3 is cancoded at chromosome 7422.1, MDZ4 is encoded at chromosome 6921.3-22.2, MDZ7 is encoded at chromosome 6921.3-22.2, MDZ7 is encoded at chromosome 6921.3-22.2, MDZ7 is encoded at chromosome 1601.2 and MDZ12 is encoded at chromosome second in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic acids and proteins are also useful for diagnosing or monitoring a disease caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic acids can also be used as probes to detect and characterize gross alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are useful in constructing microarrays for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as proteins are useful as therapeutic agents for gene therapy or as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytostatic; immunostimulant; gene therapy; vaccine; human; zinc finger protein; MDZ3; MDZ4; MDZ1; hDZ12; chromosome 7q22.1; chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer; developmental disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7 or MDZ12, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.8%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 9.6e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17 BP; 8 A; 0 C; 9 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human MDZ3 scanning oligonucleotide SEQ ID 1078.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 8; SEQ ID NO 3186; 103pp; English.
                                                                                                                                                                                                                                                                                    30-JUL-2002; 2002EP-00016874
                                                                                                                                                                                                                                                                                                                                                           02-AUG-2001; 2001US-00922181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gu Y, Nguyen C;
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les 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-423107/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                 (AEOM-) AEOMICA INC
                                                                      Homo sapiens
                                                                                                                                             EP1281758-A2
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                                                                                                                                                                                                                05-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADB00092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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AC ADB00093
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XY ZO-NOV-:
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XX Cytosta
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KW Chomos
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The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2, MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome 15p2.1.2 and MDZ12 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome cor in manufacturing a medicament for treating or preventing a disorder casociated with decreased or increased expression or activity of MDZ3. MDZ4, MDZ7, or MDZ12. The nucleic caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic acids and lso be used as probes to detect and characterize gross alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are useful in constructing microarrays for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as the present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytostatic; immunostimulant; gene therapy; vaccine; human; zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7g22.1; chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15g26.1; cancer; developmental disorder; ss.
                                                                                                                                                                                    New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.8%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 9.6e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17 BP; 2 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human MDZ7 scanning oligonucleotide SEQ ID 5253.
                                                                                                                                                                                                                                                                                       Example 8; SEQ ID NO 1078; 103pp; English.
                                                                                                                                                                                                                                                MDZ4, MDZ7 or MDZ12, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADB04267 standard; DNA; 17 BP
30-JUL-2002; 2002EP-00016874.
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                                     02-AUG-2001; 2001US-00922181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  852 TGGCCCTGCAGGAAG 866
                                                                                                             Shannon M, Gu Y, Nguyen C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shannon M, Gu Y, Nguyen C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 TGGCCCTGCAGGCAG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-NOV-2003 (first entry)
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Matches 14; Conservative
                                                                                                                                                  WPI; 2003-423107/40.
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                                                                         (AEOM-) AEOMICA INC
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The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MD23, MD24, MD27, MD21, MD23 is encoded at chromosome 7022.1, MD24 is encoded at chromosome 7022.1, MD24 is encoded at chromosome 6p21.3-22.2, MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome 16p21.3-20.2, MD27 is encoded at chromosome 16p21.3-20.2, MD24, MD27, MD24, MD27, and MD212 sequences are useful in therapy, or in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MD23, MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic caused by altered expression of MD24, MD27, or MD212. The nucleic acids can also be used as probes to detect and characterize gross acids can also be used as probes to detect and characterize gross are useful in constructing microarrays for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as proteins are useful as therapeutic agents for gene therapy or as vaccines. The present sequence was used to illustrate the invention.

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                                                                                                                                               The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is encoded at chromosome [722.1, MD24] is encoded at chromosome [513.13-22.2, MD27 is encoded at chromosome 16p1.2 and MD212 is encoded at chromosome 16p1.2 or meanistic training a medicament for treating or preventing adjicting or in manufacturing a medicament for treating or preventing adjicting associated with decreased or increased expression or activity of MD23, MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic acids can also be used as probes to detect and characterize gross alterations in MD23, MD27, or MD212. The probes are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytostatic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MDZ3; MDZ4; MDZ12; chromosome 7q22.1;
chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
                                                                                                                                                                                                                                                                                                                                                                 useful in constructing microarrays for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as vaccines. The present sequence was used to illustrate the invention.
                              New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3, MDZ4, MDZ7 or MDZ12, e.g. cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.8%; Score 13.4; DB 1; Length 17; 33.3%; Pred. No. 9.6e+02; ved. No. 9.6e+02; ved. 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17 BP; 1 A; 1 C; 1 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human MDZ4 scanning oligonucleotide SEQ ID 3188.
                                                                                                                   Example 8; SEQ ID NO 5253; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1736 AAAAAAAAAAAA 1750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADB02202 standard; DNA; 17 BP
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WPI; 2003-423107/40.
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Matches
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0.8%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 9.6e+02; ative 0; Mismatches 1; Indele

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14; Conservative

Best Local Similarity

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Query Match

ABZ59906 standard; RNA; 17 BP

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RESULT 14 ABZ59906/

Sequence 17 BP; 8 A; 0 C; 9 G; 0 T; 0 U; 0 Other;

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The invention relates to a novel short interfering RNA (siRNA) nucleic acid molecule or an enzymatic nucleic acid molecule, that modulates expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras, human immunodeficiency virus (HIV) or a component of HIV. The nucleic acid molecule of the invention has cytostatic, anti-HIV, and anti-rheumatic activity. The nucleic acid molecules are useful for reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel short interfering RNA and enzymatic nucleic acid useful for treating cancer, modulates the expression of a nucleic acid encoding HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
                                                                                                               Human, ribozyme; short interfering RNA; siRNA; HER2; K-Ras; enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV; anti-rheumatic; cancer; AIDS; 88.
                                                                                Human K-Ras DNAzyme substrate #18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 58; Page 85; 185pp; English
                                                                                                                                                                                                                                                                                                                  29-MAY-2001; 2001US-0294140P.
06-JUN-2001; 2001US-0296249P.
10-SEP-2001; 2001US-0318471P.
                                                                                                                                                                                                                                                                                   29-MAY-2002; 2002WO-US016840.
                                                                                                                                                                                                                                                                                                                                                                                      (RIBO-) RIBOZYME PHARM INC.
                                                21-MAR-2003 (first entry)
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                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                   05-DEC-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                       Mcswiggen J;
               ABZ59906;
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New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MDZ3,

Example 8; SEQ ID NO 3188; 103pp; English.

MDZ4, MDZ7 or MDZ12, e.g. cancer

30-JUL-2002; 2002EP-00016874. 02-AUG-2001; 2001US-00922181

05-FEB-2003

developmental disorder; ss

Homo sapiens EP1281758-A2 Gu Y, Nguyen C;

Shannon M,

(AEOM-) AEOMICA INC

WPI; 2003-423107/40.

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also useful for treating breast, ovarian, colorectal, lung, prostate, baladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ6524, ABZ66530 - ABZ66536 represent substrate/target sequences for the human
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel short interfering RNA and enzymatic nucleic acid useful for treating cancer, modulates the expression of a nucleic acid encoding HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras; enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV; anti-rheumatic; cancer; AIDS; ss.
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Pred. No. 9.6e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                 0.8%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 9.6e+02; tive 0; Mismatches 1; Indel8
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                                                                                                                                                   Sequence 17 BP; 1 A; 4 C; 10 G; 0 T; 2 U; 0 Other;
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06-JUN-2001; 2001US-0296249P.
10-SEP-2001; 2001US-0318471P.
                                                                                                                                                                                                                                                                                                      529 GAGCCCCCCCCACCT 543
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Best Local Similarity 80.0
Matches 12; Conservative
                                                                                                                                                                                                                                                     Matches 14; Conservative
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                                                                                                                                                                                                                             Sest Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABZ61980;
                                                                                                                                                                                                    Query Match
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ABZ61980
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                                                                                                                                                                                                                                                                                                                                                                                               Human H-Ras DNAzyme target #335.
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                                               ABZ61544 standard; RNA; 17 BP
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06-JUN-2001; 2001US-0296249P.
10-SEP-2001; 2001US-0318471P.
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                                                                                                                                                                                                                                                                             (first entry)
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ABZ61544/
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The present invention relates to nucleic acid molecules which modulate the synthesis, expression and/or stability of Hepatitis C virus (HCV) or Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes, inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed are nucleic acid decoy molecules and aptamers that bind to HBV reverse transcriptase that bind to HBV reverse transcriptase primer sequences, as well as oligonucleotides that specifically bind the Enhancer I region of HBV DNA. The nucleic acids may be used to modulate the expression of HBV compounds and/or potential theraples directed against HBV, and compounds that modulate the expression and/or replication of HCV. The compounds and the invention are useful for the treatment of degenerative and disease states related to HBV infection, replication and gene expression such as cirrhosis, liver failure, and hepatocellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  na. The present sequence represents a substrate for one of the HCV or minus strand DNAzyme sequences disclosed in the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel compound useful for treating cirrhosis, liver failure, hepatocellular carcinoma, or condition associated with hepatitis C virus
                                                                                                      RNA stability; RNA expression; RNA synthesis; antisense; enzymetic nucleic acid; hammerhead riboxyme; MYAzyme; inozyme; decoy molecule; aptamer; tribozyme; decoy molecule; aptamer; thus reverse transcriptase; Enhancer I region; viral replication; degenerative; disease state; HBV infection; HCV infection; cirrhosis; liver fallure; hepatocellular carcinoma; hepatotropic; cytostatic; virucide; antiinflammatory; substrate; ss.
                                                                                       Nucleic acid molecule, Hepatitis C virus, HCV, Hepatitis B virus, HBV;
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                                                   HCV minus strand DNAzyme substrate sequence #2172.
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08-JUN-2001; 2001US-0296876P.
24-OCT-2001; 2001US-0337055P.
05-DEC-2001; 2001US-0337055P.
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                 (first entry)
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Roberts E;
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MCSWIGGEN J.
MORRISSEY D.
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                                                                                                                                                                                                                                                       Hepatitis C virus
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DRAPER K.
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                 30-SEP-2003
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(LEEP/)
(DRAP/)
(ROBE/)
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The present invention relates to murine oligonucleotides (ACC62754-ACC68806), which are associated with tumour suppression, tumour reversion, apoptosis and virus resistance. The oligonucleotides are useful as (1) as probes and primers for detecting, identifying, quantifying and/or amplifying nucleic acid, e.g. as one component of a gene chip; in vitro as (anti)sense reagents; and (2) for production of recombinant polypeptides. The oligonucleotides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterised by development of tumours or cell degeneration,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.
                                                                                                                                                                                                                                          Cytostatic, virucide; neuroprotective; nootropic; neuroleptic; murine; tumour suppression; tumour reversion; apoptosis; virus resistance; viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
                                                                                                                                                                                                           Murine oligonucleotide associated with tumour supression, SEQ ID 2499.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tuijnder M;
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                                                                                                             ACC65252 standard; DNA; 17 BP
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882 GCACGGCCCCAGGT 896
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                16 GCAGGGCCCCAGGT 2
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                                                                                                                                                                                                                                                                                            schi zophrenia ;
                                                                                                                                                                             01-JUL-2003
                                                                                                                                                                                                                                                                                                                          Mus musculus
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                                                                                                                                             ACC65252;
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Pavco P,

Mcswiggen J, Morrissey D,

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(first entry)

01-JUL-2003

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Gaps

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17-SEP-2002; 2002WO-IB004219.

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ACC68806), which are associated with tumour suppression, tumour reversion, apoptosis and virus resistance. The oligonucleotides are useful as (1) as probes and primers for detecting, identifying, quantifying and/or amplifying nucleic acid, e.g. as one component of a gene chip; in vitro as (anti) sense reagents; and (2) for production of recombinant polypeptides. The oligonucleotides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
primer; probe; tumour suppression; tumour reversion; apoptosis;
virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies
                              Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine; tumour suppression; tumour reversion; apoptosis; virus resistance; viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
Murine oligonucleotide associated with tumour supression, SEQ ID 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention relates to murine oligonucleotides (ACC62754-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             specifically cancer but also Alzheimer's disease and schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.8%; Score 13.4; DB 1; Length 17; 33.3%; Pred. No. 9.6e+02; ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour suppression/reversion associated nucleotide #2527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of tumours or cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 33; 738pp; French.
                                                                                                                                                                                                                                                                                                               Tuijnder M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              characterised by development
                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR ENGINES LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP
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                                                                                                                                                                                                                                              17-SEP-2001; 2001FR-00011979.
                                                                                                                                                                                                                L7-SEP-2002; 2002WO-IB004210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rcracaaaaaaaa 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               transfected cells.
                                                                                                                                                                                                                                                                                                               Telerman A, Amson R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
                                                                                                                                                                                                                                                                                                                                                WPI; 2003-333167/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                 WO2003025176-A2.
                                                                                   schizophrenia;
                                                                                                                Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-DEC-2003
04-DEC-2003
                                                                                                                                                                              27-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosis.
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fragments of at least 15 consecutive nucleotides of these nucleotides, a fragments of at least 15 consecutive nucleotides of these nucleotides, a sequence having at least 8% identity, after optimal alignment, with the nucleotides, or the complement, or corresponding RNA, of the nucleotides, or the complement, or corresponding RNA, of the nucleotides The nucleotides are used as probes or primers for detecting, identifying, quantifying and/or amplifying nucleic acids, as in vitro sense and antisense sequences, of nucleotides involved in tumour suppression or reversion, apoptosis and or viral resistance, to produce recombinant polypeptides, and to preper transgenic animals, as experimental models. The nucleotides (also vectors containing them and cells containing the vectors), the encoded polypeptides and antibodies of viral infections or diseases characterized by development of tumours or cell degeneration (e.g. Alzheimer's disease or schizophrenia).

Analysis of the expression of the nucleotides can be used for diagnosis and/or prognosis of these diseases. The nucleotides and polypeptides can also be used to screen for their specific interactive molecules, the containing the polypeptides and also be used to screen for their specific interactive molecules.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss; primer; probe; tumour suppression; tumour reversion; apoptosis; virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
                                                                                                                                                                              New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related polypeptide and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumour suppression/reversion associated nucleotide #1213.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17 BP; 1 A; 9 C; 1 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                               Disclosure; Page 327; 771pp; French.
                                                                                                             Tuijnder M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADB40890 standard; DNA; 17 BP
                                                                       (MOLE-) MOLECULAR ENGINES LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression of the nucleotides
                                 17-SEP-2001; 2001FR-00011981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-SEP-2002; 2002WO-IB004219.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.3%;
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Matches 14; Conservative
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                                                                                                             Felerman A, Amson R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
                                                                                                                                                  WPI; 2003-441574/41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-2003
04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAY-2003.
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Gaps

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degeneration

17-SEP-2001; 2001FR-00011981.

WO2003040369-A2

15-MAY-2003.

Homo sapiens

Novel isolated nucleic acid molecule comprising single nucleotide polymorphism associated with fish, useful for forming PCR primers which are used for detecting single nucleotide polymorphisms in fish nucleic

Slettan A, Hoyum M, Lingaas

Lie O,

WPI; 2003-627388/59.

comprising

The present invention describes an isolated nucleic acid (I)

Claim 18; SEQ ID NO 507; 233pp; English.

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fragments of at least 15 consecutive nucleotides of these nucleotides, a gequence having at least 18 consecutive nucleotides of these nucleotides, a sequence having at least 80% identity, after optimal alignment, with the nucleotides, a sequence that hybridizes under stringent conditions with the nucleotides, or the complement, or corresponding RNA, of the cuncleotides, The nucleotides are used as probes or primers for detecting, identifying, quantifying and/or amplifying nucleic acids, as in vitro sense and antisense sequences, of nucleotides involved in tumour cupression or reversion, apoptosis and or viral resistance, to produce recombinant polypeptides, and to prepare transgenic animals, as experimental models. The nucleotides (also vectors containing them and calls containing the vectors), the encoded polypeptides and antibodies (Ab) against the polypeptide are useful for prevention and/or treatment of viral infections or diseases characterized by development of tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                 detecting,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or cell degeneration (e.g. Alzheimer's disease or schizophrenia). Analysis of the expression of the nucleotides can be used for diagnosis and/or prognosis of these diseases. The nucleotides and polypeptides can also be used to screen for their specific interactive molecules, potentially useful for treating diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single nucleotide polymorphism; SNP; fish; Salmo salar;
Orechromis niloticus; Atlantic halibut; microsatellite; cod;
polymorphic site; seabass; salmonidae; Tilapia; rainbow trout; halibut;
                                                                                                                              New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related polypeptide and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.8%; Score 13.4; DB 1; Length 17; Best Local Similarity 93.3%; Pred. No. 9.6e+02; Matches 14; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 1 A; 1 C; 1 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                      Disclosure, Page 173; 771pp; French
                                                          Tuijnder M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression of the nucleotides.
                  (MOLE-) MOLECULAR ENGINES LAB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADD19872 standard; DNA; 17 BP
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                                                          relerman A, Amson R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        detection; primer; ss
                                                                                                  WPI; 2003-441574/41
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control present invention describes an isolated an indicated acid of salmo salar SNPs, Oreochromis niloticus SNPs or Atlantic halibut SNPs; and (ii) an uncleic acid having nucleotide sequence that hybridises to conditions.

Also described: (1) an isolated oligonucleotide (II) comprising at least on its complement under highly stringent hybridisation conditions.

Also described: (1) an isolated oligonucleotide (II) comprising at least or inloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, code polymorphic sites and seabass polymorphic sites, or their complement; (2) applier pair (III) suitable for use in PCR, comprising two (II) capable of amplifying a nucleotide sequence chosen from S. salar SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, Code injoicius SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, code conjuicity of tish sample comprising providing a parent genotype comprising a collection of candidate parent genotype of candidate parent genotype to the parentage genotype database, where a match between conjuicate parent genotype to the parentage genotype database, where a match between the sample genotype and one of the candidate parent genotype in the sample conjuicate parent genotype to the parentage genotype database, where a match between the sample such as family salmonidae, S. salar, Tilapa, O. niloticus for the sample such as family salmonidae, S. salar, Tilapa, O. niloticus at sample, which is detecting nucleic acid molecule comprising contacting the sample containing nucleic acid molecule comprising contacting the sample containing nucleic acid molecule comprising contacting the sample contacting the sample, comprising contacting the sample contacting the sample contacting the sample contacting the sample contacting nucleic acid molecule confidence in a sample, comprising contacting nucleic acid molecule comprising contacting nucleic acid molecule comprising contacting nucleic acid molecule comprising contac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.8%; Score 13.4; DB 1; Length 17; 93.3%; Pred. No. 9.6e+02; tive 0; Mismatches 1; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human TRIP6 antisense oligonucleotide ISIS #198770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17 BP; 1 A; 3 C; 8 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1024 GATGGGGCTGGGGTT 1038
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18-JAN-2002; 2002US-0349950P. 16-AUG-2002; 2002US-0404200P. 17-JAN-2003; 2003WO-IB000112

#02003060160-A2 24-JUL-2003 (GENO-) GENOMAR ASA

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to antisense compounds targetted to a nucleic acid encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and zyxin-related protein-1 (SAP-1). TRIP6 DNA is located on chromosome 7q22. Antisense compounds of the invention are useful for modulating the expression of TRIP6 and for treating diseases or conditions associated with the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for disgnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as tesearch reagents and kits and in distinguishing between functions of various members of a biological pathway. The are also useful in antisense therapy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                             New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.
                                                             /note= "Phosphorothioate backbone; All cytidine residues are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Differential display of mRNA; reverse transcription; DDRT-PCR; human;
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                                                                                                                                                        /mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides
                                                                                                            /mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.8%; Score 13.4; DB 1; Length 20; 93.3%; Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                    cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                        Example 15; Page 76; 111pp; English
                                                      /mod_base= OTHER
                                                                                                                                                       base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        986 TTGGCCAGTGTGT 1000
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                                                                                                                                                                                                                                                         08-NOV-2001; 2001US-00008789.
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                                                                                                 *tag= b
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/*tag= c
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                                          /*tag=
                                                                                                                                                                                                                                                                               (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                    Bennett CF, Dobie K;
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                    Key
modified_base
                                                                                      modified base
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                                                                                                                                                                                                              15-MAY-2003.
 Synthetic
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AAT18608/
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chondrocyte; gene specific; primer; probe; isolation; interleukin-1beta;
IL-1beta; diagnosis; connective tissue disease; oseteoarthritis;
rheumatoid arthritis; polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stimulus-regulated nucleic acid; sequence profile; nucleic acid level; differentially expressed nucleic acid; disease state; cancer; autoimmune disease; infectious disease; aging; developmental disorder; proliferative disorder; neurological disorder; toxicity; primer; treatment resistance; differential expression; drug discovery; growth factor; epidermal growth factor; radiation; stress; pathogen; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        using osteopontin, calnexin, TSG-6 gene prod., genes encoding them or antibodies to them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anchored oligo(dT) primer T13V used for modified differential display.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 14 BP; 0 A; 0 C; 0 G; 13 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example; Page 15; 31pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                   94EP-00115751.
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les 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bartnik E, Margerie D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-181045/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FARH.) HOECHST AG
                                                                                                                                                                                                                                                                                                                                               02-OCT-1995;
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display, in the method of the invention. The specification describes a method for measuring the level of two or more nucleic acid molecules in a method for measuring the level of two or more nucleic acid molecules in a target. The method comprises contacting a probe with an arbitrarily or statistically sampled target and detecting the amount of specific binding of the target to the probe. The methods can be used to identify differentially expressed nucleic acid molecules associated with disease states, such as cancer, autoimmune disease, infectious disease, aging, developmental disorder, proliferative disorder or neurological disorder. Alternatively the methods can be used to assess the efficacy or toxicity of or a resistance to a treatment. Also the methods can be used to determine differential expression of nucleic acid molecules in response to a stimulus, e.g. a chemical, drug or growth factor (especially epideranial growth factor), radiation, stress or a pathogen. The methods can also be used to determine co-regulated genes that can be potential targets for drug discovery
                                                                                                                                                                                                                                                                                                                       Measuring expression of low abundance reduced complexity target nucleic acid molecules.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.8%; Score 13.2; DB 1; Length 14; 92.9%; Pred. No. 8.9e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14 BP; 0 A; 0 C; 0 G; 13 T; 0 U; 1 Other;
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                                                                                                                                                                                                    Trenkle T;
                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Page 91; 187pp; English
                                                                                                                                    CANCER CENT SIDNEY
   98US-0083331P.
98US-0098070P.
99US-0118624P.
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97US-0108152P.
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                                                                                                                                                                                                                                                                 WPI; 2000-086388/07
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les 13; Conserv
                                                                                                                                (KIMM-) KIMMEL
27-APR-1998;
27-AUG-1998;
04-FEB-1999;
                                                                                                                                                                                                 Mcclelland M,
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                 Sequential consensus region-directed amplification for sorting mixture of DNAs into 2 or more subsets or distinguishing gene expression patterns in 2 samples, useful for disease diagnosis and gene analysis.
                                                                                                                        The invention relates to a method of sequential consensus region-directed amplification for sorting a mixture of DNAs into 2 or more subsets or distinguishing gene expression patterns in 2 samples. The methods, kits and oligonucleotides are useful for sorting a mixture of DNAs into 2 or more subsets or distinguishing gene expression patterns in 2 samples e.g. for disease diagnosis and gene analysis. The present sequence is oligo dT PCR primer used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method of sequential consensus region-directed amplification for sorting a mixture of DNAs into 2 or more subsets or distinguishing gene expression patterns in 2 samples. The methods, kits and oligonucleotides are useful for sorting a mixture of DNAs into 2 or more subsets or distinguishing gene expression patterns in 2 samples e.g. for disease diagnosis and gene analysis. The present sequence is oligo dr PCR primer used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequential consensus region-directed amplification for sorting mixture of DNAs into 2 or more subsets or distinguishing gene expression patterns in 2 samples, useful for disease diagnosis and gene analysis.
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disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR,
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                                                                                        Example, Fig 1C, 19pp, English
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97US-0108152P
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hes 13; Conservative
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WPI; 2002-412824/44.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptides having at least two new nucleotides - useful as primers in RT-
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                                      Gaps
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0.8%; Score 13.2; DB 1; Length 14; 92.9%; Pred. No. 8.9e+02; tive 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                     RT-PCR primer of the invention SEQ ID 27.
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